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OM nucleic - nucleic search, using sw model
Run on: September 26, 2004, 09:37:58 ; Search time 18291 Seconds
(without alignments)
17478.444 Million cell updates/sec

Title: US-10-033-026-3
Perfect score: 7376
Sequence: 1 9cggcgccggtgcggcggt.....tgcttgagtgctacgtaccgc 7376

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rpd.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	7376	100.0	7376	6	AR198607	AR198607 Sequence
2	7342	99.5	7364	6	AR198608	AR198608 Sequence
3	7342	99.5	7364	6	AX3333697	AX3333697 Sequence
4	7342	99.5	7364	9	HUMCACHNT	M94172 Human N-typ
5	7316.4	99.2	7362	6	AR022379	AR022379 Sequence
6	7316.4	99.2	7362	6	AR063882	AR063882 Sequence
7	7316.4	99.2	7362	6	AR067882	AR067882 Sequence
8	7316.4	99.2	7362	6	AR105183	AR105183 Sequence
9	7316.4	99.2	7362	6	AR431823	AR431823 Sequence
10	7223.2	97.9	7266	6	AR118079	AR118079 Sequence
11	6958	94.3	7177	6	AR198609	AR198609 Sequence
12	6958	94.3	7177	9	HUMCACHNTA	M94173 Human N-typ
13	6932.4	94.0	7175	6	AR022380	AR022380 Sequence
14	6932.4	94.0	7175	6	AR063883	AR063883 Sequence
15	6932.4	94.0	7175	6	AR067883	AR067883 Sequence
16	6932.4	94.0	7175	6	AR105184	AR105184 Sequence
17	6932.4	94.0	7175	6	AR431824	AR431824 Sequence
18	5937	80.5	6232	6	A22938	A22938 H.sapiens m
19	5887.8	79.8	6232	6	AR150755	AR150755 Sequence
20	5717.4	77.5	7121	4	RAF13882	RAF13882 Bos tauru
21	5641	76.5	7713	4	RABBCBIII	D14157 Rabbit mRNA
22	5359.6	72.7	9695	10	AF055477	AF055477 Rattus no
23	5327.4	72.2	6984	10	AF042317	AF042317 Mus muscu
24	5289.8	71.7	7011	6	AR198610	AR198610 Sequence
25	5289.8	71.7	7011	10	RATRBI	M92905 Rat calcium
26	5049.2	68.5	7185	6	BD095100	BD095100 N-Type ca
27	5049.2	68.5	7185	10	MMU04999	U04999 Mus musculu
28	4865.4	66.0	5467	6	I12880	I12880 Sequence 12
29	3817.2	51.8	7925	5	AF173018	AF173018 Gallus ga
30	3797.2	51.5	7920	5	AF173019	AF173019 Gallus ga
31	3758.8	51.0	7892	5	AF173014	AF173014 Gallus ga
32	3738.8	50.7	7887	5	AF173015	AF173015 Gallus ga
33	3733.8	50.6	8000	5	AF173012	AF173012 Gallus ga
34	3713.8	50.3	7995	5	AF173013	AF173013 Gallus ga
35	3713.6	50.3	7967	5	AF173016	AF173016 Gallus ga
36	3693.6	50.1	7962	5	AF173017	AF173017 Gallus ga
37	3195.2	43.3	5438	6	AR150749	AR150749 Sequence
38	3194.2	43.3	5438	6	A22926	A22926 H.sapiens m
39	2833	38.4	6981	5	DYGCCALB	L12532 Discopryge o
40	2732.8	37.0	7786	5	AF461708	AF461708 Oncorhync
41	2731.2	37.0	7835	5	AY319304	AY319304 Oncorhync
42	2689.8	36.5	7819	5	AF461707	AF461707 Oncorhync
43	2582.6	35.0	6639	6	AX401910	AX401910 Sequence
44	2582.6	35.0	6639	10	RATBCCA1S	M64373 Rat calcium
45	2577.8	34.9	7236	10	AB066608	AB066608 Mus muscu

ALIGNMENTS

RESULT 1	AR198607	AR198607	7376 bp	DNA	linear	PAT 20-APR-2002
LOCUS	Sequence 3 from patent US 6353091.					
DEFINITION	Sequence 3 from patent US 6353091.					
ACCESSION	AR198607					
VERSION	AR198607.1	GI:20248456				
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 7376)					
AUTHORS	Lipscombe,D. and Schorge,S.					
TITLE	Human N-type calcium channel isoform					
JOURNAL	Patent: US 6353091-A 3 05-MAR-2002;					
FEATURES	Location/Qualifiers					

2041	Db		GGGACAGTTCAA	CTTCAGGATGAG	CTCCACAACCA	CTTCGACACCTTCCTCGCGC	2100	
2101	Qy		CATCCTCACTGTCTT	TCAGATCCCTGACGSGAGAG	AGCTGGAATG	CAGTGATGATCACGG	2160	
2101	Db		CATCCTCACTGTCTT	TCAGATCCCTGACGSGAGAG	AGCTGGAATG	CAGTGATGATCACGG	2160	
2161	Qy		GATCGAATTCGCAAG	CGCGGCTCAGCAAA	GCGATGTTCTCGT	CTCTTTTATCTTCAATGTGCTCT	2220	
2161	Db		GATCGAATTCGCAAG	CGCGGCTCAGCAAA	GCGATGTTCTCGT	CTCTTTTATCTTCAATGTGCTCT	2220	
2221	Qy		GACACTGTTTCGGA	AACCTACACTCTGCT	GAAATGCTTTCTGCG	CATCCTGCTGTGACACCT	2280	
2221	Db		GACACTGTTTCGGA	AACCTACACTCTGCT	GAAATGCTTTCTGCG	CATCCTGCTGTGACACCT	2280	
2281	Qy		GGCCAAACGCCCCA	GAGCTGACCAAGG	ATGAAGAGATG	GAAGAAGCAGCAATCAGAA	2340	
2281	Db		GGCCAAACGCCCCA	GAGCTGACCAAGG	ATGAAGAGATG	GAAGAAGCAGCAATCAGAA	2340	
2341	Qy		GCTTTGCTCTGCAA	AAGGCCAAGAGT	GGCTGAAGT	CAGCCCCCATGCTGCGCGACAT	2400	
2341	Db		GCTTTGCTCTGCAA	AAGGCCAAGAGT	GGCTGAAGT	CAGCCCCCATGCTGCGCGACAT	2400	
2401	Qy		CTCCATTCGCGCC	CAGGAGCAGAA	ACTCGGCCAAGG	CGCGCTCGGTGTGGAGCAGCGGGC	2460	
2401	Db		CTCCATTCGCGCC	CAGGAGCAGAA	ACTCGGCCAAGG	CGCGCTCGGTGTGGAGCAGCGGGC	2460	
2461	Qy		CAGCCAGCTACGG	CTGCAGAACCT	TCGGGCCAGT	CTGAGCGGATGGA	2520	
2461	Db		CAGCCAGCTACGG	CTGCAGAACCT	TCGGGCCAGT	CTGAGCGGATGGA	2520	
2521	Qy		CCCCGAGGAGCGG	CTGGCTTCGCCA	CTTACGCGCCAG	CTTCGGGCCGACATGAAGA	2580	
2521	Db		CCCCGAGGAGCGG	CTGGCTTCGCCA	CTTACGCGCCAG	CTTCGGGCCGACATGAAGA	2580	
2581	Qy		CCTCGA	CCGGCCGTGTGTGTG	AGCTGGGCCGGA	CGGGCGCGGGGGCCCGTGGAGG	2640	
2581	Db		CCTCGA	CCGGCCGTGTGTGTG	AGCTGGGCCGGA	CGGGCGCGGGGGCCCGTGGAGG	2640	
2641	Qy		CAAAAGCCGACCT	CAGGCTCGGAGG	CCCCCGAGGGCGT	GCACCTCCGCGCAGGCA	2700	
2641	Db		CAAAAGCCGACCT	CAGGCTCGGAGG	CCCCCGAGGGCGT	GCACCTCCGCGCAGGCA	2700	
2701	Qy		CCGGCA	CCGCGACAA	GGAACAAAGCCCGCGGGGGGA	CCAGAACCGAGCAGAGCGCCC	2760	
2701	Db		CCGGCA	CCGCGACAA	GGAACAAAGCCCGCGGGGGGA	CCAGAACCGAGCAGAGCGCCC	2760	
2761	Qy		GAAAGCGAGAG	CGGGAGCCCGGTG	CCCGGAAGAGCGGCGCGCGCGCA	CCGACGCCA	2820	
2761	Db		GAAAGCGAGAG	CGGGAGCCCGGTG	CCCGGAAGAGCGGCGCGCGCGCGCA	CCGACGCCA	2820	
2821	Qy		CACCAAGAGAG	CGGGAGCCCGGTG	CCCGGAAGAGCGGCGCGCGCGCGCA	CCGACGCCA	2880	
2821	Db		CACCAAGAGAG	CGGGAGCCCGGTG	CCCGGAAGAGCGGCGCGCGCGCGCGCA	CCGACGCCA	2880	
2881	Qy		CGAGGGCGCGCGG	CAACACCGCGCGGCT	CTCCCGAGAGAGCGGCGGAGCGGCGG	CGGAGCGGAGCC	2940	
2881	Db		CGAGGGCGCGCGG	CAACACCGCGCGGCT	CTCCCGAGAGAGCGGCGGAGCGGCGG	CGGAGCGGAGCC	2940	
2941	Qy		CCGA	CGCCACCGCGCA	CCGGCAACAGGAT	CCGAGCAAGAGTGC	CGCGCGCAAGGG	3000
2941	Db		CCGA	CGCCACCGCGCA	CCGGCAACAGGAT	CCGAGCAAGAGTGC	CGCGCGCAAGGG	3000
3001	Qy		CGAGGGCGCGCGG	CAACCGGGGGCCCCCGAG	CGGGCCCCCGGAGCGGAGCGG	CGGAGCGG	3060	
3001	Db		CGAGGGCGCGCGG	CAACCGGGGGCCCCCGAG	CGGGCCCCCGGAGCGGAGCGG	CGGAGCGG	3060	
3061	Qy		GGAGGAGCGCGG	CGCGGCAACCGGGCCCCCGG	CAAGCGCAGGCT	GTCTACAGAGGCTGT	3120	
3061	Db		GGAGGAGCGCGG	CGCGGCAACCGGGCCCCCGG	CAAGCGCAGGCT	GTCTACAGAGGCTGT	3120	
3121	Qy		GGAGAGGAGAG	CAACGGAGAGGAGG	CCCGAGAGAGGCT	CGAGATAGTGGAGCGGA	3180	

Db	3121	GGAGAAAGGAGACACGCGAAGAGGAGGCCACGGAGAGAGGAGCGCTGAGATAGTGGAAAGCCGA	3181
Qy	3181	CAAGGAAAAGGAGCTCCGGAAACACCAAGCCCCGGGAGGCCACACTGTGACCTCTGGAGACCAG	3241
Db	3181	CAAGGAAAAGGAGCTCCGGAAACACCAAGCCCCGGGAGGCCACACTGTGACCTCTGGAGACCAG	3241
Qy	3241	TGGGACTGTGACTGTGTGGGTCCCATGCAACACTGTGCCAGACACTGTCTCCAGAAGGTTGGA	3301
Db	3241	TGGGACTGTGACTGTGTGGGTCCCATGCAACACTGTGCCAGACACTGTCTCCAGAAGGTTGGA	3301
Qy	3301	GGAAACGACGAGAGATGACACAATCAGCGGAACGTCACCTCGCATGGCAGTCAGCCCCCC	3361
Db	3301	GGAAACGACGAGAGATGACACAATCAGCGGAACGTCACCTCGCATGGCAGTCAGCCCCCC	3361
Qy	3361	AGACCCGAAACACTATTGTGTACATATCCAGGTGATGCTGACGGGCCCTCTTGGGGAAGCCAC	3421
Db	3361	AGACCCGAAACACTATTGTGTACATATCCAGGTGATGCTGACGGGCCCTCTTGGGGAAGCCAC	3421
Qy	3421	GGTCGTTCCAGTGGTAACTGTGACCTTGGAAAGCCAAAGCAGAGAGGGGAAGAGAGGTTGGA	3481
Db	3421	GGTCGTTCCAGTGGTAACTGTGACCTTGGAAAGCCAAAGCAGAGAGGGGAAGAGAGGTTGGA	3481
Qy	3481	AGCGGATGACGTGATGAGGAGCGGCCCGCGCCCTATCGTCCCATACAGCTCCATGTTCTG	3541
Db	3481	AGCGGATGACGTGATGAGGAGCGGCCCGCGCCCTATCGTCCCATACAGCTCCATGTTCTG	3541
Qy	3541	TTTAAAGCCCCAACCAACCTGTCTCGCCGCTTCTGCGCATACATCGTGACCATGAGGTACTT	3601
Db	3541	TTTAAAGCCCCAACCAACCTGTCTCGCCGCTTCTGCGCATACATCGTGACCATGAGGTACTT	3601
Qy	3601	CGAGGTGGTCAATTCTCGTGTGTCATCGGCTTTGAGCAGCATCGCCCTGCTGTGAGGACCC	3661
Db	3601	CGAGGTGGTCAATTCTCGTGTGTCATCGGCTTTGAGCAGCATCGCCCTGCTGTGAGGACCC	3661
Qy	3661	AGTCGCACACAGCTCGCCCAAGGACACGCTCTGAATACCTGGATTACATTTTTCACCTGG	3721
Db	3661	AGTCGCACACAGCTCGCCCAAGGACACGCTCTGAATACCTGGATTACATTTTTCACCTGG	3721
Qy	3721	TGCTTTTACCTTTGAGATGGTGATAAAGATGATCGACTTGGGACTGCTGCTTTCAACCTGG	3781
Db	3721	TGCTTTTACCTTTGAGATGGTGATAAAGATGATCGACTTGGGACTGCTGCTTTCAACCTGG	3781
Qy	3781	AGCCTATTTCCGGGACTTGTGGAAACAATTCTGGAACTTCAATTGTGTGCTAGTGGCGCCCTGGT	3841
Db	3781	AGCCTATTTCCGGGACTTGTGGAAACAATTCTGGAACTTCAATTGTGTGCTAGTGGCGCCCTGGT	3841
Qy	3841	GGCGTTTTCCTTCTCGAGCTTGTGGAGGATCCAAAGGGGAAACACATCAATACCATCAA	3901
Db	3841	GGCGTTTTCCTTCTCGAGCTTGTGGAGGATCCAAAGGGGAAACACATCAATACCATCAA	3901
Qy	3901	GTCTCTCAGAGTCCCTCGTCTCGCGGCCCTCAAGACCATCAAAAGGCTGCCCAAGCT	3961
Db	3901	GTCTCTCAGAGTCCCTCGTCTCGCGGCCCTCAAGACCATCAAAAGGCTGCCCAAGCT	3961
Qy	3961	CAAGGCTGTGTTTGAAGTGTGTGGTGAATCCCTTGAAGAAATGCTCTCAACATCTTTGATTGT	4021
Db	3961	CAAGGCTGTGTTTGAAGTGTGTGGTGAATCCCTTGAAGAAATGCTCTCAACATCTTTGATTGT	4021
Qy	4021	CTACATGCTCTTCAATGTTTCATATTTGCGGTTCATTCGGCTGCAGCTCTTCAAGGGGAATT	4081
Db	4021	CTACATGCTCTTCAATGTTTCATATTTGCGGTTCATTCGGCTGCAGCTCTTCAAGGGGAATT	4081
Qy	4081	TTTTCTACTGCACAGATCAATCCAAAGAGCTGGAGAGGATCTGCAAGGGTCAGTATTTTGGAA	4141
Db	4081	TTTTCTACTGCACAGATCAATCCAAAGAGCTGGAGAGGATCTGCAAGGGTCAGTATTTTGGAA	4141
Qy	4141	TTATGAGAAGGAGGAACTGGAAGCTCAGCCCGACGTGGAAGAAATACGACTTTTCACTA	4201
Db	4141	TTATGAGAAGGAGGAACTGGAAGCTCAGCCCGACGTGGAAGAAATACGACTTTTCACTA	4201
Qy	4201	CGACAATGTGCTCTGGGCTCTGTGACGCTGTTTCAAGTGTCCACGGGAGAGGCTGGCC	4261
Db	4201	CGACAATGTGCTCTGGGCTCTGTGACGCTGTTTCAAGTGTCCACGGGAGAGGCTGGCC	4261

QY 4261 CATGGTGCCTGAAACACTCCGTGGATGCCACCTATGAGGAGCAGGGTCCAAGCCCTGGGTA 4320
DB CATGGTGCCTGAAACACTCCGTGGATGCCACCTATGAGGAGCAGGGTCCAAGCCCTGGGTA 4320
QY 4321 CGGCATGGAGCTGCTCCATCTTCTACGTGCTACTTTGTGGTCTTTCCTCTCTTCTTGGT 4380
DB CGGCATGGAGCTGCTCCATCTTCTACGTGCTACTTTGTGGTCTTTCCTCTCTTCTTGGT 4380
QY 4381 CAACATCTTTTGGGCTTTGATCATCATCACCTTCCAGGAGCAGGGGCAAGAGTGTATGTC 4440
DB CAACATCTTTTGGGCTTTGATCATCATCACCTTCCAGGAGCAGGGGCAAGAGTGTATGTC 4440
QY 4441 TGAATGCAGCCTGGAGAGAAACGAGAGGCTTGCATTGACTTTCGCGCATCAGCGCCAAACC 4500
DB TGAATGCAGCCTGGAGAGAAACGAGAGGCTTGCATTGACTTTCGCGCATCAGCGCCAAACC 4500
QY 4501 CCTGCACCGGTACATGCCCCCAAAACCGGCAGTCTTCCAGTATATAGAGTGTGACATTTGT 4560
DB CCTGCACCGGTACATGCCCCCAAAACCGGCAGTCTTCCAGTATATAGAGTGTGACATTTGT 4560
QY 4561 GGTCTCCCCGCCCTTTGAATACTTTCATATGCCCATGATAGCCCTCAACACTGTGGTGTCT 4620
DB GGTCTCCCCGCCCTTTGAATACTTTCATATGCCCATGATAGCCCTCAACACTGTGGTGTCT 4620
QY 4621 GATGATGAAGTCTATGATGCAACCTATGAGTACGAGCTGATGTGAATGCTGAAACAT 4680
DB GATGATGAAGTCTATGATGCAACCTATGAGTACGAGCTGATGTGTGAATGCTGAAACAT 4680
QY 4681 CGTGTTCACATCCATGTTCTCCATCGGAATGCGTGTGAAGTATCATCGGCTTTGGGGTGTCT 4740
DB CGTGTTCACATCCATGTTCTCCATCGGAATGCGTGTGAAGTATCATCGGCTTTGGGGTGTCT 4740
QY 4741 GAACTATTTTACAGATGCTCGGAATGTCTTTGACTTTTGTCACTGTGTTGGGAAGTATTAC 4800
DB GAACTATTTTACAGATGCTCGGAATGTCTTTGACTTTTGTCACTGTGTTGGGAAGTATTAC 4800
QY 4801 TGATATTTTGTAAACAGAGATTGCGGAACCGAACAATTTTCACTCAGCTTCTCCTCCG 4860
DB TGATATTTTGTAAACAGAGATTGCGGAACCGAACAATTTTCACTCAGCTTCTCCTCCG 4860
QY 4861 CCTCTTTTCAGCTGCGCGCTGATCAAGTGTCTCCGCGAGGCTACACCATCCGATCCT 4920
DB CCTCTTTTCAGCTGCGCGCTGATCAAGTGTCTCCGCGAGGCTACACCATCCGATCCT 4920
QY 4921 GCTGTGGACCTTTGTCCAGTTCCTTCAAGGCCCTGCCCCCTACGTGTCTGCTCATTTGCCAT 4980
DB GCTGTGGACCTTTGTCCAGTTCCTTCAAGGCCCTGCCCCCTACGTGTCTGCTCATTTGCCAT 4980
QY 4981 GCTGTCTTCTATCTACGCCATCATCGGCATGAGGTGTTGGGAATATTGCCCTGGATGA 5040
DB GCTGTCTTCTATCTACGCCATCATCGGCATGAGGTGTTGGGAATATTGCCCTGGATGA 5040
QY 5041 TGACACACGATCAACCGCCCAACAACTTCCGAGCTTTTGTGCAAGCCCTGATGCTGCT 5100
DB TGACACACGATCAACCGCCCAACAACTTCCGAGCTTTTGTGCAAGCCCTGATGCTGCT 5100
QY 5101 GTTCAGGAGCCACCGGGGAGGCTGCGACAGATCATGCTGTCTGCTGCTGAGCAACCA 5160
DB GTTCAGGAGCCACCGGGGAGGCTGCGACAGATCATGCTGTCTGCTGCTGAGCAACCA 5160
QY 5161 GGCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGTGCTTGTGCTGTGATCAT 5220
DB GGCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGTGCTTGTGCTGTGATCAT 5220
QY 5221 CGTCTCTTCTATCTTCTGTGCTCTTCTGATGTGAACCTCTTGTGGTGTGATCAT 5280
DB CGTCTCTTCTATCTTCTGTGCTCTTCTGATGTGAACCTCTTGTGGTGTGATCAT 5280
QY 5281 GGAACAATTTTGTAGTACTTCAACGCGGACTTTCATCTTAGTCTCTCACCACCTTGGATGA 5340
DB GGAACAATTTTGTAGTACTTCAACGCGGACTTTCATCTTAGTCTCTCACCACCTTGGATGA 5340

QY 5341 GTTCATCCGGCTCTGGGCTGAATACGACCGGCTGCGTGTGGGCGCATCTAGTTACAATGA 5400
DB GTTCATCCGGCTCTGGGCTGAATACGACCGGCTGCGTGTGGGCGCATCTAGTTACAATGA 5400
QY 5401 CATGTTTGAGATGCTGAAACACATGTCCCCTGCTCTGGGCTGGGGAAGAAATCCCTGTC 5460
DB CATGTTTGAGATGCTGAAACACATGTCCCCTGCTCTGGGCTGGGGAAGAAATCCCTGTC 5460
QY 5461 TCGAGTGTCTTACAAGCGCTGGTTCCGATGAAATGCCCATCTCCAAACAGGACATGAC 5520
DB TCGAGTGTCTTACAAGCGCTGGTTCCGATGAAATGCCCATCTCCAAACAGGACATGAC 5520
QY 5521 TGTTCACCTTCAAGCTGATGGGCTCATCCGACCGCATGAGATCAAGCTGGC 5580
DB TGTTCACCTTCAAGCTGATGGGCTCATCCGACCGCATGAGATCAAGCTGGC 5580
QY 5581 CCCAGCTGGGACAAAGCAGCATCATGTGACGGGAGTTGAGGAAGAGATTTCCCGTTGT 5640
DB CCCAGCTGGGACAAAGCAGCATCATGTGACGGGAGTTGAGGAAGAGATTTCCCGTTGT 5640
QY 5641 GTGGGCCAAATCTGCCCCAGAAAGACTTTGGACTTTGCTGTACCCCATAGCCTGATGA 5700
DB GTGGGCCAAATCTGCCCCAGAAAGACTTTGGACTTTGCTGTACCCCATAGCCTGATGA 5700
QY 5701 GATGACAGTGGGAAAGTTTATGACGCTCTGATGATATTTGACTTCTACAGCAGAACAA 5760
DB GATGACAGTGGGAAAGTTTATGACGCTCTGATGATATTTGACTTCTACAGCAGAACAA 5760
QY 5761 AACCCAGAGACAGATGACGAGGCTCTTGAGGCTCTCCAGATGGTCTCTGTGTC 5820
DB AACCCAGAGACAGATGACGAGGCTCTTGAGGCTCTCCAGATGGTCTCTGTGTC 5820
QY 5821 CCTGTTCCACCTCTGAAGGCCACCTGGAGCAGACACAGCCGCTGTGCTCCGAGGAGC 5880
DB CCTGTTCCACCTCTGAAGGCCACCTGGAGCAGACACAGCCGCTGTGCTCCGAGGAGC 5880
QY 5881 CCGGGTTTTCTTCGACAGAAAGTTTCCACTCCCTCAGCAATGGCGGGCCATACAATA 5940
DB CCGGGTTTTCTTCGACAGAAAGTTTCCACTCCCTCAGCAATGGCGGGCCATACAATA 5940
QY 5941 CCAAGAGTGGCATCAAGAGTCTGCTCTCTGGGCACTCAAGAGACCCAGATGACCC 6000
DB CCAAGAGTGGCATCAAGAGTCTGCTCTCTGGGCACTCAAGAGACCCAGATGACCC 6000
QY 6001 CATGAGGCGCAGCCCACTCCGAGGCTGCGCACTCCACAGAGATCCCTGTGGGCGGTC 6060
DB CATGAGGCGCAGCCCACTCCGAGGCTGCGCACTCCACAGAGATCCCTGTGGGCGGTC 6060
QY 6061 AGGAGCACTGGCTGTGGAGCTTCCAGATGAGAGCTTCCAGAGGAGGCTGATGGGGA 6120
DB AGGAGCACTGGCTGTGGAGCTTCCAGATGAGAGCTTCCAGAGGAGGCTGATGGGGA 6120
QY 6121 GCCCCAGCTGGGCTGGAGAGCCAGGCTCAGCGGCTCCATGCGGCTTTCGCGCGGA 6180
DB GCCCCAGCTGGGCTGGAGAGCCAGGCTCAGCGGCTCCATGCGGCTTTCGCGCGGA 6180
QY 6181 GACTCAGCCGCTCAGAGATGCCAGCCCATGAAAGCTTCCATCTCCAAGCTGCGCCAGCG 6240
DB GACTCAGCCGCTCAGAGATGCCAGCCCATGAAAGCTTCCATCTCCAAGCTGCGCCAGCG 6240
QY 6241 GCCCTGTGGACTCATCTTTTGAGACACACCCCGGACGCCCACTTA3CCAGGCGTC 6300
DB GCCCTGTGGACTCATCTTTTGAGACACACCCCGGACGCCCACTTA3CCAGGCGTC 6300
QY 6301 GTGCAACACCAACACCGCTGCCACCGCGCAGGAGACAGGAAGAGAGTCTCCCTGA 6360
DB GTGCAACACCAACACCGCTGCCACCGCGCAGGAGACAGGAAGAGAGTCTCCCTGA 6360
QY 6361 GAAGGGGCCAGCCTGTCTGCGGATATGATGGCAGCAACCAAGCAGTGTGTGGGGCCGG 6420
DB GAAGGGGCCAGCCTGTCTGCGGATATGATGGCAGCAACCAAGCAGTGTGTGGGGCCGG 6420
QY 6421 GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGCGGGGAACGAGAGCGCT3GAGAGAGCG 6480

||||| 6421 GCTGCCCGGAGAGGGGCTACAGGCTGCGCGGGAACAGAGCGCGGAGGAGCG 6480
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QY GGGCGGCTCCAGAGCGGAGGAGCGCTCATCTCTCTCTCTCGGAGAGGAGCGCTTCTA 6540
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Db GGGCGGCTCCAGAGCGGAGGAGCGCTCATCTCTCTCTCTCGGAGAGGAGCGCTTCTA 6540
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QY CTCCTGCGACCGCTTTTGGGGGCGGTGAGCGCCCGAAGCCCAAGCCCTCCCTCAGCAGCCA 6600
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Db CTCCTGCGACCGCTTTTGGGGGCGGTGAGCGCCCGAAGCCCAAGCCCTCCCTCAGCAGCCA 6600
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QY CCCAACCTGCGCAACACATGCGCCAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 6660
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QY GAATGGGAGCGCCCTTGTCTGCTCAACATCTGTGTCTAGCACCCCGCGCGGTGGCGGAG 6720
|||||
Db GAATGGGAGCGCCCTTGTCTGCTCAACATCTGTGTCTAGCACCCCGCGCGGTGGCGGAG 6720
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QY GCAGCTCCCCAGACGCGCCCTGATCTCCCGCCAGCATCACTTACAGAGCGGCAACTC 6780
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Db GCAGCTCCCCAGACGCGCCCTGATCTCCCGCCAGCATCACTTACAGAGCGGCAACTC 6780
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QY CTCACCCATCCACTTCCCGGGGCTCAGACGAGCGCTCCCTGCTTCTCCCGAGCGCGCT 6840
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Db CTCACCCATCCACTTCCCGGGGCTCAGACGAGCGCTCCCTGCTTCTCCCGAGCGCGCT 6840
|||||
QY CAGCGGTGGGCTTCCGAAACAAACGCGCTGCTCAGAGAGACCCCTCAGCGAGCGCCCT 6900
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Db CAGCGGTGGGCTTCCGAAACAAACGCGCTGCTCAGAGAGACCCCTCAGCGAGCGCCCT 6900
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|||||
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|||||
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RESULT 2
AR198608
LOCUS AR198608 7364 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5 from patent US 6353091.
ACCESSION AR198608
VERSION AR198608.1 GI:20248457
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 7364)
AUTHORS Lipscombe,D. and Schorge,S.
TITLE Human N-type calcium channel isoform
JOURNAL Patent: US 6353091-A 5 05-MAR-2002;
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Best Local Similarity 99.8%; Pred. No. 0;
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Db 61 GCTGCTCCGCTCTGAGCGCTGCGCGCCCGCGCGCTCCCTCCCGGGGCGCTGGGCGG 120
QY 121 GGGATGCAAGCGGGGCGCGGAGCGATGCTTGGGGGACGAGTGGGGCGGCGCTA 180
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Qy	1381	TTTGGACCTGCTGAGAGAGCGGCCACGAGAGCAGAGAAATGACTGATCCAGCAGA	1440
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RESULT 3

AX333697

LOCUS

AX333697 7364 bp DNA linear PAT 09-JAN-2002

DEFINITION Sequence 4206 from Patent WO0194629.
ACCESSION AX333697
VERSION AX333697.1 GI:18124416
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Horrikan, S., Soppet, D. R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 4206 13-DEC-2001;
Avalon Pharmaceuticals (US)
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RESULT 4

HUMCACHNT 7364 bp mRNA linear PRI 31-OCT-1994

LOCUS Human N-type calcium channel alpha-1 subunit mRNA, complete cds.

DEFINITION M94172.1 GI:179757

ACCESSION M94172.1

VERSION M94172.1

KEYWORDS N-type calcium channel alpha-1 subunit.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 7364)

AUTHORS Williams,M.E., Brust,P.F., Feldman,D.H., Patthi,S., Simerson,S., Maroufi,A., McCue,A.F., Velicellebi,G., Ellis,S.B. and Harpold,M.M.

TITLE Structure and functional expression of an omega-conotoxin-sensitive human N-type calcium channel

JOURNAL Science 257 (5068), 389-395 (1992)

MEDLINE 92355886

PUBMED 1321501

COMMENT Original source text: Homo sapiens CNS cDNA to mRNA.

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ORIGIN

Query Match 99.5%; Score 7342; DB 9; Length 7364;
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Db 6109 GCCCAACGCTGGGCTGGAGCCAGGCTCGAGCGGCTCCATGCCCGGCTTGGGGCCGA 6168
Qy 6181 GACTCAGCCCGTCCACAGATGCCAGCCCATGAAGCGCTCCATCTCCACGCTGCCCGCAGCG 6240
Db 6169 GACTCAGCCCGTCCACAGATGCCAGCCCATGAAGCGCTCCATCTCCACGCTGCCCGCAGCG 6228

Qy 661 GGTGGTCTCTCAAGGATCCCTTGCCACGGCTGGAACTGACTTCGACTCGGAACTGAG 720
Db |||||
Qy 659 GGTGGTCTCTCAAGGATCCCTTGCCACGGCTGGAACTGACTTCGACTCGGAACTGAG 718
Db |||||
Qy 721 GGTGGTGGCTGTGCTGAGGCCCTTGAAAGCTGGTGTCTGGGATCCAAAGTTTGCAAGTGGT 780
Db |||||
Qy 719 GGTGGTGGCTGTGCTGAGGCCCTTGAAAGCTGGTGTCTGGGATCCAAAGTTTGCAAGTGGT 778
Db |||||
Qy 781 GGTCAAAGTCCATCATGAAGGCCATGGTTCCACTCCTGCAGATTGGGCTGCTTCTTCTTCTT 840
Db |||||
Qy 779 GGTCAAAGTCCATCATGAAGGCCATGGTTCCACTCCTGCAGATTGGGCTGCTTCTTCTTCTT 838
Db |||||
Qy 841 TGGCATCCTCATGTTTGGCATCATGAGCTGGAGTTCTAATGAGGCAAGTTTCCAAAGGC 900
Db |||||
Qy 839 TGGCATCCTCATGTTTGGCATCATGAGCTGGAGTTCTAATGAGGCAAGTTTCCAAAGGC 898
Db |||||
Qy 901 CTGTTTCCCAACAGCAGATGGGAGCCGCTGGGTGACTTCCCTGTGGCAAGAGGC 960
Db |||||
Qy 899 CTGTTTCCCAACAGCAGATGGGAGCCGCTGGGTGACTTCCCTGTGGCAAGAGGC 958
Db |||||
Qy 961 CCCAGCCCGGCTGTGCGAGGCGGACACTGAGTGC CGGAGTACTTGGCCAGGACCCAACTT 1020
Db |||||
Qy 959 CCCAGCCCGGCTGTGCGAGGCGGACACTGAGTGC CGGAGTACTTGGCCAGGACCCAACTT 1018
Db |||||
Qy 1021 TGGCATCACCACTTTGACATAATCCTGTTTGGTTCATCTTGGCATCTTGGCATCAC 1080
Db |||||
Qy 1019 TGGCATCACCACTTTGACATAATCCTGTTTGGTTCATCTTGGCATCTTGGCATCAC 1078
Db |||||
Qy 1081 CATGGGGCTGGAATGACATCCTCTATATACAAAGATCGGCGGCAACCTGGAA 1140
Db |||||
Qy 1079 CATGGGGCTGGAATGACATCCTCTATATACAAAGATCGGCGGCAACCTGGAA 1138
Db |||||
Qy 1141 CTGGCTCTACTTCTCATCCTCTCATCATCGGCTCTTCTTCTCATGCTCAACCTGGTGC 1200
Db |||||
Qy 1139 CTGGCTCTACTTCTCATCCTCTCATCATCGGCTCTTCTTCTCATGCTCAACCTGGTGC 1198
Db |||||
Qy 1201 GGGCGTGTCTCGGGGAGTTTGCAAGAGCGAGAGGGTGAGAAACCGCGCGCTT 1260
Db |||||
Qy 1199 GGGCGTGTCTCGGGGAGTTTGCAAGAGCGAGAGGGTGAGAAACCGCGCGCTT 1258
Db |||||
Qy 1261 CCTGAAGCTGGCGGAGAGAGAGATCGAGGAGAGCTCAAGGGTACCTGGAGTGGAT 1320
Db |||||
Qy 1259 CCTGAAGCTGGCGGAGAGAGAGATCGAGGAGAGCTCAAGGGTACCTGGAGTGGAT 1318
Db |||||
Qy 1321 CTTCAAGCGGAGGAAGTCTATGCTGGCGGAGGAGAGGAATCGAGGAGGAAGTCCCC 1380
Db |||||
Qy 1319 CTTCAAGCGGAGGAAGTCTATGCTGGCGGAGGAGGACAGGAATCGAGGAGGAAGTCCCC 1378
Db |||||
Qy 1381 TTTGGACGTGTGAAGAGAGCGGCCACCAAGAGAGCAAAATGACTGTATCCACGAGA 1440
Db |||||
Qy 1379 TTTGGACGTGTGAAGAGAGCGGCCACCAAGAGAGCAAAATGACTGTATCCACGAGA 1438
Db |||||
Qy 1441 GGAGGAGAGGACCGGTTTGAGATCTGTGCTGTTGGATCCCGCTTCCCGCGCGAG 1500
Db |||||
Qy 1439 GGAGGAGAGGACCGGTTTGAGATCTGTGCTGTTGGATCCCGCTTCCCGCGCGAG 1498
Db |||||
Qy 1501 CCTCAAGAGCGGGAAGACAGAGAGCTGCTCATACTTCCGAGGAAGAGAGATGTTCCG 1560
Db |||||
Qy 1499 CCTCAAGAGCGGGAAGACAGAGAGCTGCTCATACTTCCGAGGAAGAGAGATGTTCCG 1558
Db |||||
Qy 1561 GTTTTTTATCCGGCGCATGTTGAAAGGCTAGAGCTTCTACTGGGTGTTGCTGCTGGT 1620
Db |||||
Qy 1559 GTTTTTTATCCGGCGCATGTTGAAAGGCTAGAGCTTCTACTGGGTGTTGCTGCTGGT 1618
Db |||||
Qy 1621 GGCCCTGAACACATGTTGTGGCATGGTGCATTAACACGCGCGGCGGCTTACAC 1680
Db |||||
Qy 1619 GGCCCTGAACACATGTTGTGGCATGGTGCATTAACACGCGCGGCGGCTTACAC 1678
Db |||||
Qy 1681 GACCTGTATTTGAGAGTTTGTGTTTCTGGGTCTCTTCTCAGAGAGTGTCCCTGAA 1740
Db |||||
Qy 1679 GACCTGTATTTGAGAGTTTGTGTTTCTGGGTCTCTTCTCAGAGAGTGTCCCTGAA 1738
Db |||||
Qy 1741 GATGTATGGCCTGGGGCCAGAAAGCTACTTCCGGTCTCTTCAACTGCTTCGACTTTGG 1800
Db |||||

Db 1739 GATGTATGGCCTGGGGCCAGAAAGCTACTTCCGGTCTCTCCTTCAACTGCTTCGACTTTGG 1798
Qy |||||
Db 1801 GGTCACTGTGGGAGCGTCTTTGAAGTGGTCTGGCGGCCATCAAGCCGGGAAGTCTCTT 1860
Qy |||||
Db 1799 GGTCACTGTGGGAGCGTCTTTGAAGTGGTCTGGCGGCCATCAAGCCGGGAAGTCTCTT 1858
Qy |||||
Db 1861 TGGGATCAGTGTCTCGGGCCCTCCGCTGTCTGAGGATCTTCAAAAGTCAACGAAGTACTG 1920
Qy |||||
Db 1859 TGGGATCAGTGTCTCGGGCCCTCCGCTGTCTGAGGATCTTCAAAAGTCAACGAAGTACTG 1918
Qy |||||
Db 1921 GAGCTCCCTGGGAACTGGTGGTCTCTGCTGAAGTCCATGAAGTCCATCAATCAGCCT 1980
Qy |||||
Db 1919 GAGCTCCCTGGGAACTGGTGGTCTCTGCTGAAGTCCATGAAGTCCATCAATCAGCCT 1978
Qy |||||
Db 1981 GCTCTTCTTGTCTCTCTGTTCAATGTTGGTCTTTCGCCCTGCTGGGGATGAGCTGTTGG 2040
Qy |||||
Db 1979 GCTCTTCTTGTCTCTCTGTTCAATGTTGGTCTTTCGCCCTGCTGGGGATGAGCTGTTGG 2038
Qy |||||
Db 2041 GGGACAGTTCAACTTCCAGGATGAGACTCCCAACAACCTTCCGACACTTCCCTGCGCG 2100
Qy |||||
Db 2039 GGGACAGTTCAACTTCCAGGATGAGACTCCCAACAACCTTCCGACACTTCCCTGCGCG 2098
Qy |||||
Db 2101 CATCTCACTGTCTTCCAGATCCTGACGGGAGGACTTGAATGCAATGATGATCACGG 2160
Qy |||||
Db 2099 CATCTCACTGTCTTCCAGATCCTGACGGGAGGACTTGAATGCAATGATGATCACGG 2158
Qy |||||
Db 2161 GATCGAATCGAAGCGGCGTCAAGAAAGCATGTTCTCGTCTCTTTTACTTCAATGTCCT 2220
Qy |||||
Db 2159 GATCGAATCGAAGCGGCGTCAAGAAAGCATGTTCTCGTCTCTTTTACTTCAATGTCCT 2218
Qy |||||
Db 2221 GACACTGTTGCGAAACTTACACTCTGCTGAATGTTTCTTGGCCATCGCTGTGACAACT 2280
Qy |||||
Db 2219 GACACTGTTGCGAAACTTACACTCTGCTGAATGTTTCTTGGCCATCGCTGTGACAACT 2278
Qy |||||
Db 2281 GGGCAAGCCCAAGCTGACCAAGATGAGAGGAGATGGAAGAGCAGCCCAATCAGAA 2340
Db 2279 GGGCAAGCCCAAGCTGACCAAGATGAGAGGAGATGGAAGAGCAGCCCAATCAGAA 2338
Qy 2341 GCTTGTCTTGAAGAGCCCAAGAAAGTGGCTGAAGTCAAGCCCATGCTCTCCCGGAACAT 2400
Db 2339 GCTTGTCTTGAAGAGCCCAAGAAAGTGGCTGAAGTCAAGCCCATGCTCTCCCGGAACAT 2398
Qy 2401 CTCATCGCCCGCAGGACAGAACTCGGCCAAGGCGCGCTCGGTGTGGAGCAGCGGGC 2460
Db 2399 CTCATCGCCCGCAGGACAGAACTCGGCCAAGGCGCGCTCGGTGTGGAGCAGCGGGC 2458
Qy 2461 CAGCCAGCTACGGCTGCAGAACTTGGGGCAGCTGGGAGCGCTGTACAGCGAGATGGA 2520
Db 2459 CAGCCAGCTACGGCTGCAGAACTTGGGGCAGCTGGGAGCGCTGTACAGCGAGATGGA 2518
Qy 2521 CCCCGAGGAGCGGCTGCGCTTTCGCCACTACGCCCACTTCGCCGCCGACATGAAGAGCCA 2580
Db 2519 CCCCGAGGAGCGGCTGCGCTTTCGCCACTACGCCCACTTCGCCGCCGACATGAAGAGCCA 2578
Qy 2581 CCTGGAACCGGCGCTGCTGTTGAGTGGGCGCGGACAGCGCGCGGGGGCCCTGTGGAGG 2640
Db 2579 CCTGGAACCGGCGCTGCTGTTGAGTGGGCGCGGACAGCGCGCGGGGGCCCTGTGGAGG 2638
Qy 2641 CAAAGCCGACCTGAGGCTGCGGAGGCCCCGAGGGGCTGACCCCTCCGGCAGGCAACA 2700
Db 2639 CAAAGCCGACCTGAGGCTGCGGAGGCCCCGAGGGGCTGACCCCTCCGGCAGGCAACA 2698
Qy 2701 CCGGCAACCGGCAAGGACAAAGACCCCGCGGGGGGACACAGACCCGAGAGAGGCCCC 2760
Db 2699 CCGGCAACCGGCAAGGACAAAGACCCCGCGGGGGGACACAGACCCGAGAGAGGCCCC 2758
Qy 2761 GAAGCGGAGAGCGGGAGCCCGGTCTCCGGGAGGAGCGGCGCGCGCAGCGCAGCCA 2820
Db 2759 GAAGCGGAGAGCGGGAGCCCGGTCTCCGGGAGGAGCGGCGCGCGCAGCGCAGCCA 2818
Qy 2821 CAGCAAGGAGGCGCGGGGGCCCCCGAGGCGCGGAGCGGCGGCGGAGGCCCCAGGCCC 2880
Db |||||

Db	2819	CAGCAAGAGAGGCGCGGGGGCCCCCGAGGCGGAGCGAGAGCGCGCCGAGGCCCCAGCGCC	2878
Qy	2881	CGAGGCGCGCGCGGCACACACCGGCGCGGCTCCCGGAGGAGGCGGCGGAGCGGAGCC	2940
Db	2879	CGAGGCGCGCGCGGCACACCGGCGCGGCTCCCGGAGGAGGCGGCGGAGCGGAGCC	2938
Qy	2941	CCGACGCCACCGCGCGCACCGGACACAGATCCGAGCAAGAGTGCCTCGCGCCGAAGG	3000
Db	2939	CCGACGCCACCGCGCGCACCGGACACAGATCCGAGCAAGAGTGCCTCGCGCCGAAGG	2998
Qy	3001	CGAGCGGCGCGCGGCACACCGGCGGCCCCCGAGCGGGCCCCCGGAGCGGAGAGCGG	3060
Db	2999	CGAGCGGCGCGCGGCACACCGGCGGCCCCCGAGCGGGCCCCCGGAGCGGAGAGCGG	3058
Qy	3061	GGAGGAGCGCGCGCGGCACCGCGCCCGGCACAAAGCGAGCGCTGCTCACGAGGCTGT	3120
Db	3059	GGAGGAGCGCGCGCGGCACCGCGCCCGGCACAAAGCGAGCGCTGCTCACGAGGCTGT	3118
Qy	3121	CGAGAAGGAGACACCGAGAGAGGAGCCACGAGAGAGGAGCTGAGATAGTGAAGCCGA	3180
Db	3119	GGAGAAAGGAGACACCGAGAGAGGAGCCACGAGAGAGGAGCTGAGATAGTGAAGCCGA	3178
Qy	3181	CAAGAAAAGGAGTCCGGAAACACAGCCCCGGGAGCCACCTGTGACCTCGAGACCCAG	3240
Db	3179	CAAGAAAAGGAGTCCGGAAACACAGCCCCGGGAGCCACCTGTGACCTCGAGACCCAG	3238
Qy	3241	TGGGACTGTGACTGTGGGTCCATGTCACACACTCTCCAGCACCTGTCTCAGAAGGTGA	3300
Db	3239	TGGGACTGTGACTGTGGGTCCATGTCACACTCTCCAGCACCTGTCTCAGAAGGTGA	3298
Qy	3301	GGAA CAGCAGAGGATG CAGACAA TCAGCGGAACGTCACTCGATGGGAGTCAGCCCCC	3360
Db	3299	GGAA CAGCAGAGGATG CAGACAA TCAGCGGAACGTCACTCGATGGGAGTCAGCCCCC	3358
Qy	3361	AGACCCGAACACTATTGTACATATCCAGATGATGCTGAGCGGCCCTTTGGGAAAGCCAC	3420
Db	3359	AGACCCGAACACTATTGTACATATCCAGATGATGCTGAGCGGCCCTTTGGGAAAGCCAC	3418
Qy	3421	GGTCGTTCCCAAGTGGTAAACGTGGACCTTGGAAAGC CAAAGCAGAGGGGAAGAGGGTGA	3480
Db	3419	GGTCGTTCCCAAGTGGTAAACGTGGACCTTGGAAAGC CAAAGCAGAGGGGAAGAGGGTGA	3478
Qy	3481	AGCGGATGACGTGATGAGGAGCGGCCCGCCGCTATCGTCCATACAGTCCATGTTCTG	3540
Db	3479	AGCGGATGACGTGATGAGGAGCGGCCCGCCGCTATCGTCCATACAGTCCATGTTCTG	3538
Qy	3541	TTTAAGCCCCACAACTCTGCTCGCGCTTCTGCCACTACATCGTACCAATGAGTACTT	3600
Db	3539	TTTAAGCCCCACAACTCTGCTCGCGCTTCTGCCACTACATCGTACCAATGAGTACTT	3598
Qy	3601	CGAGTGGTCAATTCGTGTGTCATCGCCTTGAAGAGTATCGAGCAGCATCGCCCTGGCTGCTGAGGAGCC	3660
Db	3599	CGAGTGGTCAATTCGTGTGTCATCGCCTTGAAGAGTATCGAGCAGCATCGCCCTGGCTGAGGAGCC	3658
Qy	3661	AGTCGCACAGACTCGCCAGGAACACCGCTCTGAATACTCTGGAATACATTTTCACTGG	3720
Db	3659	AGTCGCACAGACTCGCCAGGAACACCGCTCTGAATACTCTGGAATACATTTTCACTGG	3718
Qy	3721	TGTCTTTTACCTTTGAGATGGTGTATAAGATGATCGACTTTGGGACTGCTGCTTCAACCTGG	3780
Db	3719	TGTCTTTTACCTTTGAGATGGTGTATAAGATGATCGACTTTGGGACTGCTGCTTCAACCTGG	3778
Qy	3781	AGCTATTTCCGGGACTTGGGACATTTCTGACATTCATTTGTGTCAGTGGCGGCTTGGT	3840
Db	3779	AGCTATTTCCGGGACTTGGGACATTTCTGACATTCATTTGTGTCAGTGGCGGCTTGGT	3838
Qy	3841	GGCGTTTGCTTTCTCGAGCTTCGTGGGAGGATCCAAAGGAAAGACATCAATACATCAA	3900
Db	3839	GGCGTTTGCTTTCTC-----AGGATCCAAAGGAAAGACATCAATACATCAA	3886
Qy	3901	GTCTCTGAGAGTCTCTGCTGCTGCGGCCCTCAAGACCATCAAAAGCTGCCCAAGCT	3960
Db	3887	GTCTCTGAGAGTCTCTGCTGCTGCGGCCCTCAAGACCATCAAAAGCTGCCCAAGCT	3946

QY	3961	CAAGCTGTGTTTGACTGTGTGGTGAACTCCCTCAAGAATGTCTCTCAACATCTTGATTGT	4020
DB	3947	CAAGGCTGTGTTTGACTGTGTGGTGAACTCCCTGAAGATGTCTCTCAACATCTTGATTGT	4006
QY	4021	CTACATGCTCTTCAATGTTTCATATTTGCGGTCAATTCGGTGCAGCTCTTCAAGGGGAAGTT	4080
DB	4007	CTACATGCTCTTCAATGTTTCATATTTGCGGTCAATTCGGTGCAGCTCTTCAAGGGGAAGTT	4066
QY	4081	TTTCTTATGTCACAGATGAATCCAAAGGAGCTGGAGAGGGAATGCAAGGGTCAAGTATTTGGA	4140
DB	4067	TTTCTTACTGTCACAGATGAATCCAAAGGAGCTGGAGAGGGAATGCAAGGGTCAAGTATTTGGA	4126
QY	4141	TTATGAGAAGAGAGAAGTGGAGCTCAGCCAGGCACTGGAAGAAATACACATCTTCACTA	4200
DB	4127	TTATGAGAAGAGAGAAGTGGAGCTCAGCCAGGCACTGGAAGAAATACACATCTTCACTA	4186
QY	4201	CGACAATGTGCTCTGGGCTCTGCTGACGCTGTTCCAGATGTCCACGGGAGAGGCTGGCC	4260
DB	4187	CGACAATGTGCTCTGGGCTCTGCTGACGCTGTTCCAGATGTCCACGGGAGAGGCTGGCC	4246
QY	4261	CATGGTGTGAAACAATCCGTGGATGCCACTATGAGGAGCAGGGTCCAGGCCCTGGSTA	4320
DB	4247	CATGGTGTGAAACAATCCGTGGATGCCACTATGAGGAGCAGGGTCCAGGCCCTGGSTA	4306
QY	4321	CCGCATGAGCTGTCCATCTTCTACGTGGTCTACTTTGTGCTTTCCTCTCTCTTCTG	4380
DB	4307	CCGCATGAGCTGTCCATCTTCTACGTGGTCTACTTTGTGCTTTCCTCTCTCTTCTG	4366
QY	4381	CAACATCTTTGTGGCTTTGTATCATATCATCTTCCAGGAGCAGGGGACAAAGGTATGTC	4440
DB	4367	CAACATCTTTGTGGCTTTGTATCATATCATCTTCCAGGAGCAGGGGACAAAGGTATGTC	4426
QY	4441	TGAATGAGCCTCGAGAGACAGAGAGGCTTGCAATTGACTTCGGCATCAACGCCAAACC	4500
DB	4427	TGAATGAGCCTCGAGAGACAGAGAGGCTTGCAATTGACTTCGGCATCAACGCCAAACC	4486
QY	4501	CCTGACACGGTACATGCCCCCAAAACCGGCAGTCTGTTCCAGTATAAGAGCTGACATTTGT	4560
DB	4487	CCTGACACGGTACATGCCCCCAAAACCGGCAGTCTGTTCCAGTATAAGAGCTGACATTTGT	4546
QY	4561	GGTCTCCCGCCCTTTGAAATCTTCAATCATGGCCATGATAGCCCTCAACAATGGTGCT	4620
DB	4547	GGTCTCCCGCCCTTTGAAATCTTCAATCATGGCCATGATAGCCCTCAACAATGGTGCT	4606
QY	4621	GATGATGAAGTCTATGATGCAACCTATGAGTACAGAGCTGATGCTGGAATTCCTGACAT	4680
DB	4607	GATGATGAAGTCTATGATGCAACCTATGAGTACAGAGCTGATGCTGGAATTCCTGACAT	4666
QY	4681	CGTGTTCAATCAATGTTCTCCATGGAAATGGGTGCTGAAGATCATCGCCTTTGGGGTGCT	4740
DB	4667	CGTGTTCAATCAATGTTCTCCATGGAAATGGGTGCTGAAGATCATCGCCTTTGGGGTGCT	4726
QY	4741	GAACTATTTTCAGAGATGCTGGAATGCTTTTGACTTTGTCACTGTGTGGGAAGTATTAC	4800
DB	4727	GAACTATTTTCAGAGATGCTGGAATGCTTTTGACTTTGTCACTGTGTGGGAAGTATTAC	4786
QY	4801	TGATATTTTATGACAGAGATTCGCGAAACGAAACAATTTCAATCAACCTCACTTCCTCCG	4860
DB	4787	TGATATTTTATGACAGAGATTCGCGAAACGAAACAATTTCAATCAACCTCACTTCCTCCG	4846
QY	4861	CCTCTTTTCGAGCTGCGGCTGATCAAGCTGCTCGGCAGGGCTACACCAATCGCATCCT	4920
DB	4847	CCTCTTTTCGAGCTGCGGCTGATCAAGCTGCTCGGCAGGGCTACACCAATCGCATCCT	4906
QY	4921	GCCTGGACCTTTGTCCAGTCTTCAAGGCCCTGCCCCTACGTGTGTCTGTCTATTGCCAT	4980
DB	4907	GCCTGGACCTTTGTCCAGTCTTCAAGGCCCTGCCCCTACGTGTGTCTGTCTATTGCCAT	4966
QY	4981	GCCTGTTCTTCATACGCCATCATCGGATGCAAGGTGTGTGGGAATATTGCTCCTGGATGA	5040
DB	4967	GCCTGTTCTTCATACGCCATCATCGGATGCAAGGTGTGTGGGAATATTGCTCCTGGATGA	5026

Qy	5041	TGACACAGACATCAACCGCCACAACAATCTTCGGACGCTTTTGGAAAGCCCTGATGCTGCT	5100
Db	5027	TGACACAGACATCAACCGCCACAACAATCTTCGGACGCTTTTGGCAAGCCCTGATGCTGCT	5086
Qy	5101	GTTTCAGAGCGCCACGCGGGAGGCTTCGSCACGAGATCATGCTGTCTCTGCTGAGCAACCA	5160
Db	5087	GTTTCAGAGCGCCACGCGGGAGGCTTCGSCACGAGATCATGCTGTCTCTGCTGAGCAACCA	5146
Qy	5161	GGCCTGTGATGAGCAGGCCAAATGCCACCGAGTGTGGAAGTGACTTTTGCTTACTTCTTACTT	5220
Db	5147	GGCCTGTGATGAGCAGGCCAAATGCCACCGAGTGTGGAAGTGACTTTTGCTTACTTCTTACTT	5206
Qy	5221	CGTCTCCTTCATCTTCTCTGTGCTCCTTTCTGA TGTTGAA CCTCTTTGTGGCTGTGATCAT	5280
Db	5207	CGTCTCCTTCATCTTCTCTGTGCTCCTTTCTGA TGTTGAA CCTCTTTGTGGCTGTGATCAT	5266
Qy	5281	GGACAAATTTTGTAGTACCTCACGCGGACTCTTCCATCCTTAGTCTCTCACACATTGGATGA	5340
Db	5267	GGACAAATTTTGTAGTACCTCACGCGGACTCTTCCATCCTTAGTCTCTCACACATTGGATGA	5326
Qy	5341	GTTTCATCCGGTCTTGGGCTGAATACGACCCGGCTCGTGTGGGCGCATCAGTTTACATGA	5400
Db	5327	GTTTCATCCGGTCTTGGGCTGAATACGACCCGGCTCGTGTGGGCGCATCAGTTTACATGA	5386
Qy	5401	CATGTTTGTAGATGTGTAAACACATGTCCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5460
Db	5387	CATGTTTGTAGATGTGTAAACACATGTCCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5446
Qy	5461	TCGAGTTGCTTTACAAAGCGCTGGTTTCGATCGAATCGCAATGCCATCTCCAAACGAGACATGAC	5520
Db	5447	TCGAGTTGCTTTACAAAGCGCTGGTTTCGATCGAATCGCAATGCCATCTCCAAACGAGACATGAC	5506
Qy	5521	TGTTTCACTTTCACGCTCCAGCTGATGGGCCCTCATCCGACCGGCATCTGAGATCAAGCTGGC	5580
Db	5507	TGTTTCACTTTCACGCTCCAGCTGATGGGCCCTCATCCGACCGGCATCTGAGATCAAGCTGGC	5566
Qy	5581	CCACGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTTGAGGAAGAGATTTCCGTTGT	5640
Db	5567	CCACGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTTGAGGAAGAGATTTCCGTTGT	5626
Qy	5641	GTGGGCCAATCTGCCCCAGAGACTTTTGGACTTCTCGTACCAACCCATCAAGCTGATGA	5700
Db	5627	GTGGGCCAATCTGCCCCAGAGACTTTTGGACTTCTCGTACCAACCCATCAAGCTGATGA	5686
Qy	5701	GATGACAGTGGGGAAGTTTATGCAGCTCTGATGATATTTGACTTCTTACAAGCAGAACAA	5760
Db	5687	GATGACAGTGGGGAAGTTTATGCAGCTCTGATGATATTTGACTTCTTACAAGCAGAACAA	5746
Qy	5761	AACCAACAGAGACAGATGACGAGGCTCTTGGAGGCTCTCCAGATGGGTCTGTGTCT	5820
Db	5747	AACCAACAGAGACAGATGACGAGGCTCTTGGAGGCTCTCCAGATGGGTCTGTGTCT	5806
Qy	5821	CCTGTTTCCACCTCTGAAGGCCACCTTGGACGACACAGCCGCTGTCTCCGAGAGC	5880
Db	5807	CCTGTTTCCACCTCTGAAGGCCACCTTGGACGACACAGCCGCTGTCTCCGAGAGC	5866
Qy	5881	CCGGGTTTTTCTTCCGACAGAAGAGTTCCACTCCCTCAGCAATGGCGGGGCCATACAAAA	5940
Db	5867	CCGGGTTTTTCTTCCGACAGAAGAGTTCCACTCCCTCAGCAATGGCGGGGCCATACAAAA	5926
Qy	5941	CCAGAGAGTGGCATCAAAAGTCTGTCTCTGGGGCATCAAAAGGACCCAGGATGCACC	6000
Db	5927	CCAGAGAGTGGCATCAAAAGTCTGTCTCTGGGGCATCAAAAGGACCCAGGATGCACC	5986
Qy	6001	CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGGCGGTC	6060
Db	5987	CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGGCGGTC	6046
Qy	6061	AGGAGCACTGGCTGTGGACGTTTCAGATGACAGCATAAACCCGAGGGGCCCTGTATGGGGA	6120
Db	6047	AGGAGCACTGGCTGTGGACGTTTCAGATGACAGCATAAACCCGAGGGGCCCTGTATGGGGA	6106
Qy	6121	GCCCCAGCCTGGGCTGGAGAGCCAGGGGTTCGACGGGCTCTCATGTCCCCGGCCTTCGCCCGGA	6180

Db	6107	 GCCCCAGCGCTGGGCTGGAGAGCCAGGGTCAGCGGCTTCATGCCCCCGCTTTCGGCGCGA	6166
Qy	6181	GACTCAGCCCGTCA CAGATGCCAGCCCATGAAAGCGTTCATCTCCACGCTGCCCCAGCG	6240
Db	6167	GACTCAGCCCGTCA CAGATGCCAGCCCATGAAAGCGTTCATCTCCACGCTGCCCCAGCG	6226
Qy	6241	GCCCGTGGGACTCATCTTTGACGACACACCGCTGCCACCGCCGAGCCGCCACCCCTAGCCAGGCGTC	6300
Db	6227	GCCCGTGGGACTCATCTTTGACGACACACCGCTGCCACCGCCGAGCCGCCACCCCTAGCCAGGCGTC	6286
Qy	6301	GTGCGACCAACCAACCGCTGCCACCGCTGCCACCGCCGAGGACAGGAAGCAGAGTCCCTGGA	6360
Db	6287	GTGCGACCAACCAACCGCTGCCACCGCTGCCACCGCCGAGGACAGGAAGCAGAGTCCCTGGA	6346
Qy	6361	GAAGGGCCCGAGCGCTGTCTGCCGATATGATGCGCAGCAACAAAGCAGTCTGTGTGGGCGCGG	6420
Db	6347	GAAGGGCCCGAGCGCTGTCTGCCGATATGATGCGCAGCAACAAAGCAGTCTGTGTGGGCGCGG	6406
Qy	6421	GCTGCCCGCGGAGAGGGGGCTTACGGCTGCCGGCGGGAAACGAGAGCGCGCGCAGAGCG	6480
Db	6407	GCTGCCCGCGGAGAGGGGGCTTACGGCTGCCGGCGGGAAACGAGAGCGCGCGCAGAGCG	6466
Qy	6481	GGGCGGTCACAGAGGGGAGGGCGCTCATCTCTCTCGGAGAACGAGAGCGCGCTTCTA	6540
Db	6467	GGGCGGTCACAGAGGGGAGGGCGCTCATCTCTCTCGGAGAACGAGAGCGCGCTTCTA	6526
Qy	6541	CTCTCGACCGCTTTTGGGGCGGTGAGCGCCCGAAGCCCAAGCCCTCCCTCAGCAGCCA	6600
Db	6527	CTCTCGACCGCTTTTGGGGCGGTGAGCGCCCGAAGCCCAAGCCCTCCCTCAGCAGCCA	6586
Qy	6601	CCCAAGCTGCCAAGCTGGCGCAGAGCGGGAGCCCAACCAACAGGGCAGTGGTTCGGT	6660
Db	6587	CCCAAGCTGCCAAGCTGGCGCAGAGCGGGAGCCCAACCAACAGGGCAGTGGTTCGGT	6646
Qy	6661	GAATGGAGCGCCCTGCTGTCAACATCTGGTGTAGCACCCCGCGCGCGGTGGGCGGAG	6720
Db	6647	GAATGGAGCGCCCTGCTGTCAACATCTGGTGTAGCACCCCGCGCGCGGTGGGCGGAG	6706
Qy	6721	GCAGCTCCCCAGACGCGCCCTGACTCCCGCCCGCAGCATCACTACAAGACGGCCAACTC	6780
Db	6707	GCAGCTCCCCAGACGCGCCCTGACTCCCGCCCGCAGCATCACTACAAGACGGCCAACTC	6766
Qy	6781	CTCACCATCACTTCGCGGGGCTCAGACAGCCTCCCTGCTTCTCCCGAGCGCGGT	6840
Db	6767	CTCACCATCACTTCGCGGGGCTCAGACAGCCTCCCTGCTTCTCCCGAGCGCGGT	6826
Qy	6841	CAGCGTGGGCTTTCGAAACAAACGCGCTGTGACAGAGACACCCCTCAGCCAGCCCT	6900
Db	6827	CAGCGTGGGCTTTCGAAACAAACGCGCTGTGACAGAGACACCCCTCAGCCAGCCCT	6886
Qy	6901	GGGCGCTGGCTCTCGAATTGGCTCTGACCTTACCTGGGGGAGCGTCTGGAAGTGAAGC	6960
Db	6887	GGGCGCTGGCTCTCGAATTGGCTCTGACCTTACCTGGGGGAGCGTCTGGAAGTGAAGC	6946
Qy	6961	CTCTGTCCAGCGCCCTGCCTGAGGACACGCTCACTTTGAGAGGCTGTGTGCCAACCACTC	7020
Db	6947	CTCTGTCCAGCGCCCTGCCTGAGGACACGCTCACTTTGAGAGGCTGTGTGCCAACCACTC	7006
Qy	7021	GGGCGGCTCTCAGAGCTTCCTACGTGTCTCCCTGACCTCCAGTCTCACCCCTCTCG	7080
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Qy	7081	CCGCGTGCCCAACGGTTACCACTGCACCCCTGGGACTCAGCTCGGGGTGGCGAGCAGCGCA	7140
Db	7067	CCGCGTGCCCAACGGTTACCACTGCACCCCTGGGACTCAGCTCGGGGTGGCGAGCAGCGCA	7126
Qy	7141	CAGCTACCAACCCCTGACCAAGACCACTGGTGTAGCTGACCGTGAACCGCTCAGAGC	7200
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Db 7187 CTGATGAGCAGGCGGTGTGTTCCAGTGGATGAGTTTATATCCACACGCGGCGAGTCGG 7246
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DEFINITION Sequence 7 from patent US 5846757.
ACCESSION AR063882
VERSION AR063882.1 GI:5993190
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 7362)
AUTHORS Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F.
and Brenner,R.
TITLE Human calcium channel .alpha..sub.1.1. .alpha..sub.2. and .beta.
subunits and assays using them
JOURNAL Patent: US 5846757-A 7 08-DEC-1998;
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Qy 61 GCTGCTCCGCTCTGAGCGCTTGGCGCGCCCGCGCCCTCCCTGCGGGGCGGCTGGGCG 120
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Qy 121 GGGATGACGCGGGGCGCGGAGCCATGTCGCTTCGGGAGCAGCTGGGCGGCGCTA 180
Db 119 GGGATGACGCGGGGCGCGGAGCCATGTCGCTTCGGGAGCAGCTGGGCGGCGCTA 178

Qy 181 TGGAGCCCCGCGGGGAGCGGGCGCGGGCGCGGGCGCGGGCGCGGGCGGCGGCG 240
Db 179 TGGAGCCCCGCGGGGAGCGGGCGCGGGCGCGGGCGCGGGCGCGGGCGGCGGCG 238

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Qy 541 CACGAGGCCCTATTTTCATCGGGATCTTTTGCTTCGAGCAGGGATCAAAATTCATCGCTCT 600
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Qy 1141 CTGGCTCTATTCTCTCTCTCATCATATCGGCTCTTCTTCTCATCTCAACTGCTGCT 1200
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Qy 1441 GGAGGAGAGGAGCCGGTTTGAGATCTCTGTGCTGTTGGAATCCCTCTTGGCCGCGCAG 1500
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QY	3841	GGCGTTTGCTTTCTCGAGCTTCGTGGAGGATCCAAAGGGAAGACATCAATACCATCAA	3900
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QY	3901	GTCTCTGAGAGTCTTTCGTGTCCTGGGCCCTCAGACCATCAAAAGCGTGCCCAAGCT	3960
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QY	3961	CAAGGCTGTGTGACATGTGTGGTGAACCTCCCTGAAGAATGCTCCTCAAGGGAAGTT	4020
Db	3947	CAAGGCTGTGTGACATGTGTGGTGAACCTCCCTGAAGAATGCTCCTCAAGGGAAGTT	4006
QY	4021	CTACATGCTCTTCATGTTTCATATTTGCGCTCATTTGCGGTGCAGCTCTTCAAGGGAAGTT	4080
Db	4007	CTACATGCTCTTCATGTTTCATATTTGCGGTCAATGCGGTGCAGCTCTTCAAGGGAAGTT	4066
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Db	4067	TTTCTACTGCACAGATGAATCCAAAGAGCTGGAGAGGACTGAGAGGCTCAGTATTTGGA	4126
QY	4141	TTATGAGAAGAGGAAAGTGAAGCTCAGCCAGGCAAGTGGAGAAATACGACTTTCACTA	4200
Db	4127	TTATGAGAAGAGGAAAGTGAAGCTCAGCCAGGCAAGTGGAGAAATACGACTTTCACTA	4186
QY	4201	CGAATATGCTCTGGGCTCTGCTGACGCTGTTACAGTGTCCAAGGGAAGGCTGGCC	4260
Db	4187	CGAATATGCTCTGGGCTCTGCTGACGCTGTTACAGTGTCCAAGGGAAGGCTGGCC	4246
QY	4261	CATGGTGCTGAAACACTCCGTGATGCCACCTATGAGGAGCGGTCCAAAGCCCTGGGTA	4320
Db	4247	CATGGTGCTGAAACACTCCGTGATGCCACCTATGAGGAGCGGTCCAAAGCCCTGGGTA	4306
QY	4321	CGCATGAGCTGTGTCATCTTACGTGTGTCTACTTTGTGTCTTTCCCTCTCTTCTCGT	4380
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QY	4381	CAACATCTTTGTGGCTTTGATCATCATCACCTTCAGAGGAGGAGGGAACAGGTGATGC	4440
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QY	4441	TGAATGCAGCTGGAGAAGAACGAGAGGCTTGCATTTCGTCATCAGCGCCAAACC	4500
Db	4427	TGAATGCAGCTGGAGAAGAACGAGAGGCTTGCATTTCGTCATCAGCGCCAAACC	4486
QY	4501	CTGACACGGTACATGCCCAAAACCGGAGTCGTTCCAGTATAGAGCTGGACATTTGT	4560
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QY	4561	GGTCTCCCGCCCTTTGAATACCTTCATCATGSCCATGATAGCCCTCAACACTGGTGCT	4620
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QY	4861	CCTCTTTTCAGCTCGCGGCTGATCAAGCTGCTCCGAGGGCTACACCATCGCATCCT	4920
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QY	4981	GCTGTCTTCTCATCTACGCCATCATCGGCATCGAGGTGTTTGGGAATATTTCCCTTGGATGA	5040
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RESULT 7
AR067882
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DEFINITION Sequence 7 from patent US 5851824.
ACCESSION AR067882
VERSION AR067882.1 GI:5999104
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7362)
AUTHORS Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McQue,A.F.
TITLE Human calcium channel .alpha.-1c/.alpha.-1D, .alpha.-2, .beta.-1,
and .gamma.subunits and cells expressing the DNA
JOURNAL Patent: US 5851824-A 7 22-DEC-1998;
FEATURES Location/Qualifiers
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Query Match 99.2%; Score 7316.4; DB 6; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
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Db 3419 GGTGTTCCGAGTGGTAACTGTGGAACCTGGAAAGCCAA GCGAGGGGGAAGAGAGTGGGA 3478
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Db 4667 CGTGTTCACATCCATGTTCTCATGGAATGCGTGTGAGATCAT CGCCTTTGGGGTGT 4726
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Db 4727 GAACATTTTCAGAGATGCGCTGGAAATGCTTTGACTTTGTGTCAC TGTGTGGGAAGTATTAC 4786

QY	4801	TGATATTTAGTAAACAGAGATTGGGAAAGAAACAATTTTCATCAACCTCAGCTTCCTCCG	4860
Db	4787	TGATATTTAGTAAACAGAGATTGGGAAAGAAACAATTTTCATCAACCTCAGCTTCCTCCG	4846
QY	4861	CCTCTTTCGAGCTCGGGGCTGATCAAGCTGCTCCGACAGGGCTACACCATCCGCATCCT	4920
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QY	5041	TGACACAGCATCAACCGCCACACAACATTTCCGAGCTTTTTCGAAAGCCCTGATGTGCT	5100
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QY	6061	AGGAGCACTGGCTCTGGACCTTCAGATGCAAGAGATAAACCGGAGGGGCTCTGATGGGGA	6120
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AUTHORS Harpold,M.M., Ellis,S.B., Williams,M.E. and McCue,A.F.

TITLE Human calcium channel compositions and methods

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ORIGIN

Query Match 99.2%; Score 7316.4; DB 6; Length 7362;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

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Db 60 GCTGCTCCGCTCTGAGCGCTT-GGCGCGCCCGCGCCCTCCCTGCGGGGCGCTGGGCGG 118

Qy 121 GGGATGACCGCGGCGCGGAGCGCGCCCGGGGCGCGGCGCGGCGAGCTGGGCGCGCTA 180

Db 119 GGGATGACCGCGGCGCGGAGCGCATGTGTCGCTTCGGGGACAGCTGGGCGCGCTA 178

Qy 181 TGGAGGCGCGCGGCGGAGCGCGCCCGGGGCGCGGCGCGGCGCGGCGCGGCGCGCC 240

Db 179 TGGAGGCGCGCGGCGGAGCGCGCCCGGGGCGCGGCGCGGCGCGGCGCGGCGCGCC 238

Qy 241 GGGTCCGCGGGGCTGACGCGCGCGCGAGCGGGTCTCTTACAAGCAATCGATCGCGACGC 300

Db 239 GGGTCCGCGGGGCTGACGCGCGCGCGAGCGGGTCTCTTACAAGCAATCGATCGCGACGC 298

Qy 301 CGCGCGACCATGGCGCTGTACAACCCGATCCCGGTCAAGCAGAACTGCTTACCCTCAA 360

299 CGCGCGGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTACCCTCAA 358

Qy 361 CGCTCGCTCTTCCGTCTTTCAGCGAGGACAAACGCTGTCGCAAAATACGCGAAGCGCATCAC 420

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Qy 421 CGAGTGGCTCCATTCGAGTATATGATCTGGGCCACCATCATGCCAACTGCACTCGTCT 480

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Qy 481 GGCCTTGGAGCAGCACTCCCTCATGGGACAAAACGCCCATGTCGAGCGGCTGGAACGA 540

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Db 1379 TTTTGGACGTCTCAAGAGCGCGCCCAAGAGAGCAGAAATGACTGATTCACCGAGA 1438

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QY	2281	GGCCACCGCCCAAGAGTGAACAGGATGAAGAGATGAAGAGAGAGATGGAATCAGAA	2340
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QY	2341	GCTTCTCTGCAAAAGGCCAAGAGTGGCTGAAAGTGAAGTCAAGCCCATGTCGCGGAACAT	2400
Db	2339	GCTTCTCTGCAAAAGGCCAAGAGTGGCTGAAAGTGAAGTCAAGCCCATGTCGCGGAACAT	2398
QY	2401	CTCCATCGCGCCAGCAGAGAACTCGGCCAAGCGCGCTCGGTGTGGAGAGAGCGGC	2460
Db	2399	CTCCATCGCGCCAGCAGAGAACTCGGCCAAGCGCGCTCGGTGTGGAGAGAGCGGC	2458
QY	2461	CAGCCAGCTACGGTGCAGAACCTCGGGCCAGCTGCGAGCGCTGTACAGCGAGATGGA	2520
Db	2459	CAGCCAGCTACGGTGCAGAACCTCGGGCCAGCTGCGAGCGCTGTACAGCGAGATGGA	2518

QY	2521	CCCCGAGGAGCGGCTGCGCTTTCGCCACTACCGGCGCACTTGGCGGCCGACATGAAGACGCA	2580
Db	2519	CCCCGAGGAGCGGCTGCGCTTTCGCCACTACCGGCGCACTTGGCGGCCGACATGAAGACGCA	2578
QY	2581	CCTGGAACCGGCGCTGCTGCTGAGCTGGGCGCGAGCGCGCGCGGGGCTCCGTGGGAGG	2640
Db	2579	CCTGGAACCGGCGCTGCTGCTGAGCTGGGCGCGAGCGCGCGCGGGGCTCCGTGGGAGG	2638
QY	2641	CAAAAGCCGACCTGAGGCTGCGGAGGCCCCCGAGGGCGTCCGAGCGAGCACCA	2700
Db	2639	CAAAAGCCGACCTGAGGCTGCGGAGGCCCCCGAGGGCGTCCGAGCGAGCACCA	2698
QY	2701	CCGCGACCGCAGACAGACAGACAGACCCCGCGCGGGGGAACAGACCGAGAGGCCCC	2760
Db	2699	CCGCGACCGCAGACAGACAGACAGACCCCGCGCGGGGGAACAGACCGAGAGGCCCC	2758
QY	2761	GAAGCGGAGAGCGGGGAGGCCCCGCTGCCGAGGAGCGCGCGCGCGCGCGCGAGGAGCC	2820
Db	2759	GAAGCGGAGAGCGGGGAGGCCCCGCTGCCGAGGAGCGCGCGCGCGCGCGAGGAGCC	2818
QY	2821	CAGCAAGGAGCGCGGGGCCCCCGAGGCGCGAGCGCGCGCGCGCGAGGCCCCAGGCCC	2880
Db	2819	CAGCAAGGAGCGCGGGGCCCCCGAGGCGCGAGCGCGCGCGCGCGAGGCCCCAGGCCC	2878
QY	2881	CGAGGCGCGCGCGCGCGCACACCGCGCGCGCTCCCGGAGGAGCGCGCGCGCGAGGAGCC	2940
Db	2879	CGAGGCGCGCGCGCGCGCACACCGCGCGCGCTCCCGGAGGAGCGCGCGCGCGAGGAGCC	2938
QY	2941	CCGAGCGCAACCGCGCGCACCGCGCACAGGATCCGAGCAAGAGTGGCGCGCGCGCGAGGG	3000
Db	2939	CCGAGCGCAACCGCGCGCACCGCGCACAGGATCCGAGCAAGAGTGGCGCGCGCGAGGG	2998
QY	3001	CGAGCGCGCGCGCGCGCACCGCGCGCGCCCCCGAGCGGGGCCCCCGGAGCGG	3060
Db	2999	CGAGCGCGCGCGCGCGCACCGCGCGCGCCCCCGAGCGGGGCCCCCGGAGCGG	3058
QY	3061	GGAGGAGCGCGCGCGCGCACCGCGCGCGCAACAGGCGCAGCGCTGCTACAGAGGCTGT	3120
Db	3059	GGAGGAGCGCGCGCGCGCACCGCGCGCGCAACAGGCGCAGCGCTGCTACAGAGGCTGT	3118
QY	3121	GGAGAGAGAGACCAACCGAGAGAGAGCGCCACCGAGAGAGAGGCTGAGATAGTGAAGCCGA	3180
Db	3119	GGAGAGAGAGACCAACCGAGAGAGAGCGCCACCGAGAGAGAGGCTGAGATAGTGAAGCCGA	3178
QY	3181	CAAGGAAAAGGAGCTCCGGAAACACAGCGCGCGGAGCCACACTGTGACTGAGAGACCAAG	3240
Db	3179	CAAGGAAAAGGAGCTCCGGAAACACAGCGCGCGGAGCCACACTGTGACTGAGAGACCAAG	3238
QY	3241	TGGGACTGTGACTGTGGGTCCCATGCACACACTGCGCCAGCACCTGTCTCCAGAGGTGA	3300
Db	3239	TGGGACTGTGACTGTGGGTCCCATGCACACACTGCGCCAGCACCTGTCTCCAGAGGTGA	3298
QY	3301	GGAGACCGCAGAGGATGAGAGCAATCAGCGGAACGTCACTCGCATGGGCAATCAGGCCCC	3360
Db	3299	GGAGACCGCAGAGGATGAGAGCAATCAGCGGAACGTCACTCGCATGGGCAATCAGGCCCC	3358
QY	3361	AGACCCGAAACATATTGTATACATATCCAGTGTGTGAGCGGCGCTTGTGGAGAGCCAC	3420
Db	3359	AGACCCGAAACATATTGTATACATATCCAGTGTGTGAGCGGCGCTTGTGGAGAGCCAC	3418
QY	3421	GCTCGTTCCTGAGTGTGAG	3480
Db	3419	GCTCGTTCCTGAGTGTGAG	3478
QY	3481	AGCGGATGAGTGTGAG	3540
Db	3479	AGCGGATGAGTGTGAG	3538
QY	3541	TTTAAAGCCCAACCACTGCTCGCGCTTCTGCGCACTACATCGTGACCATGAGGTACTT	3600
Db	3539	TTTAAAGCCCAACCACTGCTCGCGCTTCTGCGCACTACATCGTGACCATGAGGTACTT	3598
QY	3601	CGAGGTGTGCTTCTCGTGTGCTCATCGGCTTGAGCAGCATCGCCCTGGGCTGTGAGGAGCCC	3660

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Qy 3721 TGTCTTTACCTTTGAGATGGTGATTAAGATGATCGACTTGGGACTGCTGCTTCAACCTGG 3780
Db 3719 TGTCTTTACCTTTGAGATGGTGATTAAGATGATCGACTTGGGACTGCTGCTTCAACCTGG 3778
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Qy 4861 CCTCTTTTCGAGCTGCGCGCTGATCAAGCTGCTCCGCGAGGGCTACACCATCCGCAATCT 4920
Db 4847 CCTCTTTTCGAGCTGCGCGCTGATCAAGCTGCTCCGCGAGGGCTACACCATCCGCAATCT 4906
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Qy 5041 TGACACAGCATCAACCGCCACAACTTTCCGGAAGTGTTCGGAAGCTTTTTCGAAAGCTGCTGT 5100
Db 5027 TGACACAGCATCAACCGCCACAACTTTCCGGAAGTGTTCGGAAGCTTTTTCGAAAGCTGCTGT 5086
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Db 5087 GTTCAGGAGCGCCACCGGGGAGGCTGGCACGAGATCATGCTGCTCCCTGCGCTGAGCAACCA 5146
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Qy 5761 AACCA CAGAGACCATGACAGGCTCTGAGGCTCTCCAGATGGCTCTCTGTC 5820
Db 5747 AACCA CAGAGACCATGACAGGCTCTGAGGCTCTCTCCAGATGGCTCTCTGTC 5806

QY	5821	CTGTGTTCCACCTCTCTGAAGGCCACCCCTGTAGAGCAGACACAGCGGGCTGTGCTCCGAGGAGC	5881
DB	5807	CTGTGTTCCACCTCTGAAGGCCACCCCTGTAGAGCAGACACAGCGGGCTGTGCTCCGAGGAGC	5866
QY	5881	CCGGGTGTTTCCCTTCGACAGAGAGTTCCACCTCCCTCAGCAATGGCGGGGCATACAAAA	5940
DB	5867	CCGGGTGTTTCCCTTCGACAGAGAGTTCCACCTCCCTCAGCAATGGCGGGGCATACAAAA	5926
QY	5941	CCAAGAGAGTGCCATCAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC	6000
DB	5927	CCAAGAGAGTGCCATCAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC	5986
QY	6001	CCATGAGGCCAGGCCACCCCTGGAGAGTGGCCATCTCCACAGATCTCTGTGGGGCGGTC	6060
DB	5987	CCATGAGGCCAGGCCACCCCTGGAGAGTGGCCATCTCCACAGATCTCTGTGGGGCGGTC	6046
QY	6061	AGGAGCACTGGCTGTGGACGTTTCAGATGTCAGAGATTAACCCGGAGGGGCCCTCATGGGA	6120
DB	6047	AGGAGCACTGGCTGTGGACGTTTCAGATGTCAGAGATTAACCCGGAGGGGCCCTCATGGGA	6106
QY	6121	GCCCAGGCTGGGCTGGAGAGCCAGGGTTCGAGCGGCTTCCATGCCCGCCTTCGCGCCGA	6180
DB	6107	GCCCAGGCTGGGCTGGAGAGCCAGGGTTCGAGCGGCTTCCATGCCCGCCTTCGCGCCGA	6166
QY	6181	GACTCAGGCCGTTCACAGATGCCAGCCCATGAGCGCTTCCATCTCAGCGTGGCCCGAGG	6240
DB	6167	GACTCAGGCCGTTCACAGATGCCAGCCCATGAGCGCTTCCATCTCAGCGTGGCCCGAGG	6226
QY	6241	GCCCCTGGGACTCATCTTTGACGACCAACCCCGGACCGCCACCCCTAGCCAGAGCGTC	6300
DB	6227	GCCCCTGGGACTCATCTTTGACGACCAACCCCGGACCGCCACCCCTAGCCAGAGCGTC	6286
QY	6301	GTCCGACCCACACACACACGCTGCCACCGCGGAGGGAACGAAACAGAGTCTCCTGGA	6360
DB	6287	GTCCGACCCACACACACACGCTGCCACCGCGGAGGGAACGAAACAGAGTCTCCTGGA	6346
QY	6361	GAAGGGGCCAGGCTGTCTGCCATATGGATGGCGCACCAAGCAGTCTGTGGGCGCGG	6420
DB	6347	GAAGGGGCCAGGCTGTCTGCCATATGGATGGCGCACCAAGCAGTCTGTGGGCGCGG	6406
QY	6421	GCTGCCCGCGGAGAGGGGCTCAGGCTGCCCGGGGGAACGAGAGCGCGGACGAGCG	6480
DB	6407	GCTGCCCGCGGAGAGGGGCTCAGGCTGCCCGGGGGAACGAGAGCGCGGACGAGCG	6466
QY	6481	GGGCGGCTCCAGAGCGGAGGAGCCCTCATCTCTCTCTCGGAGAGCAGCGTCTTA	6540
DB	6467	GGGCGGCTCCAGAGCGGAGGAGCCCTCATCTCTCTCTCGGAGAGCAGCGTCTTA	6526
QY	6541	CTCTTGGAACGGCTTTGGGGGCCGTGAGCCCGGAAGCCCAAGCCCTCTCCTCAGAGCCA	6600
DB	6527	CTCTTGGAACGGCTTTGGGGGCCGTGAGCCCGGAAGCCCAAGCCCTCTCCTCAGAGCCA	6586
QY	6601	CCCAAAGTCCCAACAGCTGGCCAGAGCGGGACCCCAACCCAGCCCTCCTCCTCAGAGCCA	6660
DB	6587	CCCAAAGTCCCAACAGCTGGCCAGAGCGGGACCCCAACCCAGCCCTCCTCCTCAGAGCCA	6646
QY	6661	GAATGGAGCCCTTGCTGTCAACATCTGGTGTAGCACCCCGCGCGGTGGCGGAG	6720
DB	6647	GAATGGAGCCCTTGCTGTCAACATCTGGTGTAGCACCCCGCGCGGTGGCGGAG	6706
QY	6721	GCAAGTCCCCCAGAGCGCCCTGACTCCCGCCCGCAGATCATCTTAAGACGGGCCAATCT	6780
DB	6707	GCAAGTCCCCCAGAGCGCCCTGACTCCCGCCCGCAGATCATCTTAAGACGGGCCAATCT	6766
QY	6781	CTCACCATCCACTTTCGCGCGGGCTCAGACCAAGCTCTCTGCTTCTCTCCAGGCGCGCT	6840
DB	6767	CTCACCATCCACTTTCGCGCGGGCTCAGACCAAGCTCTCTGCTTCTCTCCAGGCGCGCT	6826
QY	6841	CAGCGGTGGGCTTTCGAAACAAACGCTCTGTGTGAGAGACCCCTCTCAGCCAGCCCT	6900
DB	6827	CAGCGGTGGGCTTTCGAAACAAACGCTCTGTGTGAGAGACCCCTCTCAGCCAGCCCT	6886

QY	6901	GGCCCTCGCTCTCGAATTGGCTCTGACCTTACCTGCGGCGAGCGTCTGACAGTGAAGGC	6961
Db	6887	GGCCCTCGGCTCTCGAATTGGCTCTGACCTTACCTGCGGCGAGCGTCTGACAGTGAAGGC	6946
QY	6961	CTCTGTCCACGCGCTTGGCTGAGGACAGCGTCACCTTTTCGAGGAGGCTGTGACCAACAATC	7020
Db	6947	CTCTGTCCACGCGCTTGGCTGAGGACAGCGTCACCTTTTCGAGGAGGCTGTGACCAACAATC	7006
QY	7021	GGGCGCTCTCTCCAGGACTTCTTACGTGTCTCTCCTGACCTCCCAAGTCTCACCTCTCTCG	7080
Db	7007	GGGCGCTCTCTCCAGGACTTCTTACGTGTCTCTCCTGACCTCCCAAGTCTCACCTCTCTCG	7066
QY	7081	CGGCGTGCCCAAGCGTTTACCACTGCACCCCTGGGACTCAGCTCGGGTGGCCGAGCAGGCA	7140
Db	7067	CGGCGTGCCCAAGCGTTTACCACTGCACCCCTGGGACTCAGCTCGGGTGGCCGAGCAGGCA	7126
QY	7141	CAGCTACCAACACCTCTACCAAGACCACTGGTGTAGTGCACCGTACCGCTTCAGACGC	7200
Db	7127	CAGCTACCAACACCTCTACCAAGACCACTGGTGTAGTGCACCGTACCGCTTCAGACGC	7186
QY	7201	CTGCATGACGAGCGCTGTGTTTCAGTGGATGATGTTTTATCATCCACAGGGGCACTCGG	7260
Db	7187	CTGCATGACGAGCGCTGTGTTTCAGTGGATGATGTTTTATCATCCACAGGGGCACTCGG	7246
QY	7261	CCCTCGGGGAGGCGCTTGCCCACTTGTGTGAGGCTCCTGTGGCCCTCCTCCTCCCTCCT	7320
Db	7247	CCCTCGGGGAGGCGCTTGCCCACTTGTGTGAGGCTCCTGTGGCCCTCCTCCTCCCTCCT	7306
QY	7321	CCCTCTTTTACTCTTAGACGAGCAATAAGACCCCTGTGTTGAGTGTACGTACCGC	7376
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Db	1	GGGGCGGCGGCTGCGGCGGTGGGGCGGGCGGAGGTGCGGCTGCGGTGCCGGCGGCTCCG	59
QY	61	GCTGTCTCGCTCTGAGCGCGTGGCGCGCCCGCGCGCTTCTCCTGCGGGGCGGCTGGGCGG	120
Db	60	GCTGTCTCGCTCTGAGCGCGCTTGGCGCGCCCGCGCGCTTCTCCTGCGGGGCGGCTGGGCGG	118
QY	121	GGGATGCACGGGGGCGCGGAGCGCATGGTCCGCTTCGGGGGACGAGCTGGGCGGCGCTA	180
Db	119	GGGATGCACGGGGGCGCGGAGCGCATGGTCCGCTTCGGGGGACGAGCTGGGCGGCGCTA	178
QY	181	TGAGGCGCCCGCGCGCGAGAGCGGGCGCCCGGGGCGGCGGGCGCGGGGCGGGGCGCC	240
Db	179	TGAGGCGCCCGCGCGCGAGAGCGGGCGCCCGGGGCGGCGGGCGCGGGGCGGGGCGCC	238

Qy	241	GGGTCCGGGGGGCTGCAGCCCGGCCAGCGGGTCCTCTACAAGCAATCGATCGCGAGCG	300
Db	239	GGGTCCCGGGGGGCTGCAGCCCGGCCAGCGGGTCCTCTACAAGCAATCGATCGCGAGCG	298
Qy	301	CGCGGGACCAATGGCGCTGTATACAACCCCATCCCGGTCAAGCAGNACTGCTTCAACGTCAA	360
Db	299	CGCGGGACCAATGGCGCTGTATACAACCCCATCCCGGTCAAGCAGNACTGCTTCAACGTCAA	358
Qy	361	CCGCTCGCTCTTTCGCTTTTCAGCGAGGACAACGTCGTCGCGAAATACGCGAAGCGCATCAC	420
Db	359	CCGCTCGCTCTTTCGCTTTTCAGCGAGGACAACGTCGTCGCGAAATACGCGAAGCGCATCAC	418
Qy	421	CGAGTGGCCTCCATTTCGAGTATATGATTCCTGGCCACCATCATCGCCAACTGCATCGTGCT	480
Db	419	CGAGTGGCCTCCATTTCGAGTATATGATTCCTGGCCACCATCATCGCCAACTGCATCGTGCT	478
Qy	481	GGCCCTGGAGCAGCACCTCCCTGATGGGACAAAACGCCCATGTCGAGCGGCTGGACGA	540
Db	479	GGCCCTGGAGCAGCACCTCCCTGATGGGACAAAACGCCCATGTCGAGCGGCTGGACGA	538
Qy	541	CACGGAGCCATTTCATCGGGATCTTTTGCTTCGAGCGAGGGATCAAAATCATCGCTCT	600
Db	539	CACGGAGCCATTTCATCGGGATCTTTTGCTTCGAGCGAGGGATCAAAATCATCGCTCT	598
Qy	601	GGGCTTTGCTTCTTCCAAGGCGCTTACCTGCGGAACGGCTGGAACTCATGGACTTCGT	660
Db	599	GGGCTTTGCTTCTTCCAAGGCGCTTACCTGCGGAACGGCTGGAACTCATGGACTTCGT	658
Qy	661	GGTCGTCCTCACAGGGATCTCTTGGCCAGCGCTGGAACTGACTTTCGACCTGGGAACATGAG	720
Db	659	GGTCGTCCTCACAGGGATCTCTTGGCCAGCGCTGGAACTGACTTTCGACCTGGGAACATGAG	718
Qy	721	GGCTGCGGTGCTGAGGCCCTCGAAGCTGGTGTCTGGGATTCGAAGTTTCAGAGTGGT	780
Db	719	GGCTGCGGTGCTGAGGCCCTCGAAGCTGGTGTCTGGGATTCGAAGTTTCAGAGTGGT	778
Qy	781	GCTCAAGTCCATCATGAAGGCCATGCTTCACACTCCTGCAGATTTGGGCTGCTCTCTTCTT	840
Db	779	GCTCAAGTCCATCATGAAGGCCATGCTTCACACTCCTGCAGATTTGGGCTGCTCTCTTCTT	838
Qy	841	TGCCATCCTCATGTTTGCCATCATATTGGCTGGAGTTCTAATGGGCAAGTTCCACAAGGC	900
Db	839	TGCCATCCTCATGTTTGCCATCATATTGGCTGGAGTTCTAATGGGCAAGTTCCACAAGGC	898
Qy	901	CTGTTTTCCCAACAGCACAGATGCGGAGCCGTTGGGTGACTTCCCCTGTGGCAGGAGGC	960
Db	899	CTGTTTTCCCAACAGCACAGATGCGGAGCCGTTGGGTGACTTCCCCTGTGGCAGGAGGC	958
Qy	961	CCAGCCCGGCTGTGCGAGGGCGACACTGAGTGC CGGGAGTACTGGCCAGGACCCAACTT	1020
Db	959	CCAGCCCGGCTGTGCGAGGGCGACACTGAGTGC CGGGAGTACTGGCCAGGACCCAACTT	1018
Qy	1021	TGGCATCAACCACTTTGACAAATATCCTGTTTGGCATCTTGACGGTGTTCAGTGCATCAC	1080
Db	1019	TGGCATCAACCACTTTGACAAATATCCTGTTTGGCATCTTGACGGTGTTCAGTGCATCAC	1078
Qy	1081	CATGGAGGGCTGGACTGACATCTCTATATATACAAACGATGCGCCCGGCAACACCTGGAA	1140
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Qy	1141	CTGGCTCTACTTTCATCCCTCTCATCATCATCGGCTCCTTCTTATGCTCAACCTGGTGCT	1200
Db	1139	CTGGCTCTACTTTCATCCCTCTCATCATCATCGGCTCCTTCTTATGCTCAACCTGGTGCT	1198
Qy	1201	GGGCGTGCTCTCGGGGAGTTTGGCAAGGACGAGAGGGTGGAGAACCGCCGCGCTT	1260
Db	1199	GGGCGTGCTCTCGGGGAGTTTGGCAAGGACGAGAGGGTGGAGAACCGCCGCGCTT	1258
Qy	1261	CCTGAAGCTGCGCGGACGACAGATCGAGCGAGAGCTCAACGGGTACTCTGAGTGGAT	1320
Db	1259	CCTGAAGCTGCGCGGACGACAGATCGAGCGAGAGCTCAACGGGTACTCTGAGTGGAT	1318

Qy	1321	CTTCAAGCGCGAGAGAGTCAATGCTGGCCGAGAGAGACAGAAATGCAGAGAGAAAGTCCCC	1380
Db	1319	CTTCAAGCGCGAGAGAGTCAATGCTGGCCGAGAGAGGACAGAAATGCAGAGAGAAAGTCCCC	1378
Qy	1381	TTTGGACGTCTGAAGAGACGGCCACCAAGAAAGACAGAAATGCACCTGATCCACGCAGA	1440
Db	1379	TTTGGACGTCTGAAGAGACGGCCACCAAGAAAGACAGAAATGCACCTGATCCACGCAGA	1438
Qy	1441	GGAGGGAGAGAGACCGGTTTCAGATCTCTGTGCTGTTGGATCCCCCTTCGCCCGCGCCAG	1500
Db	1439	GGAGGGAGAGACCGGTTTCAGATCTCTGTGCTGTGGATCCCCCTTCGCCCGCGCCAG	1498
Qy	1501	CCTCAAGAGCGGGAAGACAGAGAGCTGTCATATCTTCGAGAGAAGAGAAAGATGTTCCG	1560
Db	1499	CCTCAAGAGCGGGAAGACAGAGAGCTGTCATATCTTCGAGAGAAGAGAAAGATGTTCCG	1558
Qy	1561	GTTTTTTATCCGGCGCATGTGAAGGCTCAGAGCTTCTACTGGGTGCTGTGTGCGTGGT	1620
Db	1559	GTTTTTTATCCGGCGCATGTGAAGGCTCAGAGCTTCTACTGGGTGCTGTGTGCGTGGT	1618
Qy	1621	GGCCCTGAAACACACTGTGTGGCCATGTTGCATTAACAACGCCGCGCGGCTTACCAC	1680
Db	1619	GGCCCTGAAACACACTGTGTGGCCATGTTGCATTAACAACGCCGCGCGGCTTACCAC	1678
Qy	1681	GACCTGTATTTGACAGAGTTGTTTTCCTGGGTCTCTTCCCTCACAGAGATGCTCCGTAA	1740
Db	1679	GACCTGTATTTGACAGAGTTGTTTTCCTGGGTCTCTTCCCTCACAGAGATGCTCCGTAA	1738
Qy	1741	GATGTATGGCTGGGCGCCAGAGACTACTTCGGGTCTCTCTCAACTGCTTCGACTTTGG	1800
Db	1739	GATGTATGGCTGGGCGCCAGAGACTACTTCGGGTCTCTCTCAACTGCTTCGACTTTGG	1798
Qy	1801	GGTCATCGTGGGAGCGTCTTTCAAGTGGTCTGGCGCGCCATCAAGCGCGGAAAGCTCCTT	1860
Db	1799	GGTCATCGTGGGAGCGTCTTTGAGTGGTCTGGCGCGCCATCAAGCGCGGAAAGCTCCTT	1858
Qy	1861	TGGGATCAGTGTGCTGGCGGCCCTTCGCCCTGCTGAGAGATCTTCAAAAGTCACGAAGTACTG	1920
Db	1859	TGGGATCAGTGTGCTGGCGGCCCTTCGCCCTGCTGAGAGATCTTCAAAAGTCACGAAGTACTG	1918
Qy	1921	GAGCTCCCTGGGAACTGTGTGTCTCCCTGCTGAAGTCCATGAAGTCCATCATCAGCCT	1980
Db	1919	GAGCTCCCTGGGAACTGTGTGTCTCCCTGCTGAAGTCCATGAAGTCCATCATCAGCCT	1978
Qy	1981	GCTCTTCTGCTCTTCTCTGTTTCAATTGTGTCCTTCGCCCTGCTGGGATGCAGCTGTTGG	2040
Db	1979	GCTCTTCTGCTCTTCTCTGTTTCAATTGTGTCCTTCGCCCTGCTGGGATGCAGCTGTTGG	2038
Qy	2041	GGGACAGTTCAACTTCAGGATGAGACTCCCAACAACAACTTCGACACCTTCCTCGCCG	2100
Db	2039	GGGACAGTTCAACTTCAGGATGAGACTCCCAACAACAACTTCGACACCTTCCTCGCCG	2098
Qy	2101	CATCCTCACTGTTCTTCAGATCTGACGGGAGAGGACTGGAATGCAGTGTATATCAGG	2160
Db	2099	CATCCTCACTGTTCTTCAGATCTGACGGGAGAGGACTGGAATGCAGTGTATATCAGG	2158
Qy	2161	GATCGAATCGCAAGCGGCGTTCAGAAAGCATGTTCTCGTCTCTTTTACTTCAATTGTCCT	2220
Db	2159	GATCGAATCGCAAGCGGCGTTCAGAAAGCATGTTCTCGTCTCTTTTACTTCAATTGTCCT	2218
Qy	2221	GACACTGTTCCGAACTACACTCTGCTGAAATGTTCTTCGGCCATCGCTGTGACAACT	2280
Db	2219	GACACTGTTCCGAACTACACTCTGCTGAAATGTTCTTCGGCCATCGCTGTGACAACT	2278
Qy	2281	GGCCAAACGCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGAGAGCCCAATCGAA	2340
Db	2279	GGCCAAACGCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGAGAGCCCAATCGAA	2338
Qy	2341	GCTTGTCTTCGAAAGGCCAAAGATGGCTGAAGTCAGCCCACTGCTCCCGCGAACAT	2400
Db	2339	GCTTGTCTTCGAAAGGCCAAAGATGGCTGAAGTCAGCCCACTGCTCCCGCGAACAT	2398
Qy	2401	CTCCATCGCGCGCAGGCGAGCAGAACTCGGCCAAAGGCGCGCTCGGTGTGGGAGCAGCGGGC	2460

QY	4621	GATGATGAAGTTCTATGATGAAACCCCTATAGTAGTACGAGCTGATGCTGAAATGCCTGAACAT	4680
Db	4607	GATGATGAAGTTCTATGATGAAACCCCTATAGTAGTACGAGCTGATGCTGAAATGCCTGAACAT	4666
QY	4681	CGTGTTACACATCCATGTTCTCCATGGAATCGGTGCTGGAAGATCATCGCCTTTGGGGTGCT	4740
Db	4667	CGTGTTACACATCCATGTTCTCCATGGAATCGGTGCTGGAAGATCATCGCCTTTGGGGTGCT	4726
QY	4741	GAACTATTTTCAGAGATGCTCGGAATGCTTTTGACTTTGTCACTGTGTGGGAAGTATTAC	4800
Db	4727	GAACTATTTTCAGAGATGCTCGGAATGCTTTTGACTTTGTCACTGTGTGGGAAGTATTAC	4786
QY	4801	TGATATTTTAGTAAACAGAGATTTGGGAAACGAAACAATTTTCACTCACTCACTCACTCCG	4860
Db	4787	TGATATTTTAGTAAACAGAGATTTGGGAAACGAAACAATTTTCACTCACTCACTCACTCCG	4846
QY	4861	CCCTTTTCGAGCTCGCGGCTGATCAAGCTGCTCCGCGAGGGCTACACCATCCGCACTCT	4920
Db	4847	CCCTTTTCGAGCTCGCGGCTGATCAAGCTGCTCCGCGAGGGCTACACCATCCGCACTCT	4906
QY	4921	GCTGTGACCTTTGTCTCAGTCCCTTCAAGGCCCTGCCCCCTAGCTGTCTGCTCACTTGCCAT	4980
Db	4907	GCTGTGACCTTTGTCTCAGTCCCTTCAAGGCCCTGCCCCCTAGCTGTCTGCTCACTTGCCAT	4966
QY	4981	GCTGTTCTTCTATCACTGACCATCACTGCGCATGCGAGTGTGTTGGGAATATTCCTCGGATGA	5040
Db	4967	GCTGTTCTTCTATCACTGACCATCACTGCGCATGCGAGTGTGTTGGGAATATTCCTCGGATGA	5026
QY	5041	TGACACCGCATCAACCGGCACACACACTTCCCGAGCTTTTTCGACGCCCTGATGCTGT	5100
Db	5027	TGACACCGCATCAACCGGCACACACACTTCCCGAGCTTTTTCGACGCCCTGATGCTGT	5086
QY	5101	GTTTCAGAGCGCCACGCGGGAGGCTTGGCACGAGATCATGCTGTCTGCTGCTGAGCAACCA	5160
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QY	5161	GGCTGTGATGAGCAGGCGCAATGCGCACCGAGTGTGGAAGTGACTTTGCGCTACTTCTACTT	5220
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QY	5221	CGTCTCCTTCTATCTTCTGTGCTCTTCTGTGATGTTGAACTCTTTGTGGCTGTGATCAT	5280
Db	5207	CGTCTCCTTCTATCTTCTGTGCTCTTCTGTGATGTTGAACTCTTTGTGGCTGTGATCAT	5266
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QY	5341	GTTTCATCCGGGTCTGGGCTGAATAAGACCCGGCTGCGTGTGGCGGCATCAGTTTACAATGA	5400
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QY	5401	CATGTTTGAGATGCTGAAACACATGTTCCCGCTCTGGGCTGGGAGAAATGCCCTGC	5460
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QY	5461	TCCAGTTGCTTAAAGCGCTGTTTGCATGAACAATGCCCATCTCCAAACGAGGACATGAC	5520
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QY	5701	GATGACAGTGGGAAGGTTTATGACAGCTCTGATGATATTTTGACTTCTACAGCAGAACAA	5760
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QY	5761	AACCCACAGAGACCAAGATGACAGGCTCTCTGAGGCTCTCCAGATGGGTCTCTGTGTC	5820
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QY	5821	CTGTGTTCCAACCTCTGAAGGCCACCTGGAGCAGACAACAGCCGGCTGTGTCCGAGGAGC	5880
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QY	6121	GCCCCAGCTGGGCTGGAGAGCCAGGGCTCAGCGGCTCTCATGCCCGCTTCGCGCCGA	6180
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QY	6181	GACTCAGCCCGTCACAGATGCCCCCATGAAAGCGCTCCATCTCCACGCTGCGCCAGCG	6240
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QY	6301	GTGCGACCAACCAACACCGCTGCCACCGCCGACAGGACAGGAAGCAGAGTCCCTGGA	6360
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QY	6361	GAAAGGCGCCAGCTGTCTGCGGATATGATGGCGGCAACCAAGCAGTGTGTGGGCGCGG	6420
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QY	6481	GGGCGCGTCCCAAGGAGCGGAGCGGCTCATCTCTCTCGGAGAGCAGCGCTTCTA	6540
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QY	6601	CCCAAGCTGCCAAACAGCTGGCGCAGAGCGGGACCCCAACCAACAGGAGATGGTTCGGT	6660
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QY	6661	GAAAGGAGCGCTTGTCTGTCAACATCTGTGTAGTACACCCCGCGCGGCGGGGAG	6720
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QY	6721	GCAGCTTCCCGCAGACGCCCTCTGATCTCCCGCGCCAGCATCACCTACAAGACGCGCACTC	6780
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AUTHORS 1. (bases 1 to 7266)
TITLE Franco.R., Chen,A.Ru.Sun. and Shuey,D.John.
JOURNAL Nucleic acid encoding human neuronal calcium channel subunits
FEATURES Patent: US 6140485-A 1 31-OCT-2000;
Location/Qualifiers
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Db 61 GGGCGGGGATGACGCGGGGCCCGGAGCCATGGTTCGGTTCGGGACAGCTGGCGG 120
Qy 175 CCGCTATGAGGCCCGCGCGGAGACGCGGCCCGGGGCGCGGCGCGGCGG 234

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Qy 355 CGTCAA CGCTCGCTCTTCTGCTTTCAGGAGGACCAAGCTCGTCGCAAAATACGGAAGCG 414
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1915	Qy	GTACTGGAGCTCCCTGCGGAACCTGGTGGTGTCCCTGCTGAACTCCAT	GAAAGTCCATCAT	1974
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1975	Qy	CAGCCTGCTCTTCTTGTCTTCTGTTTCAATGTGGTCTTCCGCTGCT	GGGATGAGCT	2034
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1981	Db	GTTTTGGGGGACAGTTCAACTTTCAGGATGAGACTCCCAACAACCTT	CCACACCTTCCC	2040
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2155	Qy	TCACGGGATCGAATCGCAAGCGCGTTCAGAAAGGATGTTCTGHTCTTT	TACTTTTCAT	2214
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2335	Qy	TCAGAGCTTGCTCTGCAAAAGCCAAAGATGGCTGAAGTCAAGCCCAT	GTCTGCCG	2394
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Qy	2515	GATGGACCCCAGAGCGGCTGCGCTTCGCCACTTAGCGCGCACCTGCGGGCCCCGACATGAA	2574
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DEFINITION Sequence 7 from patent US 6353091.
ACCESSION AR198609
VERSION AR198609.1 GI:20248458

KEYWORDS .

SOURCE Unknown.

ORGANISM

REFERENCE 1 (bases 1 to 7177)

Unclassified.

AUTHORS Lipscombe,D. and Schorge,S.

TITLE Human N-type calcium channel isoform

JOURNAL Patent: US 6353091-A 7 05-MAR-2002;

FEATURES Location/Qualifiers

1..7177

source

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DB |||||
QY 1981 GCTCTTCTTGTCTCTCTCTTCAATGTGTCTTCCGCTCTCTGGGATCGAGTGTGG 2040
DB |||||
QY 2041 GGGACAGTTTCAACTTCCAGATGAGACTCCCAACCAACTTCCGACCTTCCCTCCCGC 2100
DB |||||
QY 2041 GGGACAGTTTCAACTTCCAGATGAGACTCCCAACCAACTTCCGACCTTCCCTCCCGC 2100
DB |||||
QY 2101 CATCTCTCATGTCTTCCAGATCTTGAAGAGGAGCTGGAATGCAGTGAATGATCACGG 2160
DB |||||
QY 2101 CATCTCTCATGTCTTCCAGATCTTGAAGAGGAGCTGGAATGCAGTGAATGATCACGG 2160
DB |||||
QY 2161 GATCGAATCGAAGCGGCTCAGCAAGGCAATGTTCTGCTCTTCTTACTTTCATTTGCTCT 2220
DB |||||
QY 2161 GATCGAATCGAAGCGGCTCAGCAAGGCAATGTTCTGCTCTTCTTACTTTCATTTGCTCT 2220
DB |||||
QY 2221 GACACTGTTTGGAAACTACACTCTCTGTAATGCTTCTTCTGGCCATCGCTGTGGCAACCT 2280
DB |||||
QY 2221 GACACTGTTTGGAAACTACACTCTCTGTAATGCTTCTTCTGGCCATCGCTGTGGCAACCT 2280
DB |||||
QY 2281 GGGCAACGCCCAAGAGCTGACCAAGATGAGAGGAGATGGAAGAGCAAGCCATCAGAA 2340
DB |||||

[illegible][illegible]

QY	4501	CCTGACCGGTACATGCCCAAAACCGCAGTCGTTCCAGTATATAGACGTGGACATTTGT	4560
Db	4489	CCTGACCGGTACATGCCCAAAACCGCAGTCGTTCCAGTATATAGACGTGGACATTTGT	4548
QY	4561	GGTCTCCCGCCCTTTGAATACTTCATCATGGCCATGATAGCCCTCAACACTGTGGTGCT	4620
Db	4549	GGTCTCCCGCCCTTTGAATACTTCATCATGGCCATGATAGCCCTCAACACTGTGGTGCT	4608
QY	4621	GATGATGAAGTTCATATGATGACCCCTATGATAGTACGAGCTGATGCTGAATGCTGAAAT	4680
Db	4609	GATGATGAAGTTCATATGATGACCCCTATGATAGTACGAGCTGATGCTGAATGCTGAAAT	4668
QY	4681	CGTGTTCACATCCATGTTCTCCATGGAAATGCGTGTGAAATCATCGCCTTTGGGGTGCT	4740
Db	4669	CGTGTTCACATCCATGTTCTCCATGGAAATGCGTGTGAAATCATCGCCTTTGGGGTGCT	4728
QY	4741	GAATATTTTACAGATGCTCGAATGTCCTTTGTACTTTGTACTGTTGGGAAGTATTAC	4800
Db	4729	GAATATTTTACAGATGCTCGAATGTCCTTTGTACTTTGTACTGTTGGGAAGTATTAC	4788
QY	4801	TGATATTTTATAGTAACAGAGATTGCGAAACGAAATTTTCATCAACTCAGCTTCTCGG	4860
Db	4789	TGATATTTTATAGTAACAGAGATTGCGAAACGAAATTTTCATCAACTCAGCTTCTCGG	4848
QY	4861	CCTCTTTTCGAGCTGCGCGGTGATCAAGCTGTCCGCCAGGGCTACCATCCGCATCCT	4920
Db	4849	CCTCTTTTCGAGCTGCGCGGTGATCAAGCTGTCCGCCAGGGCTACCATCCGCATCCT	4908
QY	4921	GCTGTGACCTTTGTCAGTCCCTCAAGGCCCTGCCCTACGTGTGCTCATTTGCCAT	4980
Db	4909	GCTGTGACCTTTGTCAGTCCCTCAAGGCCCTGCCCTACGTGTGCTCATTTGCCAT	4968
QY	4981	GCTGTTCCTTCACTACGCCATCATCGGCATGAGGTGTTTGGGAATATTGCCCTCGATGA	5040
Db	4969	GCTGTTCCTTCACTACGCCATCATCGGCATGAGGTGTTTGGGAATATTGCCCTCGATGA	5028
QY	5041	TGACACAGCATCAACGGCCACACAACTTCGCGACGTTTTCGAGCCCTGATGCTCT	5100
Db	5029	TGACACAGCATCAACGGCCACACAACTTCGCGACGTTTTCGAGCCCTGATGCTCT	5088
QY	5101	GTTTCAGGAGCGCACGGGGAGGCTGGCACGAGATCATGCTGCTCCCTCGAGCAACCA	5160
Db	5089	GTTTCAGGAGCGCACGGGGAGGCTGGCACGAGATCATGCTGCTCCCTCGAGCAACCA	5148
QY	5161	GGCTGTGATGAGCGAGGCCAATGCCACCGAGTGTGGAAGTGACTTTGCTACTTCTACTT	5220
Db	5149	GGCTGTGATGAGCGAGGCCAATGCCACCGAGTGTGGAAGTGACTTTGCTACTTCTACTT	5208
QY	5221	CGTCTCCTTCATCTTCCTGCTCCTTTCTGATGTTGAACCTCTTTGTTGGCTGTGATCAT	5280
Db	5209	CGTCTCCTTCATCTTCCTGCTCCTTTCTGATGTTGAACCTCTTTGTTGGCTGTGATCAT	5268
QY	5281	GGACAATTTTGTAGTACCTCAACGGGATCTTTCCATCCTAGGTCTCTACCACTTTGGATGA	5340
Db	5269	GGACAATTTTGTAGTACCTCAACGGGATCTTTCCATCCTAGGTCTCTACCACTTTGGATGA	5328
QY	5341	GTTTCATCGGGTCTGGGCTGAATAGCACCGGCTGCGTGTGGGCGCATTCAGTTACAATGA	5400
Db	5329	GTTTCATCGGGTCTGGGCTGAATAGCACCGGCTGCGTGTGGGCGCATTCAGTTACAATGA	5388
QY	5401	CATGTTTGAGATGCTGAAACACATGTCCTCCCTCTGGGGCTGGGGAAGAAATGCCCTGC	5460
Db	5389	CATGTTTGAGATGCTGAAACACATGTCCTCCCTCTGGGGCTGGGGAAGAAATGCCCTGC	5448
QY	5461	TCGAGTTGCTTACAAGCGCCTGGTTTGGATGAAATGCCCCATCTCCAAACGAGGACATGAC	5520
Db	5449	TCGAGTTGCTTACAAGCGCCTGGTTTGGATGAAATGCCCCATCTCCAAACGAGGACATGAC	5508
QY	5521	TGTTCACTTCACGTCACGCTGATGGCCCTCATCCGACCGGCACTGAGATCAAGCTGGC	5580
Db	5509	TGTTCACTTCACGTCACGCTGATGGCCCTCATCCGACCGGCACTGAGATCAAGCTGGC	5568

QY	5581	CCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGAGTTGAGGAAGGAGATTTCCGTTGT	5640
Db	5569	CCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGAGTTGAGGAAGGAGATTTCCGTTGT	5628
QY	5641	GTGGGCCAATCTGCCCCAGAGACTTTGGACTTCTGTTAGTACCAACCCCATATAGCCCTGATGA	5700
Db	5629	GTGGGCCAATCTGCCCCAGAGACTTTGGACTTCTGTTAGTACCAACCCCATATAGCCCTGATGA	5688
QY	5701	CATGACATGTGGGGAAGGTTTATGACAGTCTGATGATATTTGACTTCTTACAGAGAGAACAA	5760
Db	5689	CATGACATGTGGGGAAGGTTTATGACAGTCTGATGATATTTGACTTCTTACAGAGAGAACAA	5748
QY	5761	AACACACAGAGACAGATGACAGAGGCTCTTGAGAGGCTCTCCAGATGGGTCTCTGTGTC	5820
Db	5749	AACACACAGAGACAGATGACAGAGGCTCTTGAGAGGCTCTCCAGATGGGTCTCTGTGTC	5808
QY	5821	CCTGTTCCACCTCTGAAGGCCACCTTGAGAGACACACGCGGCTCTCTCGAGAGGAGC	5880
Db	5809	CCTGTTCCACCTCTGAAGGCCACCTTGAGAGACACACGCGGCTCTCTCGAGAGGAGC	5868
QY	5881	CCGGGTTTTCTTCGACAGAGAGTTCCACTCTCAGCAATGGCGGGGCTCATACAAA	5940
Db	5869	CCGGGTTTTCTTCGACAGAGAGTTCCACTCTCAGCAATGGCGGGGCTCATACAAA	5928
QY	5941	CCAAGAGAGTGGCATCAAGAGTCTGCTCTCTGGGGCACTCAAGAGACCCAGATGACCC	6000
Db	5929	CCAAGAGAGTGGCATCAAGAGTCTGCTCTCTGGGGCACTCAAGAGACCCAGATGACCC	5988
QY	6001	CCATGAGGCGCAGGCCACCCCTTGAGAGGCTGCCACTCCACAGAGATCCCTGTGGGGCGGTC	6060
Db	5989	CCATGAGGCGCAGGCCACCCCTTGAGAGGCTGCCACTCCACAGAGATCCCTGTGGGGCGGTC	6048
QY	6061	AGGAGCACTGGCTGTGAGCGTTTTCAGATGACAGAGATAAACCCGAGGGGCTTGATGGGA	6120
Db	6049	AGGAGCACTGGCTGTGAGCGTTTTCAGATGACAGAGATAAACCCGAGGGGCTTGATGGGA	6108
QY	6121	GCCTCAGCTGGGCTGGAGAGCCAGGCTCGAGCGGCTCCATGCCCCCGCTTGGGGCCGA	6180
Db	6109	GCCTCAGCTGGGCTGGAGAGCCAGGCTCGAGCGGCTCCATGCCCCCGCTTGGGGCCGA	6168
QY	6181	GACTCAGCCGCTCAGATGCGGCCCATGAAGCGCTCCATCTCCACGCTGGCCAGCG	6240
Db	6169	GACTCAGCCGCTCAGATGCGGCCCATGAAGCGCTCCATCTCCACGCTGGCCAGCG	6228
QY	6241	GCCTCCTGCGACTCATCTTTTTCAGACACCCCGGACCGCCACCCCTTACCCAGCGCTC	6300
Db	6229	GCCTCCTGCGACTCATCTTTTTCAGACACCCCGGACCGCCACCCCTTACCCAGCGCTC	6288
QY	6301	GTGCAACCAACCAACCAACCGCTGCGACCGCGCAGGGACAGAGACGTCCCTGGA	6360
Db	6289	GTGCAACCAACCAACCAACCGCTGCGACCGCGCAGGGACAGAGACGTCCCTGGA	6348
QY	6361	GAAGGGCCCGACCTGTCTGCCGATATGATGCGCGACCAAGCAGCTGTGTGGGGCCGG	6420
Db	6349	GAAGGGCCCGACCTGTCTGCCGATATGATGCGCGACCAAGCAGCTGTGTGGGGCCGG	6408
QY	6421	GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGCGGGGAACGAGAGCGCCGCGAGAGCG	6480
Db	6409	GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGCGGGGAACGAGAGCGCCGCGAGAGCG	6468
QY	6481	GGGCGGCTCCAGAGAGCGGAGGCGCTCATCTCTCTCGGAGAGAGCGCTTCTA	6540
Db	6469	GGGCGGCTCCAGAGAGCGGAGGCGCTCATCTCTCTCGGAGAGAGCGCTTCTA	6528
QY	6541	CTCTCTGCGACCGCTTTTGGGGCGGCTGAGCGCCCGGAGCCCAAGCCCTTCTCAGAGCCA	6600
Db	6529	CTCTCTGCGACCGCTTTTGGGGCGGCTGAGCGCCCGGAGCCCAAGCCCTTCTCAGAGCCA	6588
QY	6601	CCCAACGTCGCCAACAGCTGCGCCAGGAGCGCGGACCCCAACAGGCGAGTGGTTCGT	6660
Db	6589	CCCAACGTCGCCAACAGCTGCGCCAGGAGCGCGGACCCCAACAGGCGAGTGGTTCGT	6631
QY	6661	GAATGGGAGCCCCCTTGTGTCACATCTGTGTGTAGCACCCCCCGGCGGCGGAG	6720

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Db	1261	CCTGAAGCTGCGCGCAGCAGCAGATCGAGCGAGAGCTCAA	CGGCTAC	CTGGAGTGGAT	1320	
Qy	1321	CTTTAAAGCGGAGGAAGTCA	TGCTGGCGCGGAGGAGCAGGAATGC	GAGCAGCAGGAAGTCCCC	1380	
Db	1321	CTTTAAAGCGGAGGAAGTCA	TGCTGGCGCGGAGGAGCAGGAATGC	GAGCAGCAGGAAGTCCCC	1380	
Qy	1381	TTTGGACGTGTGAAGAGAGCGGCC	ACCAAGAAAGACAGAAATG	ACTGATCCACGCAGA	1440	
Db	1381	TTTGGACGTGTGAAGAGAGCGGCC	ACCAAGAAAGACAGAAATG	ACTGATCCACGCAGA	1440	
Qy	1441	GGAGGAGAGGACCGGTTTC	GCAGATCTCTGTGTTGGATCC	CCCTTCCCGCGGCCAG	1500	
Db	1441	GGAGGAGAGGACCGGTTTC	GCAGATCTCTGTGTTGGATCC	CCCTTCCCGCGGCCAG	1500	
Qy	1501	CCTCAAGAGCGGGAAGACAGAGAGCTCGT	CA	TACTTCCGGAGGAAGGAGAGATG	1560	
Db	1501	CCTCAAGAGCGGGAAGACAGAGAGCTCGT	CA	TACTTCCGGAGGAAGGAGAGATG	1560	
Qy	1561	GTTTTTTTATCCGGCGCATGTG	GAAGGCTCAGAGCTTCTACT	TGGGTGGTGC	TGTGCGTGGT	1620
Db	1561	GTTTTTTTATCCGGCGCATGTG	GAAGGCTCAGAGCTTCTACT	TGGGTGGTGC	TGTGCGTGGT	1620
Qy	1621	GGCCCTGAACACACTGTGTGTGGCCATGTGT	GCATTA	CAACACAGCCCGCGCGCTT	ACCAC	1680
Db	1621	GGCCCTGAACACACTGTGTGTGGCCATGTGT	GCATTA	CAACACAGCCCGCGCGCTT	ACCAC	1680
Qy	1681	GACCTGTATTTTCAGAGTTT	TTTTCTTGGGTCTCTTCT	CACAGAGATGTCCCTG	GAA	1740
Db	1681	GACCTGTATTTTCAGAGTTT	TTTTCTTGGGTCTCTTCT	CACAGAGATGTCCCTG	GAA	1740
Qy	1741	GATGTATGGCTGGGGCC	AAGAAGTACTTCCGGTCTCTCT	CACTGCTTCACTTTGG	1800	
Db	1741	GATGTATGGCTGGGGCC	AAGAAGTACTTCCGGTCTCTCT	CACTGCTTCACTTTGG	1800	
Qy	1801	GGTCATCGTGGGAGCGTCTT	TGAAGTGTCTGGCGGCCATCA	AGCCGGAGAGCTCTT	1860	
Db	1801	GGTCATCGTGGGAGCGTCTT	TGAAGTGTCTGGCGGCCATCA	AGCCGGAGAGCTCTT	1860	
Qy	1861	TGGGATCAGTGTCTCGGGCC	TCCGCTCGCTGAGGATCTT	CAAGTCA	CAGAACTG	1920
Db	1861	TGGGATCAGTGTCTCGGGCC	TCCGCTCGCTGAGGATCTT	CAAGTCA	CAGAACTG	1920
Qy	1921	GAGCTCCCTCGGAACCTGGTGGTGTCT	CTGCTGA	ACTCCATGAAGTCCAT	CATCAGCCT	1980
Db	1921	GAGCTCCCTCGGAACCTGGTGGTGTCT	CTGCTGA	ACTCCATGAAGTCCAT	CATCAGCCT	1980
Qy	1981	GCTCTTCTTCTCTCTCTCTCTCT	TTCA	TGTGGTCTTCCGCTCGCTGGGGATG	CAGTGTGG	2040
Db	1981	GCTCTTCTTCTCTCTCTCTCTCT	TTCA	TGTGGTCTTCCGCTCGCTGGGGATG	CAGTGTGG	2040
Qy	2041	GGGACAGTTCAACTTCCAGGATGAGACT	CCCA	CAACCACTTCCGACCTT	CCCTCGCGC	2100
Db	2041	GGGACAGTTCAACTTCCAGGATGAGACT	CCCA	CAACCACTTCCGACCTT	CCCTCGCGC	2100
Qy	2101	CATCTCTCACTGTCTTCCAGATCCT	GACGGGAGAGACTGGA	ATGAGTGA	TGTATCAGG	2160
Db	2101	CATCTCTCACTGTCTTCCAGATCCT	GACGGGAGAGACTGGA	ATGAGTGA	TGTATCAGG	2160
Qy	2161	GATCGAATCGAAGGGGGT	CAGCAAGGCA	TGTTCTGCTCTTTTACT	TCATGTCCT	2220
Db	2161	GATCGAATCGAAGGGGGT	CAGCAAGGCA	TGTTCTGCTCTTTTACT	TCATGTCCT	2220
Qy	2221	GACACTGTTGGGAACTA	CATCTGCTGAATGTCTT	TGCGCCATCGCTG	TGGACAACT	2280
Db	2221	GACACTGTTGGGAACTA	CATCTGCTGAATGTCTT	TGCGCCATCGCTG	TGGACAACT	2280
Qy	2281	GGCAACGCCAAGACTCA	CAAGATGAAGAGAGATGGA	AGACAGTCAATCAGAA	2340	
Db	2281	GGCAACGCCAAGACTCA	CAAGATGAAGAGAGATGGA	AGACAGTCAATCAGAA	2340	
Qy	2341	GCTTGTCTGCAAAAGGCC	CAAAAGATGGCTG	AGCTCAGCCCCATGTCTG	CGCGAACAT	2400
Db	2341	GCTTGTCTGCAAAAGGCC	CAAAAGATGGCTG	AGCTCAGCCCCATGTCTG	CGCGAACAT	2400

QY 2401 CTCATCCGCGCCAGGAGAGAGAACTCGGCCAAGGCGCGTCTCGTGTGGAGAGCAGCGGCG 2460
DB CTCATCCGCGCCAGGAGAGAGAACTCGGCCAAGGCGCGTCTCGTGTGGAGAGCAGCGGCG 2460
QY 2461 CAGCCAGCTACGGCTGCAGAACCTGCGGGCCAGCTGCGAGCGCTGTACAGCGAGATGGA 2520
DB CAGCCAGCTACGGCTGCAGAACCTGCGGGCCAGCTGCGAGCGCTGTACAGCGAGATGGA 2520
QY 2521 CCCGAGGAGCGGCTGCGCTTCGCCACTAGCGGCACCTGCGGCCCGACATGAAGACGCA 2580
DB CCCGAGGAGCGGCTGCGCTTCGCCACTAGCGGCACCTGCGGCCCGACATGAAGACGCA 2580
QY 2581 CTTGGAACCGGCGCTGTGTGTGAGCTGTGGGCGGGA CGGCGCGCGGGGCGCCGTGTGGAGG 2640
DB CTTGGAACCGGCGCTGTGTGTGAGCTGTGGGCGGGA CGGCGCGCGGGGCGCCGTGTGGAGG 2640
QY 2641 CAAGCCCGACCTGAGGCTGCGGAGGCGCCCGGAGGGCGTGACCTCCGCGCAGGACCA 2700
DB CAAGCCCGACCTGAGGCTGCGGAGGCGCCCGGAGGGCGTGACCTCCGCGCAGGACCA 2700
QY 2701 CCGGCACCGGCAAGACCAAGACCCCGCGCGGGGGGACAGACCCGAGCAGAGGCGCCC 2760
DB CCGGCACCGGCAAGACCAAGACCCCGCGCGGGGGGACAGACCCGAGCAGAGGCGCCC 2760
QY 2761 GAAGCGGAGAGCGGGAGCCCGGTGCCCGGGAGGAGCGCGCGCCGACCGCACCA 2820
DB GAAGCGGAGAGCGGGAGCCCGGTGCCCGGGAGGAGCGCGCGCCGACCGCACCA 2820
QY 2821 CAGCAAGGCGCGCGGGCGCCCGGAGGCGCGGAGCGCGGCGCGCGCGCGCGCGCGCG 2880
DB CAGCAAGGCGCGCGGGCGCCCGGAGGCGCGGAGCGCGGCGCGCGCGCGCGCGCGCG 2880
QY 2881 CGAGGCGCGCGCGCGCACCAACCGCGCGCTCCCGAGAGGCGCGCGCGCGCGCGCGCG 2940
DB CGAGGCGCGCGCGCGCACCAACCGCGCGCTCCCGAGAGGCGCGCGCGCGCGCGCGCG 2940
QY 2941 CCGACGCCACCGCGCGCACCGGCAACAGGATCCGAGCAAGGAGTGCGCGCGCGCGCGCG 3000
DB CCGACGCCACCGCGCGCACCGGCAACAGGATCCGAGCAAGGAGTGCGCGCGCGCGCGCG 3000
QY 3001 CGAGCGCGCGCGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3060
DB CGAGCGCGCGCGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3060
QY 3061 GGAGGAGCGCGCGCGCGCACCGCGCGCGCGCGCACAGCGCGCGCTGCTCAACAGGCTGT 3120
DB GGAGGAGCGCGCGCGCGCACCGCGCGCGCGCGCACAGCGCGCGCTGCTCAACAGGCTGT 3120
QY 3121 GGAGAGGAGACCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3180
DB GGAGAGGAGACCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3180
QY 3181 CAAGGAAAGGAGCTCCGGAGACCAACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3240
DB CAAGGAAAGGAGCTCCGGAGACCAACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3240
QY 3241 TGGGACTGTGACTGTGGGTCCATGCAACACTCCAGCACTCCCGAGCACTGTCTCCAGAGGTTGA 3300
DB TGGGACTGTGACTGTGGGTCCATGCAACACTCCAGCACTCCCGAGCACTGTCTCCAGAGGTTGA 3300
QY 3301 GGAACAGCCAGAGGATCGAGACATAGCGGAAAGCTCACTCGCATGGGCGAGTCAGCCGCC 3360
DB GGAACAGCCAGAGGATCGAGACATAGCGGAAAGCTCACTCGCATGGGCGAGTCAGCCGCC 3360
QY 3361 AGACCCGAAACATTTGTACATATCCAGTGATGCTGACGGGCGCTCTTGGGAGGCGAC 3420
DB AGACCCGAAACATTTGTACATATCCAGTGATGCTGACGGGCGCTCTTGGGAGGCGAC 3420
QY 3421 GGTGTTCCAGTGGTAACTGGACCTGGAAAGCCAGAGGAGGAGGAGGAGGAGGAGGAG 3480
DB GGTGTTCCAGTGGTAACTGGACCTGGAAAGCCAGAGGAGGAGGAGGAGGAGGAGGAG 3480

QY 3481 AGCGGATGACGTGATGAGGAGCGGCGCGCGCGCTATCGTCCCATACAGCTCCATGTTCTG 3540
DB AGCGGATGACGTGATGAGGAGCGGCGCGCGCGCTATCGTCCCATACAGCTCCATGTTCTG 3540
QY 3541 TTTAAGCCCGACCAACCTGCTCCGCGCTTCTGCACTACATCGTGACCAATGAGGTACTT 3600
DB TTTAAGCCCGACCAACCTGCTCCGCGCTTCTGCACTACATCGTGACCAATGAGGTACTT 3600
QY 3601 CGAGGTGGTCAATCTCGTGGTCAATCGCTTTGAGCAGCATCGCCCTGCTGCTGAGGACCC 3660
DB CGAGGTGGTCAATCTCGTGGTCAATCGCTTTGAGCAGCATCGCCCTGCTGCTGAGGACCC 3660
QY 3661 AGTGCGCAGAGCTCCGCCAGGAAACACGCTCTGAATACCTGGATACATTTTCACTGG 3720
DB AGTGCGCAGAGCTCCGCCAGGAAACACGCTCTGAATACCTGGATACATTTTCACTGG 3720
QY 3721 TGTCTTTTACCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780
DB TGTCTTTTACCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780
QY 3781 AGCTATTTTCCGGGACTTTGTGGAACATTTCTGGAATTTCAATTTGAGTGGCGCCCTGGT 3840
DB AGCTATTTTCCGGGACTTTGTGGAACATTTCTGGAATTTCAATTTGAGTGGCGCCCTGGT 3840
QY 3841 GCGGTTTGTCTTCTCGAGCTTCTGCGGAGGATCCAAAGGGAAGAGACATCAATACCAAC 3900
DB GCGGTTTGTCTTCTCGAGCTTCTGCGGAGGATCCAAAGGGAAGAGACATCAATACCAAC 3888
QY 3901 GTCTCTGAGAGTCTTCTGCTGCTGCGGCGCTCAAGACCATCAAGCGGCTGCCCAAGCT 3960
DB GTCTCTGAGAGTCTTCTGCTGCTGCGGCGCTCAAGACCATCAAGCGGCTGCCCAAGCT 3948
QY 3961 CAAAGGCTGTGTTTGAATGCTGTGTTGAACTCCCTGGAAGAAATGCTCTCAACATTTGAT 4020
DB CAAAGGCTGTGTTTGAATGCTGTGTTGAACTCCCTGGAAGAAATGCTCTCAACATTTGAT 4008
QY 4021 CTACATGCTCTTCTGATGTTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4080
DB CTACATGCTCTTCTGATGTTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4068
QY 4081 TTTCTACTGCACAGATGAATCCCAAGGAGCTGGAAGAGGAGCTGCAAGGCTCAGTATTTTGA 4140
DB TTTCTACTGCACAGATGAATCCCAAGGAGCTGGAAGAGGAGCTGCAAGGCTCAGTATTTGA 4128
QY 4141 TTAATGAGAGGAGGAGGAGTGGAGCTCAGCCAGGCGAGTGGAGAAATACGACTTTTCACTA 4200
DB TTAATGAGAGGAGGAGGAGTGGAGCTCAGCCAGGCGAGTGGAGAAATACGACTTTTCACTA 4188
QY 4201 CGACATGCTCTGCGGCTCTGCTGAGCTGTTTCAAGTGTCCACGGGAGAGGCTGGCC 4260
DB CGACATGCTCTGCGGCTCTGCTGAGCTGTTTCAAGTGTCCACGGGAGAGGCTGGCC 4248
QY 4261 CATGGTGTCAACACTCCGTTGATGCCACTATGAGGAGCGGCTCCAGGCTGGGTA 4320
DB CATGGTGTCAACACTCCGTTGATGCCACTATGAGGAGCGGCTCCAGGCTGGGTA 4308
QY 4321 CCGCATGGAGCTCTCCATCTTTTACGTTGCTCTACTTTTGTGGTCTTTTCCCTTTCTTCTGT 4380
DB CCGCATGGAGCTCTCCATCTTTTACGTTGCTCTACTTTTGTGGTCTTTTCCCTTTCTTCTGT 4368
QY 4381 CAACATCTTTTGTGGCTTTGATCATCATCTTTTCCAGGAGGAGGAGGAGGAGGAGGAG 4440
DB CAACATCTTTTGTGGCTTTGATCATCATCTTTTCCAGGAGGAGGAGGAGGAGGAGGAG 4428
QY 4441 TGAATCGACGCTGGAGAGAAACGAGAGGCTTGCATTTGATTTTCCCATCAGCCCAAAACC 4500
DB TGAATCGACGCTGGAGAGAAACGAGAGGCTTGCATTTGATTTTCCCATCAGCCCAAAACC 4488
QY 4501 CTTGACACGCTACATGCCCGCAAAACCGGCGAGTGGTCCAGTATAAGACGTTGGACATTTGT 4560
DB CTTGACACGCTACATGCCCGCAAAACCGGCGAGTGGTCCAGTATAAGACGTTGGACATTTGT 4548
QY 4561 GGTCTCCCCCGCCTTTTGAATACTTTTCAATCATGCGCATGATAGCCCTCAACACTGTGTGCT 4620

Db		4549	GGTCTCCCGCCCTTTGAAATCTTCATCATGGCCATGATAGCCCTCAACACATGTGTGCT	4608
Qy		4621	GATGATGAAGTCTTATGATGACCCCTATGATGATGAGGCTGATGCTGAAATGCTGAAAT	4680
Db		4609	GATGATGAAGTCTTATGATGACCCCTATGATGATGAGGCTGATGCTGAAATGCTGAAAT	4668
Qy		4681	CGTGTTCACATCCATGATTTCTCCATGGAATGCGTGTCTGAAGATCATCGCTTTGGGGTGT	4740
Db		4669	CGTGTTCACATCCATGATTTCTCCATGGAATGCGTGTCTGAAGATCATCGCTTTGGGGTGT	4728
Qy		4741	GAATATTTTACAGATGCTCTGGAATGTCTTTGATCTTTGTACATGTTGGGAAGTATTAC	4800
Db		4729	GAATATTTTACAGATGCTCTGGAATGTCTTTGATCTTTGTACATGTTGGGAAGTATTAC	4788
Qy		4801	TGATATTTTATGAACAGAGATTCGCGAAGACCAATTTTCATCAACCTCAGCTTCTCGG	4860
Db		4789	TGATATTTTATGAACAGAGATTCGCGAAGACCAATTTTCATCAACCTCAGCTTCTCGG	4848
Qy		4861	CTCTTTTCAGAGTTCGCGGCTGATCAAGCTGTCTCCGCAAGGCTACACCATCCGATCCT	4920
Db		4849	CTCTTTTCAGAGTTCGCGGCTGATCAAGCTGTCTCCGCAAGGCTACACCATCCGATCCT	4908
Qy		4921	GCTGTGGAAGTCTTGTCCAGTCTTCAAGGCCCTGCCCTACGTTGTCTCATTTGCCAT	4980
Db		4909	GCTGTGGAAGTCTTGTCCAGTCTTCAAGGCCCTGCCCTACGTTGTCTCATTTGCCAT	4968
Qy		4981	GCTGTCTTTCATCTACGCCATCATCGGCATGAGAGTGTGGAATATTTGCCCTGGATGA	5040
Db		4969	GCTGTCTTTCATCTACGCCATCATCGGCATGAGAGTGTGGAATATTTGCCCTGGATGA	5028
Qy		5041	TGACACAGCATCAACCGCCACAACAACTTCCGGAGCTTTTTCGAAAGCCCTGATCCTCT	5100
Db		5029	TGACACAGCATCAACCGCCACAACAACTTCCGGAGCTTTTTCGAAAGCCCTGATCCTCT	5088
Qy		5101	GTTTCAGGAGCGCACGGGGAGCCCTGSCACAGATCATGCTGCTCCTGCTGAGCAACA	5160
Db		5089	GTTTCAGGAGCGCACGGGGAGCCCTGSCACAGATCATGCTGCTCCTGCTGAGCAACA	5148
Qy		5161	GGCCTGTGATGAGCAGGCCCAATGCCACCGAGTGTGGAAGTGAATTTTGCTACTTCTACT	5220
Db		5149	GGCCTGTGATGAGCAGGCCCAATGCCACCGAGTGTGGAAGTGAATTTTGCTACTTCTACT	5208
Qy		5221	CCTCTCCTTCACTTCTCTGTGCTCTTTCTGATGTTGAACCTCTTTTGGCTGTGATCAT	5280
Db		5209	CCTCTCCTTCACTTCTCTGTGCTCTTTCTGATGTTGAACCTCTTTTGGCTGTGATCAT	5268
Qy		5281	GGACAAATTTGATACCTCAGCGGAGCTCTTCCATCCTTAGTCTCACCACCTTTGGATGA	5340
Db		5269	GGACAAATTTGATACCTCAGCGGAGCTCTTCCATCCTTAGTCTCACCACCTTTGGATGA	5328
Qy		5341	GTTTCATCCGGGCTCGGGCTGAATACGACCCGGCTGCTGTGGGGCATCAGTTACAATGA	5400
Db		5329	GTTTCATCCGGGCTCGGGCTGAATACGACCCGGCTGCTGTGGGGCATCAGTTACAATGA	5388
Qy		5401	CATGTTTACAGATGCTGAAACACATGTCCTCGGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5460
Db		5389	CATGTTTACAGATGCTGAAACACATGTCCTCGGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5448
Qy		5461	TCGAGTTGCTTACAAGCCCTGTTTCGATCAATGACATGCTTCCATCCTTAGTCTCAGGATGAC	5520
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Qy		5581	CCCAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGAGATTTCCGTTGT	5640
Db		5569	CCCAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGAGATTTCCGTTGT	5628
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Db		5629	GTGGGCCAATCTGCCCCAGAGAATTTTGGACTTGTGTGTACCAACCCCATTAAGCCTGATGA	5688
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Db		5689	GATGACAGTGGGAAGGTTTATGACGCTCTGATGATATTTTGAATTTTACAAAGCAGAAACA	5748
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AUTHORS Harpold,M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F.
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Qy 61 GCTGCTCGGCTCTGAGCGCTTGGGCGCGCCCGCCCTCCCTGCGGGGCGGCTGGGCGG 120
Db 120

Db 60 GCTGCTCGGCTCTGAGGGCCT- GGGGCGCCCGCGGCCCTCCTGCGGGGGCGGCTGGGCGG 118
Qy 121 GGGATGCACGCGGGGCGCGGAGCCATGTGTCGCTTCGGGGAGAGCTGGGCGGCGCTA 180
Db 119 GGGATGCACGCGGGGCGCGGAGCCATGTGTCGCTTCGGGGAGAGCTGGGCGGCGCTA 178
Qy 181 TGAAGGCGCGGGGCGGAGAGCGGGCGCGGGGCGGGGCGGGGCGGGGCGGGGCGG 240
Db 179 TGAAGGCGCGGGGCGGAGAGCGGGCGCGGGGCGGGGCGGGGCGGGGCGGGGCGG 238
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QY	1321	CTTCAAGGCGGAGGAGTCAATGCTGCGCGAGAGGACAGGAATGACAGAGAAATGTCCTT	1380
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QY	1381	TTTGGAGCTGCTCAAGAGAGCGGCCCAAGAGAGCAGAAATGACCTGATCCACGCGAGA	1440
Db	1379	TTTGGAGCTGCTCAAGAGAGCGGCCCAAGAGAGCAGAAATGACCTGATCCACGCGAGA	1438
QY	1441	GGAGGAGAGGACCGGTTTGCAGATCTCTGTGCTGTGTGGATCCCCCTTCGCGCGGCCAG	1500
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Db 4667 CGTGTTCACATCCATGTTCTCCATGGAATCGTGTGAAAGATCATCGCCTTTGGGGTGTCT 4726
Qy 4741 GAACTATTTTCAGAGATGCTGGAAATGCTTTGACTTTGTGACTGTGTTGGGAAGTATTAC 4800
Db 4727 GAACTATTTTCAGAGATGCTGGAAATGCTTTGACTTTGTGACTGTGTTGGGAAGTATTAC 4786
Qy 4801 TGATATTTTAGTAAACAGAGATTGCGGAAACGAAACAATTTTCACTCAAGCTCAGCTTCTCCG 4860
Db 4787 TGATATTTTAGTAAACAGAGATTGCGGAAACGAAACAATTTTCACTCAAGCTCAGCTTCTCCG 4846
Qy 4861 CCTCTTTTCGAGCTGCGCGCTGATCAAGCTGTCTCCGCAAGGCTACACCATCCGCACTCT 4920
Db 4847 CCTCTTTTCGAGCTGCGCGCTGATCAAGCTGTCTCCGCAAGGCTACACCATCCGCACTCT 4906
Qy 4921 GCTGTGGAACCTTTGCTCAGTCCCTTCAAGGCCCTGCCCTAGCTGTGCTGCTCAITGGCCAT 4980
Db 4907 GCTGTGGAACCTTTGCTCAGTCCCTTCAAGGCCCTGCCCTAGCTGTGCTGCTCAITGGCCAT 4966
Qy 4981 GCTGTTCCTTCATCTACGCCATCATCGCATGCAAGTGTTTGGGAAATATTCGCCCTGGATGA 5040
Db 4967 GCTGTTCCTTCATCTACGCCATCATCGCATGCAAGTGTTTGGGAAATATTCGCCCTGGATGA 5026
Qy 5041 TGACACAGCATCAACCGCCACAACTTTCCGAGCTTTTTCGCAAGCCCTGATGTGCT 5100
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Qy 5101 GTTCAGAGGCCACCGGGGAGGCTTGGCAAGATCATGCTGTCTGCTCCTGAGCAACCA 5160
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Qy 5161 GGCCTGTGATGAGCAGGCCAAATGSCACCGAGTGTGGAAGTGAATTTGCTTCTACTTT 5220
Db 5147 GGCCTGTGATGAGCAGGCCAAATGCCACCGAGTGTGGAAGTGAATTTGCTTCTACTTT 5206
Qy 5221 CGTCTCTTCATCTTCTGTGCTCTTTCTGATGTTTGAACCTCTTTTGTGGCTGTGATCAT 5280
Db 5207 CGTCTCTTCATCTTCTGTGCTCTTTCTGATGTTTGAACCTCTTTTGTGGCTGTGATCAT 5266
Qy 5281 GGAACAATTTTGAATACCTCAACCGGGAGCTTTCCATCTTAGTCTCTCAACACTTGGATGA 5340
Db 5267 GGAACAATTTTGAATACCTCAACCGGGAGCTTTCCATCTTAGTCTCTCAACACTTGGATGA 5326
Qy 5341 GTTCATCCGGCTCTGGCTGAAATACGACCGGCTGGTGTGGCGCATCAGTTTACAAATGA 5400
Db 5327 GTTCATCCGGCTCTGGCTGAAATACGACCGGCTGGTGTGGCGCATCAGTTTACAAATGA 5386
Qy 5401 CATGTTTGAATGCTGAAACACATGTCCCCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC 5460
Db 5387 CATGTTTGAATGCTGAAACACATGTCCCCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC 5446
Qy 5461 TCAGTGTGCTTCAAGGGCTGTGCTGCAATGAATGCAATGCCCATCTCCAAAGAGACATGAC 5520
Db 5447 TCAGTGTGCTTCAAGGGCTGTGCTGCAATGAATGCAATGCCCATCTCCAAAGAGACATGAC 5506
Qy 5521 TGTTCATCTTCAGCTCCACCTGATGCCCTCATCCGGAAGGCACTGAGATCAAGCTGGC 5580
Db 5507 TGTTCATCTTCAGCTCCACCTGATGCCCTCATCCGGAAGGCACTGAGATCAAGCTGGC 5566

[illegible]

QY	6661	GAATGGAGCCCTTGTGTCAACATCTGGTGTAGCACCCCGCGCCGCTGTGGGCGGAG	6721
Db	6630	-----	6629
QY	6721	GCAGCTCCCCCAGACGCCCCCTGACTCCCGGCCAGCATCACCTACAAGACGGCCAATC	6780
Db	6630	-----	6629
QY	6781	CTACCCATCCACTTCGCGCGGGCTCAGACCAAGCTTCCTCCCTTCCTCCCGAGCCGCT	6840
Db	6630	-----	6639
QY	6841	CAGCCGTGGCTTTCGGAACAACACGCGCTGCTGCAGAGAGACCCCTCAGCAGCCCT	6900
Db	6640	CAGCCGTGGCTTTCGGAACAACACGCGCTGCTGCAGAGAGACCCCTCAGCAGCCCT	6699
QY	6901	GGCCCTGGCTCTCGAATTGGCTCTGACCCCTTACCTGGGGCAGCGTCTGGACAGTGAGGC	6960
Db	6700	GGCCCTGGCTCTCGAATTGGCTCTGACCCCTTACCTGGGGCAGCGTCTGGACAGTGAGGC	6759
QY	6961	CTCTGTCCACGCGCTGCTGAGNACAGCTCACTTTTCGAGGAGCGTGTGGCCACCAATC	7020
Db	6760	CTCTGTCCACGCGCTGCTGAGNACAGCTCACTTTTCGAGGAGCGTGTGGCCACCAATC	6819
QY	7021	GGCGCGCTCTCCAGGACTTCTCACTGCTGCTCCTCCCTGACCTCCACGCTCTCACCTCTCCG	7080
Db	6820	GGCGCGCTCTCCAGGACTTCTCACTGCTGCTCCTCCCTGACCTCCACGCTCTCACCTCTCCG	6879
QY	7081	CCGCGTGGCCAAACGGTTTACACTGCACTGGACCTGAGCTCGGGTGGCCAGCAGGCA	7140
Db	6880	CCGCGTGGCCAAACGGTTTACACTGCACTGGACCTGAGCTCGGGTGGCCAGCAGGCA	6939
QY	7141	CAGCTACACACCCCTGACCAAGACCACTGGTGTCTAGCTGCACCGTAGCCCTCAGACGC	7200
Db	6940	CAGCTACACACCCCTGACCAAGACCACTGGTGTCTAGCTGCACCGTAGCCCTCAGACGC	6999
QY	7201	CTGATCGACAGCGGTGTGTTCCAGTGGATGTTTTATCATCCACAGCGGCAAGTCGG	7260
Db	7000	CTGATCGACAGCGCGTGTGTTCCAGTGGATGTTTTATCATCCACAGCGGCAAGTCGG	7059
QY	7261	CCCTCGGGGAGCGCTTGCCACCTTGTGTAGGCTCCTGTGGCCCTCCCTCCCTCCT	7320
Db	7060	CCCTCGGGGAGCGCTTGCCACCTTGTGTAGGCTCCTGTGGCCCTCCCTCCCTCCT	7119
QY	7321	CCCTCTTTTACTCTAGACGAAATAAGCCCTGTGTGAGTGTAGTACCGC	7376
Db	7120	CCCTCTTTTACTCTAGACGAAATAAGCCCTGTGTGAGTGTAGTACCGC	7175
RESULT 14			
AR063883			
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DEFINITION	Sequence 8 from patent US 5846757.		
ACCESSION	AR063883		
VERSION	AR063883.1	GI:5993191	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 7175)		
AUTHORS	Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F. and Brenner,R.		
TITLE	Human calcium channel .alpha. .sub.1. .alpha. .sub.2. and .beta. subunits and assays using them		
JOURNAL	Patent: US 5846757-A 8 08-DEC-1998;		
FEATURES	Location/Qualifiers		
source	1. .7175		
ORIGIN	/organism="unknown"		
	/mol_type="unassigned DNA"		

Query Match 94.0%; Score 6932.4; DB 6; Length 7175;
Best Local Similarity 97.3%; Pred. No. 0;

Matches 7174; Conservative 0; Mismatches 1; Indels 201; Gaps 4;			
Qy	1	GGCGCGCGGCTGCGGCGGTGGGCGCGGCGAGGTCCGCTGCGGTCCCGCGGCTCCGCTG	60
Db	1	GGCGCGCGGCTGCGGCGGTGGGCGCGGCGAGGTCCG-TCGGTCCCGCGGCTCCGCTG	59
Qy	61	GCTGCTCCGCTCTGAGCGCCTGGCGCGCGCGCGCGCCCTCCCTGCGGGGCGGCTGGGCGG	120
Db	60	GCTGCTCCGCTCTGAGCGCCT-GGCGCGCGCGCGCCCTCCCTGCGGGGCGGCTGGGCGG	118
Qy	121	GGGATGCACGCGGGCGCGGAGGCATGTGTCGGCTTCGGGAGCAGAGCTGGCGCGCCGCTA	180
Db	119	GGGATGCACGCGGGCGCGGAGGCATGTGTCGGCTTCGGGAGCAGAGCTGGCGCGCCGCTA	178
Qy	181	TGGAGGCCCGCGCGGAGAGCGGGCCCGGGCGGGCGGGCGCGCGGGCGGGGGCCCC	240
Db	179	TGGAGGCCCGCGCGGAGAGCGGGCCCGGGCGGGCGGGCGGGCGGGGGCCCC	238
Qy	241	GGGTCCCGGGGGCTGAGCCCGGCGAGCGGGTCTCTACAAGCAATCGATCGGCGAGCG	300
Db	239	GGGTCCCGGGGGCTGAGCCCGGCGAGCGGGTCTCTACAAGCAATCGATCGGCGAGCG	298
Qy	301	CGCGCGACCATGCGGCTGTACAAACCCATCCGSGTCAAGCAGAACTGCTTCAACGTCAA	360
Db	299	CGCGCGACCATGCGGCTGTACAAACCCATCCGSGTCAAGCAGAACTGCTTCAACGTCAA	358
Qy	361	CCGCTCGCTCTTCTTCAGCAGGAGCAACGTCGTCGCAAAATACGCGAAGCGCATCAC	420
Db	359	CCGCTCGCTCTTCTTCAGCAGGAGCAACGTCGTCGCAAAATACGCGAAGCGCATCAC	418
Qy	421	CGAGTGGCTCCATTCGAGTATATGATCTTGGGCCAACCATATGCCAACTGCACTGCTGCT	480
Db	419	CGAGTGGCTCCATTCGAGTATATGATCTTGGGCCAACCATATGCCAACTGCACTGCTGCT	478
Qy	481	GGCCCTCGAGCAGCACCTCCCTGATGCGGACAAACGCCCATGTCGAGCGGCTGGACGA	540
Db	479	GGCCCTCGAGCAGCACCTCCCTGATGGGAGCAAAACGCCCATGTCGAGCGGCTGGACGA	538
Qy	541	CACGAGCCCTATTTCATCGGGATCTTTTGTCTCGAGCGAGGGATCAAAATCATCGCTCT	600
Db	539	CACGAGCCCTATTTCATCGGGATCTTTTGTCTCGAGCGAGGGATCAAAATCATCGCTCT	598
Qy	601	GGGCTTGTCTTCCAAAGGGCTCTTACCTGCGGAAACGGCTGGAAAGTCAAGCTTCGT	660
Db	599	GGGCTTGTCTTCCAAAGGGCTCTTACCTGCGGAAACGGCTGGAAAGTCAAGCTTCGT	658
Qy	661	GGTGGCTCTCACAGGATCCTTGGCCAGGCTGGAACCTGACCTCGACCTGCGAACACTGAG	720
Db	659	GGTGGCTCTCACAGGATCCTTGGCCAGGCTGGAACCTGACCTCGACCTGCGAACACTGAG	718
Qy	721	GGCTGTGCGTGTGTGAGGGCCCTGAAAGCTGCTGCTGGGATTCAAAGTTTGCAGGTGGT	780
Db	719	GGCTGTGCGTGTGTGAGGGCCCTGAAAGCTGCTGCTGGGATTCCAAGTTTGCAGGTGGT	778
Qy	781	GCTCAAGTCCATATGAAGGCACTGGTTCCACTCCTGCGAGATTGGGCTGCTTCTTCTT	840
Db	779	GCTCAAGTCCATATGAAGGCACTGGTTCCACTCCTGCGAGATTGGGCTGCTTCTTCTT	838
Qy	841	TGCCATCTCATGTTTGCCATCATTCGCTGGAGTTCTACATGGCAAGTTCCACAGGC	900
Db	839	TGCCATCTCATGTTTGCCATCATTCGCTGGAGTTCTACATGGCAAGTTCCACAGGC	898
Qy	901	CTGTTTCCCAACAGCAGATGCGAGCCCGTGGGTGACTTCCCTCTGTGGCAAGGAGGC	960
Db	899	CTGTTTCCCAACAGCAGATGCGAGCCCGTGGGTGACTTCCCTCTGTGGCAAGGAGGC	958
Qy	961	CCAGCCCGGCTGTGCGAGGCGACACTGAGTCCGGAGTACTGGCCAGGACCCAACTT	1020
Db	959	CCAGCCCGGCTGTGCGAGGCGGACACTGAGTCCGGAGTACTGGCCAGGACCCAACTT	1018
Qy	1021	TGGCATCACCAACTTTGACATATCCTGTTGGCATCTTGACGGTGTTCAGTGCATCAC	1080
Db	1019	TGGCATCACCAACTTTGACATATCCTGTTGGCATCTTGACGGTGTTCAGTGCATCAC	1078

Qy	1081	CATGGAGGGCTGGACTGAACATCTCTATATAAATAAAACGATGCGGCGCGCAACCTGGAA	1140
Db	1079	CATGGAGGGCTGGACTGAACATCTCTATATAAATAAAACGATGCGGCGCGCAACCTGGAA	1138
Qy	1141	CTGGCTCTACTTTCATCCCTCTCATCATATCGGCTCTTCTTCTATGCTCAACCTGGTCT	1200
Db	1139	CTGGCTCTACTTTCATCCCTCTCATCATATCGGCTCTTCTTCTATGCTCAACCTGGTCT	1198
Qy	1201	GGCGCTGCTCTCGGGGGAGTTTCCCAAGAGCGAGAGGGTGGAGAACCGCGCGCCTT	1260
Db	1199	GGCGCTGCTCTCGGGGGAGTTTCCCAAGAGCGAGAGGGTGGAGAACCGCGCGCCTT	1258
Qy	1261	CTTGAAGCTGCGCGCGGAGCAGATCGAGCGAGAGCTCAACGGGTACTCTGAGTGGAT	1320
Db	1259	CTTGAAGCTGCGCGCGGAGCAGATCGAGCGAGAGCTCAACGGGTACTCTGAGTGGAT	1318
Qy	1321	CTTCAAGCGGAGGAAGTCAATGCTGCGCGGAGGACAGGAATGCAGAGAGAAAGTCCCC	1380
Db	1319	CTTCAAGCGGAGGAAGTCAATGCTGCGCGGAGGACAGGAATGCAGAGAGAAAGTCCCC	1378
Qy	1381	TTTGAAGCTGCTGAAGAGAGCGGCCAACAAAGAGAGCAGAAATGAACCTGATCCACGAGA	1440
Db	1379	TTTGAAGCTGCTGAAGAGAGCGGCCAACAAAGAGAGCAGAAATGAACCTGATCCACGAGA	1438
Qy	1441	GGAGGAGAGGACCGGTTTGAGATCTCTGTGCTGTGTGGATCCCTTTCGCCCGCGCAG	1500
Db	1439	GGAGGAGAGGACCGGTTTGAGATCTCTGTGCTGTGTGGATCCCTTTCGCCCGCGCAG	1498
Qy	1501	CCTCAAGCGGGAAGACAGAGAGCTCGTCATACTTCCGGAGGAAGAGAGATGTCG	1560
Db	1499	CCTCAAGCGGGAAGACAGAGAGCTCGTCATACTTCCGGAGGAAGAGAGATGTCG	1558
Qy	1561	GTTTTTTATCCGCGCATGTTGAAGCTCAGAGCTTCTACTGGGTGTGTGCTGCGTGGT	1620
Db	1559	GTTTTTTATCCGCGCATGTTGAAGCTCAGAGCTTCTACTGGGTGTGTGCTGCGTGGT	1618
Qy	1621	GGCCCTGAAACACACTGTGTGGCCATGTTGCATTAACAACGCGCGCGGCTTACAC	1680
Db	1619	GGCCCTGAAACACACTGTGTGGCCATGTTGCATTAACAACGCGCGCGGCTTACAC	1678
Qy	1681	GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTTCTTCTCACAGAGATGTCCTGAA	1740
Db	1679	GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTTCTTCTCACAGAGATGTCCTGAA	1738
Qy	1741	GATGATGGCTCGGCGCCAGAAAGTACTTCCGGTCTCTCTCAACTGCTTCGACTTTGG	1800
Db	1739	GATGATGGCTCGGCGCCAGAAAGTACTTCCGGTCTCTCTCAACTGCTTCGACTTTGG	1798
Qy	1801	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCCATCAAGCGGGAAGCTCCTT	1860
Db	1799	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCCATCAAGCGGGAAGCTCCTT	1858
Qy	1861	TGGGATCAGTGTGCTGGGGCCCTCGCCTGCTGAGGATCTTCAAAGTCAAGTACTG	1920
Db	1859	TGGGATCAGTGTGCTGGGGCCCTCGCCTGCTGAGGATCTTCAAAGTCAAGTACTG	1918
Qy	1921	GAGCTCCCTCGGAACTCGTGTGTGTCCTGCTGAACTCCATGAAGTCCATCATCAGCCT	1980
Db	1919	GAGCTCCCTCGGAACTCGTGTGTGTCCTGCTGAACTCCATGAAGTCCATCATCAGCCT	1978
Qy	1981	GCTCTTCTTGTCTTCTGTTTCATTTGTGCTTTCGCCCTGCTGGGAGTACAGCTTTGG	2040
Db	1979	GCTCTTCTTGTCTTCTGTTTCATTTGTGCTTTCGCCCTGCTGGGAGTACAGCTTTGG	2038
Qy	2041	GGGAGAGTTCAACTTCCAGATGAGACTCCCAACCAACTTTCGACACTTCCCTGCCG	2100
Db	2039	GGGAGAGTTCAACTTCCAGATGAGACTCCCAACCAACTTTCGACACTTCCCTGCCG	2098
Qy	2101	CATCTCACCTGCTTCCAGATCCCTGAGGAGGAGTGGAAATGCAGTGTATATCACGG	2160
Db	2099	CATCTCACCTGCTTCCAGATCCCTGAGGAGGAGTGGAAATGCAGTGTATATCACGG	2158

Qy	2161	GATCGAATCGCAAGCGCGGCTCAGCAAAAGGCAATGTTCTCGTCCCTTTTACTTCATTTGTCCT	2222
Db	2159	GATCGAATCGCAAGCGCGGCTCAGCAAAAGGCAATGTTCTCGTCCCTTTTACTTCATTTGTCCT	2218
Qy	2221	GACACTGTTCCGAAACTACACTCTGCTCAATGTCTTTCTGGCCATCGCTGTGGACAACCT	2280
Db	2219	GACACTGTTCCGAAACTACACTCTGCTCAATGTCTTTCTGGCCATCGCTGTGGACAACCT	2278
Qy	2281	GCCCAACGCCCAAGAGCTGAACAAGGATGAAGAGAGATGAAGAAGCAGCCAAATCAGAA	2340
Db	2279	GCCCAACGCCCAAGAGCTGAACAAGGATGAAGAGAGATGAAGAAGCAGCCAAATCAGAA	2338
Qy	2341	GCTTGCTCTGCAAAAGGCCAAAGAGTGGCTGAAGTCAGCGCCCATGCTCGCGGACAT	2400
Db	2339	GCTTGCTCTGCAAAAGGCCAAAGAGTGGCTGAAGTCAGCGCCCATGCTCGCGGACAT	2398
Qy	2401	CTCCATCCGCGCCAGCAGCAGAACTACGCGCCAAAGCGCGCTCGTGTGGAGCAGCGCGC	2460
Db	2399	CTCCATCCGCGCCAGCAGCAGAACTACGCGCCAAAGCGCGCTCGTGTGGAGCAGCGCGC	2458
Qy	2461	CAGCCAGCTACGGCTGCAGAACCTCGCGGCCAGCTGCGAGCGCTGTACAGCAGATGGA	2520
Db	2459	CAGCCAGCTACGGCTGCAGAACCTCGCGGCCAGCTGCGAGCGCTGTACAGCAGATGGA	2518
Qy	2521	CCCAGAGAGCGGCTGCGCTTCGCGCACTACGCGCCAGCTGCGGCCCGCACATGAAGACGA	2580
Db	2519	CCCAGAGAGCGGCTGCGCTTCGCGCACTACGCGCCAGCTGCGGCCCGCACATGAAGACGA	2578
Qy	2581	CCTGGAACCGCCGCTGTGTGTGTGAGCTGTGGCCGCGAAGCGCGCGGGGCCCTGTGGAGG	2640
Db	2579	CCTGGAACCGCCGCTGTGTGTGTGAGCTGTGGCCGCGAAGCGCGCGGGGCCCTGTGGAGG	2638
Qy	2641	CAAAAGCCGACCTCAGGCTGCGAGGCGCCCGAGGGCGTGCACCTCCGCGCAGGACCA	2700
Db	2639	CAAAAGCCGACCTCAGGCTGCGAGGCGCCCGAGGGCGTGCACCTCCGCGCAGGACCA	2698
Qy	2701	CCGGCACCGCGACAAGGACAAGACCCCTCGCGGGGGGACCAAGACCGAGCAGAGCCCC	2760
Db	2699	CCGGCACCGCGACAAGGACAAGACCCCTCGCGGGGGGACCAAGACCGAGCAGAGCCCC	2758
Qy	2761	GAAGGCGGAGAGCGGGAGCCCGGTGCCCAGGAGGAGCGGCGCGCGCGCACCGCAGCCA	2820
Db	2759	GAAGGCGGAGAGCGGGAGCCCGGTGCCCAGGAGGAGCGGCGCGCGCGCACCGCAGCCA	2818
Qy	2821	CAGCAAGGAGGCGCGGGGCCCGGAGGCGCGAGCGAGCGCGCGCGCGCCAGGCCCC	2880
Db	2819	CAGCAAGGAGGCGCGGGGCCCGGAGGCGCGAGCGAGCGCGCGCGCGCCAGGCCCC	2878
Qy	2881	CGAGGCGGCGCGGGGACCAACCGCGCGGCTCCCGGAGGAGCGGCGCGCGCGGAGCC	2940
Db	2879	CGAGGCGGCGCGGGGACCAACCGCGCGGCTCCCGGAGGAGCGGCGCGCGCGGAGCC	2938
Qy	2941	CCGACGCCACCGCGCGCACCGCGCACCAAGGATCCGAGCAAGGAGTGCCTCGCGCCCAAGG	3000
Db	2939	CCGACGCCACCGCGCGCACCGCGCACCAAGGATCCGAGCAAGGAGTGCCTCGCGCCCAAGG	2998
Qy	3001	CGAGCGCGCGCGGGGACCGCGGGGCCCGCCAGCGGGGCCCGGGAGCGGAGCGG	3060
Db	2999	CGAGCGCGCGCGGGGACCGCGGGGCCCGCCAGCGGGGCCCGGGAGCGGAGCGG	3058
Qy	3061	GGAGGAGCCGCGCGGGCGCACCGGGGCCGGCACAAAGGCGACGCTGCTCAGAGGCTGT	3120
Db	3059	GGAGGAGCCGCGCGGGCGCACCGGGGCCGGCACAAAGGCGACGCTGCTCAGAGGCTGT	3118
Qy	3121	GGAGAAGGACCAACCGAGAGAGGCGCAACGAGAGAGAGGCTGTGATGTGGAAGCCGA	3180
Db	3119	GGAGAAGGACCAACCGAGAGAGGCGCAACGAGAGAGAGGCTGTGATGTGGAAGCCGA	3178
Qy	3181	CAAGGAAAAGAGCTCCGGAACCAACAGCCCCCGGAGGCCACACTGTGACCTGGAGACAG	3240
Db	3179	CAAGGAAAAGAGCTCCGGAACCAACAGCCCCCGGAGGCCACACTGTGACCTGGAGACAG	3238
Qy	3241	TGGGACTGTGACTGTGGGTCCCATGACACACTGCCCCGACACTGTCTCCAGAGGTGGA	3300

[illegible]

Db 4307 CCGCATGGAGCTGTCACATCTTTCTACGTGGTCTACTTTGTGGTCTTTCCCTCTCTTCTTCGT 4366
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Db 4367 CAACATCTTTGTGCTTTGTATCATCATCACTTCCAGGAGCAGGGGACAAAGTGATGTC 4426
Qy 4441 TGAATGAGCCTGGAGAAGAAACGAGAGGGCTTGCAATTGACTTGGCCATCAGCGCAAAACC 4500
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Qy 4741 GAACTATTTTCAGAGATGCTTGGAAATGCTTTGACTTTGTCACTGTGTGGGAAGTATTAC 4800
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Qy 5161 GGCTGTGATGAGCAGCGCAATGCCACCGAGTGTGGAAGTGACTTTGCCCTACTTCTACTT 5220
Db 5147 GGCTGTGATGAGCAGCGCAATGCCACCGAGTGTGGAAGTGACTTTGCCCTACTTCTACTT 5206
Qy 5221 CGTCTCCTTCTATCTTCTGCTGCTCTTCTGATGTTGAACTCTTTGTGCTGTGATCAT 5280
Db 5207 CGTCTCCTTCTATCTTCTGCTGCTCTTCTGATGTTGAACTCTTTGTGCTGTGATCAT 5266
Qy 5281 GGACAAATTTTGTAGTACCTCACCGGGGACTCTTCCATCTAGGTCTCTCAACACTTGGATGA 5340
Db 5267 GGACAAATTTTGTAGTACCTCACCGGGGACTCTTCCATCTAGGTCTCTCAACACTTGGATGA 5326
Qy 5341 GTTCATCCGGGTCTGGCTGAATACGACCCGGCTGCTGTGGGCGCATCAGTTTACAATGA 5400
Db 5327 GTTCATCCGGGTCTGGCTGAATACGACCCGGCTGCTGTGGGCGCATCAGTTTACAATGA 5386
Qy 5401 CATGTTTGTAGTGTGAAACATGTTCCCGCCTCTTGGGGCTGGGGAAGAAATGCCCTGC 5460
Db 5387 CATGTTTGTAGTGTGAAACATGTTCCCGCCTCTTGGGGCTGGGGAAGAAATGCCCTGC 5446

Qy 5461 TCGAGTTGCTTACAACGCGCTGGTTCGCATGAACATGCCCATCTCCAAGAGACATGAC 5520
Db 5447 TCGAGTTGCTTACAAGCGCTGGTTCGCATGAACATGCCCATCTCCAAGAGACATGAC 5506
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Qy 5581 CCAGCTGGGACAAAACGAGCATCAGTGTGACGCGGAGTTGAGGAAGGAGATTTCCGTTGT 5640
Db 5567 CCAGCTGGGACAAAACGAGCATCAGTGTGACGCGGAGTTGAGGAAGGAGATTTCCGTTGT 5626
Qy 5641 GTGGGCAATCTGCCCCCAGAAAGACTTTTGGACTTTGTGGTACCAACCCCATTAAGCCTGATGA 5700
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Db 5687 GATGACAGTGGGGAAGGTTTATGACGCTCTGATGATATTTGACTTCTACAAGCAGAACAA 5746
Qy 5761 AACACACAGAGACAGATGACAGGCTCTCTGGAGGCTCTTCCAGATGGGTCTCTGTGTC 5820
Db 5747 AACACACAGAGACAGATGACAGGCTCTCTGGAGGCTCTTCCAGATGGGTCTCTGTGTC 5806
Qy 5821 CTTGTTTCCAACCTCTGAAGGCCACCTCTGAGCAGACACAGCCGGCTGTGCTCCGAGAGC 5880
Db 5807 CTTGTTTCCAACCTCTGAAGGCCACCTCTGAGCAGACACAGCCGGCTGTGCTCCGAGAGC 5866
Qy 5881 CCGGGTTTTCTTCGACAGAAAGTTTCCACCTCCCTCAGCAATGGCGGGCCATACAAA 5940
Db 5867 CCGGGTTTTCTTCGACAGAAAGTTTCCACCTCCCTCAGCAATGGCGGGCCATACAAA 5926
Qy 5941 CCAAGAGAGTGGCATCAAAGAGTCTCTCTGGGGCACTCAAAGGACCCAGAGATGCACC 6000
Db 5927 CCAAGAGAGTGGCATCAAAGAGTCTCTCTGGGGCACTCAAAGGACCCAGAGATGCACC 5986
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RESULT 15
LOCUS AR067883
DEFINITION Sequence 8 from patent US 5851824.
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VERSION AR067883.1 GI:5999105
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7175)
AUTHORS Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McQue,A.F.
and Brenner,R.
TITLE Human calcium channel .alpha.-1C/.alpha.-1D, .alpha.-2, .beta.-1,
and .gamma.subunits and cells expressing the DNA
JOURNAL Patent: US 5851824-A 8 22-DEC-1998;

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Query Match
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Job time : 18363 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2004, 03:06:37 ; Search time 1700 Seconds
(without alignments)
18432.182 Million cell updates/sec

Title: US-10-033-026-3
Perfect score: 7376
Sequence: 1 gggcgccgctgcggcggt.....tgcttgagtgatcgtaccgc 7376

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7376	100.0	7376	2 AAX88001	Aax88001 N-type ca
2	7342	99.5	7364	6 ABLE5869	Ab165869 Lung canc
3	7342	99.5	7364	7 ABZ58366	Abz58366 Human N-t
4	7316.4	99.2	7362	2 AAV42685	AAV42685 DNA encod
5	7316.4	99.2	7362	3 AAA71703	Aaa71703 Human cal
6	7316.4	99.2	7362	6 AAD39955	Aad39955 Human cal
7	7314.8	99.2	7362	2 AAQ84657	Aaq84657 Human neu
8	7313.2	99.1	7362	2 AAQ37817	Aaq37817 Sequence
9	7223.2	97.9	7266	2 AAV29059	Avv29059 Human cal
10	6958	94.3	7177	7 ABZ58367	Abz58367 Human N-t
11	6932.4	94.0	7175	2 AAQ84658	Aaq84658 Human neu
12	6932.4	94.0	7175	2 AAV42686	Aav42686 DNA encod
13	6932.4	94.0	7175	3 AAA71704	Aaa71704 Human cal
14	6932.4	94.0	7175	6 AAD39956	Aad39956 Human cal
15	6913.2	93.7	7175	2 AAQ37818	Aaq37818 Sequence
16	5935.4	80.5	6232	2 AAQ29269	Aaq29269 Human cal
17	5049.2	68.5	7185	4 AAH21860	Aah21860 Mouse N-c
18	3173	43.0	5438	2 AAQ29263	Aaq29263 Human cal
19	2582.6	35.0	6639	6 ABK63679	Abk63679 Rat sequ
20	2512	34.1	7808	2 AAQ84659	Aaq84659 Human neu
21	2512	34.1	7808	3 AAA71718	Aaa71718 Human cal
22	2512	34.1	7808	6 AAD39970	Aad39970 Human cal
23	2512	34.1	7808	7 ABZ58368	Abz58368 Human cal

24	2502.8	33.9	6822	4 AAF32541	Aaf32541 Rabbit P/
25	2502.2	33.9	7791	2 AAQ84660	Aaq84660 Human neu
26	2502.2	33.9	7791	3 AAA71719	Aaa71719 Human cal
27	2502.2	33.9	7791	6 AAD39971	Aad39971 Human cal
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30	2449.6	33.2	6789	2 AAV29372	Avv29372 Calcium i
31	2408.4	32.7	7179	8 ADA13409	Adal13409 Human tra
32	2402.4	32.6	7032	2 AAQ84662	Aaq84662 Human neu
33	2402.4	32.6	7032	3 AAA71720	Aaa71720 Human cal
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35	2356.2	31.9	7089	2 AAQ84663	Aaq84663 Human neu
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39	2341.6	31.7	7088	6 ABZ35344	Abz35344 Human gen
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41	1225.2	16.6	3563	2 AAZ23429	Aaz23429 Human SCA
42	1225.2	16.6	3596	2 AAV61588	Avv61588 Alpha-1A
43	1177.6	16.0	3632	2 AAV61586	Avv61586 Alpha-1A
44	1153.2	15.6	3632	2 AAV61587	Avv61587 Alpha-1A
45	1091.4	14.8	1100	2 AAQ29275	Aaq29275 Human cal

ALIGNMENTS

RESULT 1
AAX88001
ID AAX88001 standard; cDNA; 7376 BP.
XX
AC AAX88001;
XX
DT 06-DEC-1999 (first entry)
XX
DE N-type calcium channel h-alpha-1B+SFVG subunit IIIS3-S4 cDNA.
XX
KW N-type calcium channel; h-alpha-1B+SFVG; human; splice variant;
XX signal transduction; stroke; pain; brain injury; therapy; diagnosis; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 146..7177
FT /*tag= a
FT misc_difference 3856..3867
FT /*tag= b
FT /*note= "12-base insert"
XX
PN WO9946383-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US005392.
XX
PR 13-MAR-1998; 98US-0077901P.
XX (UYBR-) UNIV BROWN RES FOUND.
XX
PI Lipscombe D, Schorge S;
XX WPI; 1999-561677/47.
DR P-PSDB; AAY31809.
XX
PT New isolated human N-type calcium channel isoform, used to develop
PT products, for treating, e.g. stroke or traumatic brain injury.
XX
PS Claim 7; Page 73-84; 141pp; English.
XX
CC This the nucleotide sequence of cDNA coding for a human N-type calcium
CC channel isoform (splice variant), h-alpha-1B-SFVG (see AAY31808), that is
CC involved in central nervous system signalling. The sequence includes a 12
CC nucleotide insert (see also AAX88000) that is not present in previously

published human alpha-1B Ca channel isoform sequences. The insert encodes a 4-amino acid insert (see AAY31808) corresponding to residues 1238-41 of the protein. The h-alpha-1B-SVFG subunit makes up a significant portion of the N-type Ca channel alpha-1B subunit mRNA in human brain, and is differentially distributed in different parts of the brain. The invention also includes fragments and biologically functional variants of the h-alpha-1B-SVFG channel, as well as inhibitors of h-alpha-1B-SVFG expression or function. The h-alpha-1B-SVFG nucleic acids, polypeptides and inhibitors can be used in the treatment and/or diagnosis of conditions characterized by aberrant brain neuronal calcium current, such as stroke, pain (e.g. neuropathic pain) and traumatic brain injury

SQ Sequence 7376 BP; 1445 A; 2280 C; 2222 G; 1429 T; 0 U; 0 Other;

Query Match		100.0%;	Score 7376;	DB 2;	Length 7376;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 7376;		Conservative	0;	Mismatches	0;
		Indels	0;	Gaps	0;
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QY	61	GCTGCTCCGCTCTGAGCGCTGCGCGCGCCCGCGCGCCCTCCCTGCGCGGGCGCGCTGGGCGG	120		
Db	61	GCTGCTCCGCTCTGAGCGCTGCGCGCGCCCGCGCGCCCTCCCTGCGCGGGCGCGCTGGGCGG	120		
QY	121	GGGATGCAAGCGGGCGCGCGAGCCATGCTGCTTCGTTGCGGAGCAGACTGGCGCGCGCTA	180		
Db	121	GGGATGCAAGCGGGCGCGCGAGCCATGCTGCTTCGTTGCGGAGCAGACTGGCGCGCGCTA	180		
QY	181	TGGAGGCCCGCGCGGAGAGCGGGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	240		
Db	181	TGGAGGCCCGCGCGGAGAGCGGGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	240		
QY	241	GGGTCCCGGGGGCTGCAAGTCCCGCGCAGCGGGTCTCTACAAGCAATCGATCGCGCAGCG	300		
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QY	301	CGCGCGACCATGGCGCTGTACAACCCCATCCCGGTCAAGCAACCTCATCGCAAGCTCTCACCGTCAA	360		
Db	301	CGCGCGACCATGGCGCTGTACAACCCCATCCCGGTCAAGCAACCTCATCGCAAGCTCTCACCGTCAA	360		
QY	361	CGCTCGCTCTTCGTTTCAGCGAGGACAACGTCGTCGCAAAATACGCAAGCGCATCAC	420		
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QY	421	CGAGTGGCTCCATTCGAGTATATGATTCGCGCCACCATCATCGCAAACTGCAATCGTGCT	480		
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QY	481	GGCCCTGGAGCAGCACTCCCTGATGGGACAACAGCCCATGTCGAGCGGCTGGACGA	540		
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Db	541	CACGAGCCCTATTTTCATCGGGATCTTTGCTTCGAGGAGGAGTCAAAATCATCGCTCT	600		
QY	601	GGGCTTTGTCTTCCACAAGGCTCTTACCTGCGGAACGGCTGGAACTGATGACTTCGT	660		
Db	601	GGGCTTTGTCTTCCACAAGGCTCTTACCTGCGGAACGGCTGGAACTGATGACTTCGT	660		
QY	661	GGTCGTCTCACAAGGATCTTTCGCAAGGTGGAACTGACTTCGACTCGAAGCTGAG	720		
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QY	781	GCTCAAGTCCATCATGAAGCCATGGTTCATCTTCGCAGATTGGGCTCTTCTCTTT	840		
Db	781	GCTCAAGTCCATCATGAAGCCATGGTTCATCTTCGCAGATTGGGCTCTTCTCTTT	840		

QY 1921 GAGCTCCTCGGGAACCTGGTGTGTCCCTGCTGAACTCCATGAAGTCCATCATCAGCCT 1980
DB 1921 GAGCTCCTCGGGAACCTGGTGTGTCCCTGCTGAACTCCATGAAGTCCATCATCAGCCT 1980
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QY 3901 GTCTCTGAGAGTCTTCTGAGTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3960
DB 3901 GTCTCTGAGAGTCTTCTGAGTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3960
QY 3961 CAAAGGCTGTGTTGAGCTGTGTTGAGCTGTGTTGAGCTGTGTTGAGCTGTGTTGAGCTGTG 4020
DB 3961 CAAAGGCTGTGTTGAGCTGTGTTGAGCTGTGTTGAGCTGTGTTGAGCTGTGTTGAGCTGTG 4020
QY 4021 CTAACATGCTCTTCAATGTTTCAATGTTTCAATGTTTCAATGTTTCAATGTTTCAATGTTTCA 4080
DB 4021 CTAACATGCTCTTCAATGTTTCAATGTTTCAATGTTTCAATGTTTCAATGTTTCAATGTTTCA 4080
QY 4081 TTTTCTACTGCAAGATGATTCAGAGGAGTGGAGAGGAGTGGAGAGGAGTGGAGAGGAGTGGAG 4140

Db 4081 TTTCTACTGCACAGATGAATCCAAAGGAGCTGGAGGGAGCTGCAGGGGTCAGTATTGGGA 4140
Qy 4141 TTATGAGAAGGAGAGTGGAGAGCTCAGCCCGAGGAGTGAAGAAATACGACTTTCACTA 4200
Db 4141 TTATGAGAAGGAGAGTGGAGAGCTCAGCCCGAGGAGTGAAGAAATACGACTTTCACTA 4200
Qy 4201 CGACAATGTGCTCTGGGCTCTGTGACGCTGTTACAGTGTCCACGGGAGAGGCTGGCC 4260
Db 4201 CGACAATGTGCTCTGGGCTCTGTGACGCTGTTACAGTGTCCACGGGAGAGGCTGGCC 4260
Qy 4261 CATGGTCTGTAACACATCCCTGTGATGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4320
Db 4261 CATGGTCTGTAACACATCCCTGTGATGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4320
Qy 4321 CCGCATGGAGCTGTCCATCTTCTACGTGTGCTACTTTGTGGTCTTTTCCCTTTCTTCTGGT 4380
Db 4321 CCGCATGGAGCTGTCCATCTTCTACGTGTGCTACTTTGTGGTCTTTTCCCTTTCTTCTGGT 4380
Qy 4381 CAACATCTTTGTGGCTTTGATCATCATCACTTTCCAGGAGCAGGGGGAACAAGTGTATGTC 4440
Db 4381 CAACATCTTTGTGGCTTTGATCATCATCACTTTCCAGGAGCAGGGGGAACAAGTGTATGTC 4440
Qy 4441 TGAATGCAGCTCGAGAGAACAGAGGGCTTGCACTTGATTCGCCATCAGCGCCAAACC 4500
Db 4441 TGAATGCAGCTCGAGAGAACAGAGGGCTTGCACTTGATTCGCCATCAGCGCCAAACC 4500
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Db 4501 CCTGACACGGTACATGCCCAAAACCGGCAGTGTCTCCAGTATTAAGAGCTGACATTTGT 4560
Qy 4561 GGTCTCCCGCCCTTTGATATCTTCATCATGAGCAGTATGAGCCCTCAACACTGTGGTGTCT 4620
Db 4561 GGTCTCCCGCCCTTTGATATCTTCATCATGAGCAGTATGAGCCCTCAACACTGTGGTGTCT 4620
Qy 4621 GATGATGAAGTCTATGATGACCCCTATGAGTACGAGCTGATCTGAAATGCGCTGAACAT 4680
Db 4621 GATGATGAAGTCTATGATGACCCCTATGAGTACGAGCTGATCTGAAATGCGCTGAACAT 4680
Qy 4681 CGTGTTCACATCATCATGTTCTCCATGGAATGCGTGTGAGAGATCATCGCCTTTGGGGTGTCT 4740
Db 4681 CGTGTTCACATCATCATGTTCTCCATGGAATGCGTGTGAGAGATCATCGCCTTTGGGGTGTCT 4740
Qy 4741 GAACTATTTTCAGAGATGCGCTGGAATGTCTTTGACTTTGTCACTGTGTTGGGAATATTAC 4800
Db 4741 GAACTATTTTCAGAGATGCGCTGGAATGTCTTTGACTTTGTCACTGTGTTGGGAATATTAC 4800
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Db 4801 TGATATTTTGTAGTACAGAGATTTGCGGAAACGAAATTTTCATCAACCTCAGCTTCCTCCG 4860
Qy 4861 CCTCTTTCAGAGCTGCGGCTGTATCAAGCTGTCTCGCCAGGGCTACACCATCCGATCCT 4920
Db 4861 CCTCTTTCAGAGCTGCGGCTGTATCAAGCTGTCTCGCCAGGGCTACACCATCCGATCCT 4920
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Db 4921 GCTGTGGACCTTTGTCCAGTCTTCAAGGCCCTGCTCACTGTGTTGGGAATATTGCCCTGGATGA 5040
Qy 4981 GCTGTCTTCTAFTACGCCATCATCGGCATCAGGTGTTTGGGAATATTGCCCTGGATGA 5040
Db 4981 GCTGTCTTCTAFTACGCCATCATCGGCATCAGGTGTTTGGGAATATTGCCCTGGATGA 5040
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Db 5041 TGACACCAAGATCAACCGCCACACACTTCGGACGCTTTTGGACCCCTGATGTGCT 5100
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Db 5101 GTTCAGGAGCCACCGGGGAGGCTTGGCAGAGATCATGCTGTCTGCTGCTGAGCAACCA 5160
Qy 5161 GGCCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGACTTTGCCCTACTTCTACTT 5220
Db 5161 GGCCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGACTTTGCCCTACTTCTACTT 5220

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Db 5281 GGACAATTTTGAGTACCTTCACGGGGACTCTTCTCATCTCTAGTCTCTCACCTTGGATGA 5340
Qy 5341 GTTTCATCCGGTCTGGGCTGAATACGACCGGCTGGTGTGGGGCATCAGTTTACATGA 5400
Db 5341 GTTTCATCCGGTCTGGGCTGAATACGACCGGCTGGTGTGGGGCATCAGTTTACATGA 5400
Qy 5401 CATGTTTGAGATGCTGAAAACATGTCCCCTCTGGGGCTGGGGAGAAATGCCCTGC 5460
Db 5401 CATGTTTGAGATGCTGAAAACATGTCCCCTCTGGGGCTGGGGAGAAATGCCCTGC 5460
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Db 5641 GTGGGCAATCTGCCCCAGAAAGACTTTTGGACTTTGTGTGTACACCCCATTAAGCCTGATGA 5700
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Db 5761 AACCCACAGAGACCAAGATGCAGCGCTCTGGAGGCTCTCCAGAGTGGTCTGTGTGTC 5820
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Db 5821 CTTGTTTCCACCTCTGAAGGCCACCTTGAGCAGACACAGCCGCTGTGTGTC 5880
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Db 5881 CCGGGTTTTCTTCGACAGAGAGTTTCCACCTCTCCAGCAATGGCGGGGTCATACAAA 5940
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Db 5941 CCAAGAGAGTGGCATCAAAGAGTCTGTCTCTTGGGGCACTCAAAGGACCCAGGATGCACC 6000
Qy 6001 CCATGAGGCCAGGCCACCCCTGGAGCTGGCACTCCACAGAGATCCCTGTGGGCGGTC 6060
Db 6001 CCATGAGGCCAGGCCACCCCTGGAGCTGGCACTCCACAGAGATCCCTGTGGGCGGTC 6060
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Db 6061 AGGAGCAGTGGCTGTGGAGCTTCAGATGCAGAGATACCCGGAGGGGCTTGTATGGGA 6120
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Db 6121 GCCCCAGCTTGGGCTGGAGAGCCAGGGTTCGAGCGGCTCTCCATGCCCGGCTTGGCGCGGA 6180
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Db 6181 GACTCAGCCCTGTCAGATGCGCCCATGAAGGCTTCATCTTCAGCTTGGCCACAGCG 6240
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Qy 6361 GAAGGGCCCGAGCGCTGTGTCGATATGATGAGCGCACCAAGCAGTGTGTGGGCGCGG 6420
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Db 6421 GCTCCCGCGGAGAGGGGCTTACAGGCTGCCGCGGGAACGAGAGCGCGGACGAGGCG 6480
Qy 6481 GGGCGGTGCCAGAGCGGAGCGCTCATCTCTCTCTCGAGAGAGAGCGCTTCTA 6540
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Db 6541 CTCCTGCGACCGCTTTGGGGCGGTGAGCGCCCGAAGCCCTCCCTCAGCAGCCA 6600
Qy 6601 CCCAACGTGCGCAACAGCTGSCCAGGAGCGGGACCCACCCACAGGGCAGTGGTCCGT 6660
Db 6601 CCCAACGTGCGCAACAGCTGSCCAGGAGCGGGACCCACCCACAGGGCAGTGGTCCGT 6660
Qy 6661 GAATGGAGCGCCCTGTGTCAACATCTGTGTAGCAACCCCGCGCGCGGTGGCGGAG 6720
Db 6661 GAATGGAGCGCCCTGTGTCAACATCTGTGTAGCAACCCCGCGCGCGGTGGCGGAG 6720
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Db 6721 GCAGCTCCCGCAGAGCGCCCTGACTCCCGCCGAGCATCACTTACAGAGCGGCAACTC 6780
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Db 6781 CTCACCCATCCACTTCGCGGGGCTCAGACAGGCTCCCTGCTTCTCCCGAGCGGCT 6840
Qy 6841 CAGCGGTGGGCTTTCGAAACAAAGCGGCTGCTGAGAGAGCGGCTCAGCGAGCGGCT 6900
Db 6841 CAGCGGTGGGCTTTCGAAACAAAGCGGCTGCTGAGAGAGCGGCTCAGCGAGCGGCT 6900
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Db 6901 GGCGCTGGCTTCGAATTGCTCTGACCTTACCTGGGGCAGGCTGTGACAGTGAAGC 6960
Qy 6961 CTCTGTCCAGCGCTTCCAGGAGCAGCTCACTTTCGAGAGGCTGTGGCCACCAACTC 7020
Db 6961 CTCTGTCCAGCGCTTCCAGGAGCAGCTCACTTTCGAGAGGCTGTGGCCACCAACTC 7020
Qy 7021 GGGCGGTCTCCAGGACTTCTTACGTGTCTCTGACCTCCAGTCTCACTCTCTCG 7080
Db 7021 GGGCGGTCTCTCCAGGACTTCTTACGTGTCTCTGACCTCCAGTCTCACTCTCTCG 7080
Qy 7081 CCGGTGCCAAGGTTACCTACCTCGGACTCAGCTCGGGTGGCGAGCAGCGCA 7140
Db 7081 CCGGTGCCAAGGTTACCTACCTCGGACTCAGCTCGGGTGGCGAGCAGCGCA 7140
Qy 7141 CAGCTACCAACCGCTTACCAAGACCACTGTGTGTAGTGCACCGCTCAGACGC 7200
Db 7141 CAGCTACCAACCGCTTACCAAGACCACTGTGTGTAGTGCACCGCTCAGACGC 7200
Qy 7201 CTGATGAGAGCGGTGTGTCAGTGAATGATTTTATCATCAACAGGGGAGTGG 7260
Db 7201 CTGATGAGAGCGGTGTGTCAGTGAATGATTTTATCATCAACAGGGGAGTGG 7260
Qy 7261 CCCTCGGGGAGGCTTGGCCACCTTGGTGAAGCTCTGTGGGCGGCTCCCTCCCTCCCT 7320
Db 7261 CCCTCGGGGAGGCTTGGCCACCTTGGTGAAGCTCTGTGGGCGGCTCCCTCCCTCCCT 7320
Qy 7321 CCCCTCTTTTACTTAGACGAGCAATAAGCCCTTGTGTGAGTACGTACCGC 7376
Db 7321 CCCCTCTTTTACTTAGACGAGCAATAAGCCCTTGTGTGAGTACGTACCGC 7376

RESULT 2
ABL65869
ID ABL65869 standard; DNA; 7364 BP.
XX
AC ABL65869;
XX
DT 15-MAY-2002 (first entry)
XX
Lung cancer related gene sequence SEQ ID NO:4206.
XX
DE Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233161P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WFI; 2002-188264/24.
XX

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 4206; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour

Sequence 7364 BP; 1444 A; 2278 C; 2216 G; 1426 T; 0 U; 0 Other;

Query Match 99.5%; Score 7342; DB 6; Length 7364;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 7364; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

PT	Screening for anti-neoplastic agent involves exposing cells to a chemical	
PT	agent to be tested for anti-neoplastic activity, and determining a change	
PT	in expression of a gene of a signature gene set.	
XX		
PS	Claim 1; SEQ ID NO 4206; 44pp; English.	
XX		
CC	The present invention describes a method (M1) for screening for an anti-	
CC	neoplastic agent. The method involves exposing cells to a chemical agent	
CC	to be tested for anti-neoplastic activity, determining a change in	
CC	expression of at least one gene (I) of a signature gene set, where (I)	
CC	comprises a sequence (S) selected from 847 sequences (given in ABL61664	
CC	to ABL70110), or is at least 95% identical to (S), where a change in	
CC	expression is indicative of anti-neoplastic activity. (I) has cytostatic	
CC	activity and can be used in gene therapy. M1 can be used for screening an	
CC	anti-neoplastic agent, and can be used for producing a product which is	
CC	the data collected with respect to the anti-neoplastic agent as a result	
CC	of M1, and the data is sufficient to convey the chemical structure and/or	
CC	properties of the agent. M1 can be used in the treatment of cancer such	
CC	as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,	
CC	prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell	
CC	cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous	
CC	cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'	
CC	tumour	
XX		
SQ	Sequence 7364 BP; 1444 A; 2278 C; 2216 G; 1426 T; 0 U; 0 Other;	
	Query Match 99.5%; Score 7342; DB 6; Length 7364;	
	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 7364; Conservative 0; Mismatches 0; Indels 12; Gaps 1;	
Qy	1 GCGGCGGCGGCTGCGGCGGTGGGGCGGGCGAGGTCCGTGCGGTCCGGGCGGCTCCGTG 60	
Db		
Qy	1 GCGGCGGCGGCTGCGGCGGTGGGGCGGGCGAGGTCCGTGCGGTCCGGGCGGCTCCGTG 60	
Db		
Qy	61 GCTGCTCCGCTGTAGCGCTGTGCGCGCCCGCGCCCTCCCTGCGGGCGGCTGGGCGG 120	
Db		
Qy	61 GCTGCTCCGCTGTAGCGCTGTGCGCGCCCGCGCCCTCCCTGCGGGCGGCTGGGCGG 120	
Db		
Qy	121 GGGATGACCGCGGGGCCCGGGAGCCATGCTCGCTTCGGGGACGAGCTGGGCGGCGGCTA 180	
Db		
Qy	121 GGGATGACCGCGGGGCCCGGGAGCCATGCTCGCTTCGGGGACGAGCTGGGCGGCGGCTA 180	
Db		
Qy	181 TGGAGGCCCGGGCGGGAGAGGGGCCCGGGCGGCGGCGGCGGCGGGCGGCGGCGGCGG 240	
Db		
Qy	181 TGGAGGCCCGGGCGGGAGAGGGGCCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240	
Db		
Qy	241 GGGTCCCGGGGGGCTGCGAGCCCGGCGAGCGGGTCTCTACAGCAATCGATCGGCGAGCG 300	
Db		
Qy	241 GGGTCCCGGGGGGCTGCGAGCCCGGCGAGCGGGTCTCTACAGCAATCGATCGGCGAGCG 300	
Db		
Qy	301 CGCGGGACCATGGGCGCTGTACAACCCCATCCCGGTCAAGAGAACTGCTTTACCGTCAA 360	
Db		
Qy	301 CGCGGGACCATGGGCGCTGTACAACCCCATCCCGGTCAAGAGAACTGCTTTACCGTCAA 360	
Db		
Qy	361 CGGCTCGCTCTTCGTTTTCAGCGAGGACAAAGTGTGTCGCGCAATACCGAGCGGCATCAC 420	
Db		
Qy	361 CGGCTCGCTCTTCGTTTTCAGCGAGGACAAAGTGTGTCGCGCAATACCGAGCGGCATCAC 420	
Db		
Qy	421 CGAGTGGGCTCCATTCGAGTATATGATCTCGGCCACCATCATCGCCAACTGCATCGTGTCT 480	
Db		
Qy	421 CGAGTGGGCTCCATTCGAGTATATGATCTCGGCCACCATCATCGCCAACTGCATCGTGTCT 480	
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Qy	481 GGGCTTGGAGGACGACCTCCCTGTATGGGGAACAAACGCCCCATGTCCGAGCGGCTGGACGA 540	
Db		
Qy	481 GGGCTTGGAGGACGACCTCCCTGTATGGGGAACAAACGCCCCATGTCCGAGCGGCTGGACGA 540	
Db		
Qy	541 CACGAGCGCTATTTCATCGGGATCTTTTGTCTCGAGCGAGGATCAAAATCATCGCTCT 600	
Db		
Qy	541 CACGAGCGCTATTTCATCGGGATCTTTTGTCTCGAGCGAGGATCAAAATCATCGCTCT 600	
Db		
Qy	601 GGGCTTTGCTTCCACAAAGGCTCTTACCTCGGAAACGGCTGGAAACGTCATGGACTTCGT 660	
Db		
Qy	601 GGGCTTTGCTTCCACAAAGGCTCTTACCTCGGAAACGGCTGGAAACGTCATGGACTTCGT 660	
pB		

Qy	661 GGTGCTCTCACAGGATCCCTTGCCACGCGTGGAACTGACTTCGACCTGCGAAACACTGAG 720	
Db		
Qy	661 GGTGCTCTCACAGGATCCCTTGCCACGCGTGGAACTGACTTCGACCTGCGAAACACTGAG 720	
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Qy	721 GGCTGTGGTGTGCTGAGGCGCCCTGAAAGCTGTCTGGGATTCGAAGTTTGCAGGTGGT 780	
Db		
Qy	721 GGCTGTGGTGTGCTGAGGCGCCCTGAAAGCTGTGTCTGGGATTCGAAGTTTGCAGGTGGT 780	
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Qy	781 GCTCAAGTTCATCATGAAGGCCATGGTTTCCATCTCTCGAGATTGGGCTGCTTCTTCTT 840	
Db		
Qy	781 GCTCAAGTTCATCATGAAGGCCATGGTTTCCATCTCTCGAGATTGGGCTGCTTCTTCTT 840	
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Qy	841 TGCCATCTCATGTTTGGCCATCATTTGGCTGGAGTCTTACATGGGCAAGTTTCCAAGGC 900	
Db		
Qy	841 TGCCATCTCATGTTTGGCCATCATTTGGCTGGAGTCTTACATGGGCAAGTTTCCAAGGC 900	
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Qy	901 CTGTTTCCCAACACAGACAGATCGGAGCCGCTGGGTGACTTCCCTGTGCGAAGGAGGC 960	
Db		
Qy	901 CTGTTTCCCAACACAGACAGATCGGAGCCGCTGGGTGACTTCCCTGTGCGAAGGAGGC 960	
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Qy	961 CCGAGCCGCGTGTGCGAGGGCGACACTGAGTGC CGGAGTACTTGGCCAGSACCCCACTT 1020	
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Qy	961 CCGAGCCGCGTGTGCGAGGGCGACACTGAGTGC CGGAGTACTTGGCCAGSACCCCACTT 1020	
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Qy	1021 TGGCATCACCAACTTTTGACAATATCCTGTTTGGCATCTTGAACGGTGTTCAGTGCATCAC 1080	
Db		
Qy	1021 TGGCATCACCAACTTTTGACAATATCCTGTTTGGCATCTTGAACGGTGTTCAGTGCATCAC 1080	
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Qy	1081 CATGGAGGCTGGACATGACATCTCTATATAAACAACGATGCGGCGGCAACACTGGAA 1140	
Db		
Qy	1141 CTGGCTTACTTTCATCCCTCTCATCATCATCATCATCATCATCATCATCATCATCATCAT 1200	
Db		
Qy	1141 CTGGCTTACTTTCATCCCTCTCATCATCATCATCATCATCATCATCATCATCATCATCAT 1200	
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Db		
Qy	1201 GGGCGTCTCTCGGGGAGTTTCCCAAGGAGCGAGAGGGTGGAGAACGCGCGGCCCTT 1260	
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Qy	1441 GAGGAGAGAGGACCGGTTTTCAGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500	
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Qy	1441 GAGGAGAGAGGACCGGTTTTCAGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500	
Db		
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Db		
Qy	1501 CCTCAAGAGCGGAGACAGAGAGGCTGCTCATCTTCCGGAGGAGGAGAGATGTTCCG 1560	
Db		
Qy	1561 GTTTTTTATCCGCGCATGTGTGAAGGCTCAGAGCTTCTACTGGGTGTGTGTGTGTGTGTGTGT 1620	
Db		
Qy	1561 GTTTTTTATCCGCGCATGTGTGAAGGCTCAGAGCTTCTACTGGGTGTGTGTGTGTGTGTGTGT 1620	
Db		
Qy	1621 GGGCTTGAACACACTGTGTGTGGCCATGGTGCATTAACCAAGCCGCGCGGCTTACCAC 1680	
Db		
Qy	1621 GGGCTTGAACACACTGTGTGTGGCCATGGTGCATTAACCAAGCCGCGCGGCTTACCAC 1680	
Db		
Qy	1681 GACCTGTATTTTGCAGAGTTTGT 1740	
Db		
Qy	1681 GACCTGTATTTTGCAGAGTTTGT 1740	
Db		

QY 1741 GATGTATGGCCCTGGGGCCAGAGTACTTCCGGTCTCTTCAACTGCTTCGACTTTGG 1800
Db 1741 GATGTATGGCCCTGGGGCCAGAGTACTTCCGGTCTCTTCAACTGCTTCGACTTTGG 1800
QY 1801 GGTTCATCGTGGGAGCGTCTTTGAAGTGTCTGGCGGCCCATCAAGCCGGGAAGCTCCTT 1860
Db 1801 GGTTCATCGTGGGAGCGTCTTTGAAGTGTCTGGCGGCCCATCAAGCCGGGAAGCTCCTT 1860
QY 1861 TGGGATCAGTGTGCTGGGGGCCCTCCGCTCTCTGAGGATCTTCAAAGTACAGAGTACTG 1920
Db 1861 TGGGATCAGTGTGCTGGGGGCCCTCCGCTCTCTGAGGATCTTCAAAGTACAGAGTACTG 1920
QY 1921 GAGCTCCCTGGGAACTCTGTGTGTCTCCCTGCTGAACTCATGATGAAGTCCATCAGCCT 1980
Db 1921 GAGCTCCCTGGGAACTCTGTGTGTCTCCCTGCTGAACTCATGATGAAGTCCATCAGCCT 1980
QY 1981 GCTCTTCTTGTCTCTTCTGTTTCATTGTGTCTTCGCCCTGCTGGGATGCAAGCTGTTTGG 2040
Db 1981 GCTCTTCTTGTCTCTTCTGTTTCATTGTGTCTTCGCCCTGCTGGGATGCAAGCTGTTTGG 2040
QY 2041 GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCAACTTCGACACCTTCCCTGCCGC 2100
Db 2041 GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCAACTTCGACACCTTCCCTGCCGC 2100
QY 2101 CATCTCATCTGCTTCAGATCTCTGACGGAGAGACTGGAAATGCAATGATGATCAGG 2160
Db 2101 CATCTCATCTGCTTCAGATCTCTGACGGAGAGACTGGAAATGCAATGATGATCAGG 2160
QY 2161 GATCGAATCGCAAGCGCGTCAGCAAGGATGTTCTCGTCCCTTTTACTTCAATGTCCCT 2220
Db 2161 GATCGAATCGCAAGCGCGTCAGCAAGGATGTTCTCGTCCCTTTTACTTCAATGTCCCT 2220
QY 2221 GACACTGTTCCGAACTACACTCTGCTGAAATGTCTTTCTGGCCATCGTGTGGACAACCT 2280
Db 2221 GACACTGTTCCGAACTACACTCTGCTGAAATGTCTTTCTGGCCATCGTGTGGACAACCT 2280
QY 2281 GGCCAAAGCCCAAGAGTGCACAAAGGATGAAGAGGAGATGAAGAGCAGCAATCAGAA 2340
Db 2281 GGCCAAAGCCCAAGAGTGCACAAAGGATGAAGAGGAGATGAAGAGCAGCAATCAGAA 2340
QY 2341 GCTTGTCTCTCAAAGGCCAAAGAGTGGCTGAAGTCAAGCCCATGCTGCCCGGACAT 2400
Db 2341 GCTTGTCTCTCAAAGGCCAAAGAGTGGCTGAAGTCAAGCCCATGCTGCCCGGACAT 2400
QY 2401 CTCCATCGCCCGCAGGACAGAACTCGGCCAAAGCGCGCTCGGTGTGGAGACAGCGGC 2460
Db 2401 CTCCATCGCCCGCAGGACAGAACTCGGCCAAAGCGCGCTCGGTGTGGAGACAGCGGC 2460
QY 2461 CAGCCAGTACGGCTGCAGAACTCTGGGCGCAGCTGCGAGCGCTGTACAGCGAGATGGA 2520
Db 2461 CAGCCAGTACGGCTGCAGAACTCTGGGCGCAGCTGCGAGCGCTGTACAGCGAGATGGA 2520
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Db 2521 CCCGAGAGCGGCTGCGCTTCGCACTACGCGCCACTCGCGGCCCGCACATGAAGACGA 2580
QY 2581 CCTGGACCGGCGCTGTGTGTGAGCTGGGCGCGCAAGCGCGCGCGCGCGCGTGGAGG 2640
Db 2581 CCTGGAACGGCGCTGTGTGTGAGCTGGGCGCGCAAGCGCGCGCGCGCGTGGAGG 2640
QY 2641 CAAAGCCGACCTGAGGCTGGAGGCGCCCGGAGGCGTGCACCTCCGCGCAGGACCA 2700
Db 2641 CAAAGCCGACCTGAGGCTGGAGGCGCCCGGAGGCGTGCACCTCCGCGCAGGACCA 2700
QY 2701 CCGGACCGGACAGGACAGACCCCGCGCGCGGGAACAGACCGAGCAGAGGCCCC 2760
Db 2701 CCGGACCGGACAGGACAGACCCCGCGCGCGGGAACAGACCGAGCAGAGGCCCC 2760
QY 2761 GAAGCGGAGCGGGAGCCCGTGTCCCGGAGGAGCGCGCGCGGCGCACCCAGCCA 2820
Db 2761 GAAGCGGAGCGGGAGCCCGTGTCCCGGAGGAGCGCGCGCGGCGCACCCAGCCA 2820
QY 2821 CAGCAAGGAGCGCGGGCGCCCGAGGCGCGGAGCGAGCGCGCGCGCGCGCC 2880

Db 2821 CAGCAAGGAGCGCGGGCGCCCGGAGCGCGAGCGAGCGCGCGCGCGCGCGCC 2880
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Db 2881 CGAGGGCGCGCGCGCACCAACCGGGCGCTCCCGGAGAGGCGCGCGCGAGCGGAGCC 2940
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QY 3181 CAAGGAAAAGAGCTCCGGAAACCAACAGCGCCCGGAGGCCACACTGTGACCTGGAGACCAG 3240
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QY 3421 GGTCTGTTCCAGTGTAACTGTGACCTTGGAAAGCAGAGAGGGAAGAGAGGTGGA 3480
Db 3421 GGTCTGTTCCAGTGTAACTGTGACCTTGGAAAGCAGAGAGGGAAGAGAGGTGGA 3480
QY 3481 AGCGGATGACGTGATGAGGAGCGCGCCCGCTATGCTCCCATACAGCTCCCATGTTCTG 3540
Db 3481 AGCGGATGACGTGATGAGGAGCGCGCCCGCTATGCTCCCATACAGCTCCCATGTTCTG 3540
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QY 3601 CGAGGTGGTCATTCTCGTGTGTCATCGCTTGACGATCGCTGCTGAGGAGCC 3660
Db 3601 CGAGGTGGTCATTCTCGTGTGTCATCGCTTGACGATCGCTGCTGAGGAGCC 3660
QY 3661 AGTGCACAGACTCGCCCAAGAACACGCTCTGAAATACCTGGAATTACATTTCACTGG 3720
Db 3661 AGTGCACAGACTCGCCCAAGAACACGCTCTGAAATACCTGGAATTACATTTCACTGG 3720
QY 3721 TGTCTTTAATCTTTGAGATGATGAAGATGATGCACTTGGGACTGCTGCTTCAACCTGG 3780
Db 3721 TGTCTTTAATCTTTGAGATGATGAAGATGATGCACTTGGGACTGCTGCTTCAACCTGG 3780
QY 3781 AGCCTATTTCCGGGACTTGGGAACATTCTGGAATTTCTGAGTCAAGTGGCGCCCTGGT 3840
Db 3781 AGCCTATTTCCGGGACTTGGGAACATTCTGGAATTTCTGAGTCAAGTGGCGCCCTGGT 3840
QY 3841 GCGGTTTGTCTTC-----AGGATCCAAAGGGAAGAGCATCAATACCATCAA 3900
Db 3841 GCGGTTTGTCTTC-----AGGATCCAAAGGGAAGAGCATCAATACCATCAA 3900
QY 3901 GTCTCTGAGAGTCTTCTGTTCTCTGCGGCCCTCAAGACCATCAACCGGTGCCCAAGCT 3960
Db 3901 GTCTCTGAGAGTCTTCTGTTCTCTGCGGCCCTCAAGACCATCAACCGGTGCCCAAGCT 3960

Db 3889 GTCTGTGAGAGTCCTTGGTGTCTGGGCGCCCTCAAGACCATCAAAACGGCTGCCAAGCT 3948
Qy 3961 CAAGGCTGTGTTGACTGTGGTGAATCCCTCGTAAGAATGCTCAACATCTTCATTGT 4020
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Qy 4081 TTTCTACTGCCACAGATGAATCCAAGAGCTTGAGAGGAGCTGCAGGGTCAATTTGGA 4140
Db 4069 TTTCTACTGCCACAGATGAATCCAAGAGCTTGAGAGGAGCTGCAGGGTCAATTTGGA 4128
Qy 4141 TTATGAGAAGGAGGAAGTGAAGCTCAGCCAGGCAAGTGAAGAAATACGACTTTCACCTA 4200
Db 4129 TTATGAGAAGGAGGAAGTGAAGCTCAGCCAGGCAAGTGAAGAAATACGACTTTCACCTA 4188
Qy 4201 CGACAATGTCTCTGGGCTCTGCTGACGCTGTTCACAGTGTCCACGGGAGAAGCTGGCC 4260
Db 4189 CGACAATGTCTCTGGGCTCTGCTGACGCTGTTCACAGTGTCCACGGGAGAAGCTGGCC 4248
Qy 4261 CATGTGCTGAACACTCGGTGGATGCCACCTATGAGAGCAAGGTCCAAGCCCTGGGTA 4320
Db 4249 CATGTGCTGAACACTCGGTGGATGCCACCTATGAGGAGCAAGGTCCAAGCCCTGGGTA 4308
Qy 4321 CGCATGAGAGCTGTCCATCTCTACGTGTCTACTTTGTGGTCTTTCCCTCTCTCTTCGT 4380
Db 4309 CGCATGAGAGCTGTCCATCTCTACGTGTCTACTTTGTGGTCTTTCCCTCTCTCTTCGT 4368
Qy 4381 CAACTACTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGGAACAAGGTGATGTC 4440
Db 4369 CAACTACTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGGAACAAGGTGATGTC 4428
Qy 4441 TGAATGCAGCTCGAGAGAGCAAGAGGCTTGCAATTCATTCGCAATCAGGCGCAAAACC 4500
Db 4429 TGAATGCAGCTCGAGAGAGCAAGAGGCTTGCAATTCATTCGCAATCAGGCGCAAAACC 4488
Qy 4501 CCTGACAGGTTACATGCCCCAAAACCGGCAGTCGTTCCAGTATTAAGAGTGAACATTTGT 4560
Db 4489 CCTGACAGGTTACATGCCCCAAAACCGGCAGTCGTTCCAGTATTAAGAGTGAACATTTGT 4548
Qy 4561 GGTCTCCCGCCCTTTGAATACTTCATCATGCGCCATGATAGCCCTCAACACTGTGGTGT 4620
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Db 4609 GATGATGAAGTTCTATGATGACCCCTATGAGTACAGCTGATGCTGAATCCCTGACAT 4668
Qy 4681 CGTGTTCACATCCATGTTCTCCATGGAATGGGTGCTGAAGATCATCGGCTTTGGGGTGT 4740
Db 4669 CGTGTTCACATCCATGTTCTCCATGGAATGGGTGCTGAAGATCATCGGCTTTGGGGTGT 4728
Qy 4741 GAACTATTTACAGATGCTCGAATGTTCTTTGACTTTGCTCACTGTGTTGGGAAGTATTAC 4800
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Qy 4801 TGATATTTTACTACAGAGATTGCGGAACGAACAAATTTTCATCAACTCAGCTTCCTCCG 4860
Db 4789 TGATATTTTACTACAGAGATTGCGGAACGAACAAATTTTCATCAACTCAGCTTCCTCCG 4848
Qy 4861 CCTCTTTCCAGCTGCGCGGCTGATCAAGCTGTCTCGCGCAGGGCTACACCATCCGATCCT 4920
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Qy 4921 GCTGTGGAACCTTTGTCCAGTCCCTTCAAGGCCCTGCCCCCTACGTTGTCTGCTCATTTGCCAT 4980
Db 4909 GCTGTGGAACCTTTGTCCAGTCCCTTCAAGGCCCTGCCCCCTACGTTGTCTGCTCATTTGCCAT 4968
Qy 4981 GCTGTTCCTTACTACGCCATCATCGGCATGACAGTGTGTTGGGAATATTGCCCTGGATGA 5040
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Qy 5161 GGCCTGTGATGAGCAGGCGCAATGCCACCGAGTGTGGAAGTGAATTTGGCTACTTCTACTT 5220
Db 5149 GGCCTGTGATGAGCAGGCGCAATGCCACCGAGTGTGGAAGTGAATTTGGCTACTTCTACTT 5208
Qy 5221 CGTCTCTCTCATCTTCTGCTGCTCTTCTGATGTTGAACTCTTCTGCTGGTGTGATCAT 5280
Db 5209 CGTCTCTCTCATCTTCTGCTGCTCTTCTGATGTTGAACTCTTCTGCTGGTGTGATCAT 5268
Qy 5281 GGACAAATTTTGAATPACTCTACGCGGACTCTTCCATCCTAGGTCCTCACACTTTGGATGA 5340
Db 5269 GGACAAATTTTGAATPACTCTACGCGGACTCTTCCATCCTAGGTCCTCACACTTTGGATGA 5328
Qy 5341 GTTCATCCGGGCTTGCGCTGAATACGACCCGGCTGCGTGTGGGGGCATCAGTTACAATGA 5400
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Qy 5401 CATGTTTGAGATGTGAAACAATGTCCTCCCGCTCTGCGGCTGCGGGAAGAAATGCCCTGC 5460
Db 5389 CATGTTTGAGATGTGAAACAATGTCCTCCCGCTCTGCGGCTGCGGGAAGAAATGCCCTGC 5448
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Db 5449 TCGAGTTGCTTACAAGCGCTGTTGCAATGAACATGCCCCATCTCCAACGAGGACATGAC 5508
Qy 5521 TGTTCACCTTCACTGTCAGCGCTGATGCGCCCTCATCCGACGGCATCGAGATCAAGCTGGC 5580
Db 5509 TGTTCACCTTCACTGTCAGCGCTGATGCGCCCTCATCCGACGGCATCGAGATCAAGCTGGC 5568
Qy 5581 CCCAGCTGGGACAAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGAGAGATTTCCCGTGT 5640
Db 5569 CCCAGCTGGGACAAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGAGAGATTTCCCGTGT 5628
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Qy 5701 GATGACAGTGGGGAAGTTTTATGCACTCTGATGATATTTGACTTCTACAAGCAGAACAA 5760
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Db 5749 AACCCACAGAGACAGATGACAGGCTCCTGGAGGCTCTCCACAGATGGGTCTCTGTGTC 5808
Qy 5821 CTTGTTCCACCTCTGAAGGCCACCTCGAGAGCAGACACAGCCGGCTGTGCTCGAGAGAC 5880
Db 5809 CTTGTTCCACCTCTGAAGGCCACCTCGAGAGCAGACACAGCCGGCTGTGCTCGAGAGAC 5868
Qy 5881 CCGGTTTTCTTCGACAGAGAGTTCCACCTCCCTCAGCAATGGCGGGCCATACAAA 5940
Db 5869 CCGGTTTTCTTCGACAGAGAGTTCCACCTCCCTCAGCAATGGCGGGCCATACAAA 5928
Qy 5941 CCAAGAGTGGCATCAAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC 6000
Db 5929 CCAAGAGTGGCATCAAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC 5988
Qy 6001 CCAATGAGCCAGGCCACCTCTGAGGCGTGCACATCCACAGATCCCTGTGGGGCGGTC 6060
Db 5989 CCAATGAGCCAGGCCACCTCTGAGGCGTGCACATCCACAGATCCCTGTGGGGCGGTC 6048
Qy 6061 AGGAGCACTGGCTGTGACGTTCAAGATGACAGCAAAACCGGAGGGCCCTCATGGGGA 6120
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Qy 6121 GCCCAGCTGGGCTGGAGAGCCAGGGTCTGAGCGGCTCTCATGCCCCCGCTTTCGGCGCGA 6180
Db 6109 GCCCAGCTGGGCTGGAGAGCCAGGGTCTGAGCGGCTCTCATGCCCCCGCTTTCGGCGCGA 6168
Qy 6181 GACTCAGCCGCTCAGATGCCAGCCCACTGAAGCGTCTCATCTCCACGCTGGCCAGCG 6240
Db 6169 GACTCAGCCGCTCAGATGCCAGCCCACTGAAGCGTCTCATCTCCACGCTGGCCAGCG 6228
Qy 6241 GCCCGTGGGACTCATCTTTGACACACACCCCGGACCGGCCCTAGCCAGGGGTC 6300
Db 6229 GCCCGTGGGACTCATCTTTGACACACACCCCGGACCGGCCCTAGCCAGGGGTC 6288
Qy 6301 GTCCACACACACACACCGCTGCCACCGCCGAGGACAGGAGAGAGAGTCCCTGGA 6360
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Qy 6361 GAAGGGGCCAGCTGTCTGCCGATATGGATGGCGCACCAAGCAGTGTGTGGGGCCGG 6420
Db 6349 GAAGGGGCCAGCTGTCTGCCGATATGGATGGCGCACCAAGCAGTGTGTGGGGCCGG 6408
Qy 6421 GCTGCCCGCGGAGAGGGGCTTACAGGCTGCCGGCGGGAACGAGAGCGCCGCGAGAGCG 6480
Db 6409 GCTGCCCGCGGAGAGGGGCTTACAGGCTGCCGGCGGGAACGAGAGCGCCGCGAGAGCG 6468
Qy 6481 GGGCGGTCAGGAGGAGGAGCGCTCATCTCTCTCTCGGAGAGAGCGCTTCTA 6540
Db 6469 GGGCGGTCAGGAGGAGGAGCGCTCATCTCTCTCTCGGAGAGAGCGCTTCTA 6528
Qy 6541 CTCCTGGAGCGCTTTGGGGCGGTGAGCGCCCGAAGCCCAAGCCCTCCCTCAGCAGCCA 6600
Db 6529 CTCCTGGAGCGCTTTGGGGCGGTGAGCGCCCGAAGCCCAAGCCCTCCCTCAGCAGCCA 6588
Qy 6601 CCCAACGTCGCAACAGTGCGCCAGGAGCGGAGCCCAACCCACAGAGGAGTGTTCCT 6660
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Qy 6661 GAATGGAGGCCCTTGTCTCAACATCTGTGTAGCACCCCGCGCGCGGTGGCGGAG 6720
Db 6649 GAATGGAGGCCCTTGTCTCAACATCTGTGTAGCACCCCGCGCGCGGTGGCGGAG 6708
Qy 6721 GCAGCTCCCGCAGAGCGCCCTGACTCCCGCGCCAGCATCACTTACAGAGCGGCAACTC 6780
Db 6709 GCAGCTCCCGCAGAGCGCCCTGACTCCCGCGCCAGCATCACTTACAGAGCGGCAACTC 6768
Qy 6781 CTCACCATCACTTCGCGGGGCTCAGACAGAGCTCTCCGCTTCTCCCGAGCGCGCT 6840
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Qy 6841 CAGCGTGGGCTTTCCGAAACAACAGCGCTGTCTGAGAGAGACCCCTCAGCCAGCCCT 6900
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Qy 6901 GGCCCTGGCTCTGAAATGGCTCTGACCTTACTTGGGGCAGCGCTGGACAGTGAAGC 6960
Db 6889 GGCCCTGGCTCTGAAATGGCTCTGACCTTACTTGGGGCAGCGCTGGACAGTGAAGC 6948
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Qy 7081 CCGGTCGCCAAGGTTACCACTCCACCTGGGACTCAGCTCGGGTGGCGAGCAGCGCA 7140
Db 7069 CCGGTCGCCAAGGTTACCACTCCACCTGGGACTCAGCTCGGGTGGCGAGCAGCGCA 7128
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Db 7129 CAGCTACCAACCCCTGACCAAGACCACTGTGTGTAGCTGACCGTACCGCTCAGACGC 7188
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Db 7189 CTGCATGACAGCGGCTGTGTTCAGGATAGTATTTATCATCCACAGGGGCGAGTCGG 7248
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Db 7249 CCCTCGGGGAGAGGCTTGGCCACCTTGGTGAGGCTCTGTGGCCCTTCCCTCCCCCTCT 7308
Qy 7321 CCCTCTTTTACTCTCTAGACGACGAATAAAGCCCTGTGTGTGAGTGATGATACCGC 7376
Db 7309 CCCTCTTTTACTCTCTAGACGACGAATAAAGCCCTGTGTGTGAGTGATGATACCGC 7364

RESULT 3
ABZ58366
ID ABZ58366 standard; cDNA; 7364 BP.
XX AC ABZ58366;
XX AC
XX AC
DT 28-APR-2003 (first entry)
XX Human N-type calcium channel alpha-1B subunit coding sequence.
DE Human; calcium channel; voltage-gated ion channel; splice variant; gene;
KW ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 146..7165
XX FT /*tag= a
XX FT /product= "Human calcium channel, alpha-1B subunit"
XX PN WO2003006103-A2.
XX XX
XX 23-JAN-2003.
XX PF 12-JUL-2002; 2002WO-US022161.
XX XX
XX 12-JUL-2001; 2001US-0304955P.
XX (MERI) MERCK & CO INC.
XX Augustine PR, Bennett PB, Bugianesi RM, Garyantes TA, Imredy JP;
PI Kath GS, Mcmanus OB;
XX WPI: 2003-221676/21.
DR P-PSDB; ABP72255.
XX
PT Identifying modulators of the activity of a voltage-gated ion channel,
PT comprises altering the transmembrane potential of a portion of the cell
PT membrane expressing the voltage-gated ion channel by electric field
PT stimulation.
XX Disclosure; Fig 20A-C; 188pp; English.
XX
CC The present sequence is the coding sequence for a splice variant of the
CC alpha-1B subunit of the human T-type calcium channel. The invention
CC provides methods of identifying activators and inhibitors of voltage-
CC gated ion channels (VC). The methods use electrical field stimulation of
CC calls via extracellular electrodes to manipulate the open/close state
CC transitions of the VCs. This allows for more convenient, more precise
CC manipulation of these transitions and, coupled with efficient methods of
CC detecting ion flux or membrane potential, results in methods that are
CC especially suitable for high-throughput screening of compounds as
CC potential activators and inhibitors of VCs. The VC may be a sodium,
CC potassium calcium channel. The cells are e.g. HEK293 (ATCC 1573) cells
CC transfected with DNA encoding the VC, and may contain a fluorescent
CC indicator compound. Defective sodium, calcium and potassium VCs have been
CC implicated in a variety of disorders including long QT syndrome, ataxia,
CC migraine, muscle paralysis, deafness, seizures, and cardiac conduction
CC diseases
XX Sequence 7364 BP; 1444 A; 2278 C; 2216 G; 1426 T; 0 U; 0 Other;

Query Match 99.5%; Score 7342; DB 7; Length 7364;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 7364; Conservative 0; Mismatches 0; Indels 12; Gaps 1;									
QY	1	GC	GC	GC	GC	GC	GC	GC	GC
DB	1	GC	GC	GC	GC	GC	GC	GC	GC
QY	61	GC	GC	GC	GC	GC	GC	GC	GC
DB	61	GC	GC	GC	GC	GC	GC	GC	GC
QY	121	GG	GA	TC	CA	CG	GG	GC	GC
DB	121	GG	GA	TC	CA	CG	GG	GC	GC
QY	181	TG	AG	GC	CC	CG	GC	GC	GC
DB	181	TG	AG	GC	CC	CG	GC	GC	GC
QY	241	GG	GC	CC	CG	GC	GC	GC	GC
DB	241	GG	GC	CC	CG	GC	GC	GC	GC
QY	301	CG	CG	CG	CG	CG	CG	CG	CG
DB	301	CG	CG	CG	CG	CG	CG	CG	CG
QY	361	CG	CG	CG	CG	CG	CG	CG	CG
DB	361	CG	CG	CG	CG	CG	CG	CG	CG
QY	421	CG	AG	TC	CA	CG	GC	GC	GC
DB	421	CG	AG	TC	CA	CG	GC	GC	GC
QY	481	GG	CC	TC	GA	GG	GA	AA	AA
DB	481	GG	CC	TC	GA	GG	GA	AA	AA
QY	541	CA	CG	AG	CC	TC	GA	GG	GA
DB	541	CA	CG	AG	CC	TC	GA	GG	GA
QY	601	GG	GC	TC	CA	CG	GC	GC	GC
DB	601	GG	GC	TC	CA	CG	GC	GC	GC
QY	661	GG	TC	TC	CA	CG	GC	GC	GC
DB	661	GG	TC	TC	CA	CG	GC	GC	GC
QY	721	GG	TC	TC	CA	CG	GC	GC	GC
DB	721	GG	TC	TC	CA	CG	GC	GC	GC
QY	781	GC	TC	AG	TC	CA	CG	GC	GC
DB	781	GC	TC	AG	TC	CA	CG	GC	GC
QY	841	TG	CC	AT	TC	CA	CG	GC	GC
DB	841	TG	CC	AT	TC	CA	CG	GC	GC
QY	901	CT	GT	TC	CA	CG	GC	GC	GC
DB	901	CT	GT	TC	CA	CG	GC	GC	GC
QY	961	CC	AG	CC	CG	GC	GC	GC	GC
DB	961	CC	AG	CC	CG	GC	GC	GC	GC

QY	1021	TG	GC	AT	CA	CG	GC	GC	GC
DB	1021	TG	GC	AT	CA	CG	GC	GC	GC
QY	1081	CA	TG	AG	GC	TC	GA	TC	CA
DB	1081	CA	TG	AG	GC	TC	GA	TC	CA
QY	1141	CT	GC	TC	CA	TC	CA	TC	CA
DB	1141	CT	GC	TC	CA	TC	CA	TC	CA
QY	1201	GG	GC	TC	CA	TC	CA	TC	CA
DB	1201	GG	GC	TC	CA	TC	CA	TC	CA
QY	1261	CT	GA	AG	TC	CA	TC	CA	TC
DB	1261	CT	GA	AG	TC	CA	TC	CA	TC
QY	1321	CT	TC	CA	CG	GC	GC	GC	GC
DB	1321	CT	TC	CA	CG	GC	GC	GC	GC
QY	1381	TT	TC	GA	AG	TC	CA	TC	CA
DB	1381	TT	TC	GA	AG	TC	CA	TC	CA
QY	1441	GG	GC	AG	TC	CA	TC	CA	TC
DB	1441	GG	GC	AG	TC	CA	TC	CA	TC
QY	1501	CT	TC	CA	CG	GC	GC	GC	GC
DB	1501	CT	TC	CA	CG	GC	GC	GC	GC
QY	1561	GT	TT	TC	GA	AG	TC	CA	TC
DB	1561	GT	TT	TC	GA	AG	TC	CA	TC
QY	1621	GG	CC	TC	GA	AG	TC	CA	TC
DB	1621	GG	CC	TC	GA	AG	TC	CA	TC
QY	1681	GA	CC	TC	GA	AG	TC	CA	TC
DB	1681	GA	CC	TC	GA	AG	TC	CA	TC
QY	1741	GA	TC	TC	CA	CG	GC	GC	GC
DB	1741	GA	TC	TC	CA	CG	GC	GC	GC
QY	1801	GG	TC	TC	CA	CG	GC	GC	GC
DB	1801	GG	TC	TC	CA	CG	GC	GC	GC
QY	1861	TG	GC	AT	CA	CG	GC	GC	GC
DB	1861	TG	GC	AT	CA	CG	GC	GC	GC
QY	1921	GA	GC	TC	CA	CG	GC	GC	GC
DB	1921	GA	GC	TC	CA	CG	GC	GC	GC
QY	1981	GC	TC	TC	CA	CG	GC	GC	GC
DB	1981	GC	TC	TC	CA	CG	GC	GC	GC
QY	2041	GG	GA	TC	CA	CG	GC	GC	GC
DB	2041	GG	GA	TC	CA	CG	GC	GC	GC
QY	2101	CA	TC	TC	CA	CG	GC	GC	GC

Db 2101 CATCCTCACTGTCTTCAGATCTCTGACGGGAGAGACTGGAAATGCAGTGATATCACGG 2160
Qy 2161 GATCGAATCGCAAGCGCGCTCAGCAAGAGCATGTTCTCGTCCCTTTTACCTTCATTTGTCCT 2220
Db 2161 GATCGAATCGCAAGCGCGCTCAGCAAGAGCATGTTCTCGTCCCTTTTACCTTCATTTGTCCT 2220
Qy 2221 GACACTGTTGCGAAATACACTCTGCTGGAATGTTCTTTCTGGCCATCGCTGTGGAACAACCT 2280
Db 2221 GACACTGTTGCGAAATACACTCTGCTGGAATGTTCTTTCTGGCCATCGCTGTGGAACAACCT 2280
Qy 2281 GGCCAAAGCGCCAGAGCTGACCAAGGATGAAGAGGATGAAGAGCAAGCAAGCCATCAGAA 2340
Db 2281 GGCCAAAGCGCCAGAGCTGACCAAGGATGAAGAGGATGAAGAGCAAGCAAGCCATCAGAA 2340
Qy 2341 GCTTTGCTCTGCAAAAGGCCAAAGAGTGGCTGGAAGTCAAGCCCATGTTCTGCGCGCAACAT 2400
Db 2341 GCTTTGCTCTGCAAAAGGCCAAAGAGTGGCTGGAAGTCAAGCCCATGTTCTGCGCGCAACAT 2400
Qy 2401 CTCATCGCCGCCAGGACGACGAACTCGGCCAAGCGCGCTCGTGTGGAGCAGCGGGC 2460
Db 2401 CTCATCGCCGCCAGGACGACGAACTCGGCCAAGCGCGCTCGTGTGGAGCAGCGGGC 2460
Qy 2461 CAGCAGCTACGGCTGCAGAACCTCGCGGCCAGCTGCGAGCGCTGTACAGCGAGATGGA 2520
Db 2461 CAGCAGCTACGGCTGCAGAACCTCGCGGCCAGCTGCGAGCGCTGTACAGCGAGATGGA 2520
Qy 2521 CCCCGAGAGCGGTGGCTTCGGCACTACCGCGCACTCGCGGCCCGACATGAAGACGCA 2580
Db 2521 CCCCGAGAGCGGTGGCTTCGGCACTACCGCGCACTCGCGGCCCGACATGAAGACGCA 2580
Qy 2581 CCTGGACCGGCGCTGTGTGTGGAGCTGGCGCGCGACCGCGCGCGGGCGCGTGGGAGG 2640
Db 2581 CCTGGACCGGCGCTGTGTGTGGAGCTGGCGCGCGACCGCGCGCGGGCGCGTGGGAGG 2640
Qy 2641 CAAGCCCGACCTGAGCTGGGAGGCCCCCGAGGGGTGCACTCTCGCGCAGGACCA 2700
Db 2641 CAAGCCCGACCTGAGCTGGGAGGCCCCCGAGGGGTGCACTCTCGCGCAGGACCA 2700
Qy 2701 CCGGCACCGCGACAAGACAAGACCCCGCGCGGGGACACAGACCGAGCAGAGGCCCC 2760
Db 2701 CCGGCACCGCGACAAGACAAGACCCCGCGCGGGGACACAGACCGAGCAGAGGCCCC 2760
Qy 2761 GAAGCGGAGAGCGGGAGCGCCGTGCGCGGAGAGCGGCGCGCGCGCAACGACGCA 2820
Db 2761 GAAGCGGAGAGCGGGAGCGCCGTGCGCGGAGAGCGGCGCGCGCGCAACGACGCA 2820
Qy 2821 CAGCAAGAGGCGCGGGGCCCCCGAGGCGCGAGCGAGCGCGCGCGCGAGGCCCGCC 2880
Db 2821 CAGCAAGAGGCGCGGGGCCCCCGAGGCGCGAGCGAGCGCGCGCGCGAGGCCCGCC 2880
Qy 2881 CGAGGCGCGCGCGGACCAACCGCGCGGCTCCCGAGAGAGCGGCGCGAGCGGGAGCC 2940
Db 2881 CGAGGCGCGCGCGGACCAACCGCGCGGCTCCCGAGAGAGCGGCGCGAGCGGGAGCC 2940
Qy 2941 CCGACGCAACCGCGCAGCAGGACACAGGATCCGAGCAAGAGTGCAGCGCGCCAGAGG 3000
Db 2941 CCGACGCAACCGCGCAGCAGGACACAGGATCCGAGCAAGAGTGCAGCGCGCCAGAGG 3000
Qy 3001 CGAGCGGCGCGCGGACCGCGCGGCCCCCGAGCGGGGCCCCCGGAGAGCGGAGCGG 3060
Db 3001 CGAGCGGCGCGCGGACCGCGCGGCCCCCGAGCGGGGCCCCCGGAGAGCGGAGCGG 3060
Qy 3061 GGAGAGCGCGCGGGGACCGGGCCCGGCAACAGCGCGAGCTGCTCAAGAGGCTGT 3120
Db 3061 GGAGAGCGCGCGGGGACCGGGCCCGGCAACAGCGCGAGCTGCTCAAGAGGCTGT 3120
Qy 3121 GGAGAAGGAGACCAAGAGAGGAGGCGCACGAGAGAGGAGCTGATAGTGGAGCGCA 3180
Db 3121 GGAGAAGGAGACCAAGAGAGGAGGCGCACGAGAGAGGAGCTGATAGTGGAGCGCA 3180
Qy 3181 CAAGGAAAAGAGCTTCGGAAACCAACAGCCCCCGGAGCGCACACTGTGACTGTGGAGCAG 3240

Db 3181 CAAGGAAAAGGAGCTCGGAAACCAACAGCCCCCGGAGGCCACACTGTGACTGTGAGACCAG 3240
Qy 3241 TGGGACTGTGACTGTGGGTCCCATGACACACACTGCCAGACACCTGTCTCAGAAAGGTGGA 3300
Db 3241 TGGGACTGTGACTGTGGGTCCCATGACACACACTGCCAGACACCTGTCTCAGAAAGGTGGA 3300
Qy 3301 GGAACAGCCAGAGATGCAGAAATCAGCGGAACGTCACTGCGATGGGAGTCAAGCCCCC 3360
Db 3301 GGAACAGCCAGAGATGCAGAAATCAGCGGAACGTCACTGCGATGGGAGTCAAGCCCCC 3360
Qy 3361 AGACCCGGAACACTATTGTACATATCCAGTGATGCTGACGGGCCCTCTTGGGAAAGCCAC 3420
Db 3361 AGACCCGGAACACTATTGTATCATATCCAGTGATGCTGACGGGCCCTCTTGGGAAAGCCAC 3420
Qy 3421 GGTCTGTTCCAGTGGTAAACGTGGACCTCGGAAAGCCAAAGCAGAGGGGAAGAGGTGGA 3480
Db 3421 GGTCTGTTCCAGTGGTAAACGTGGACCTCGGAAAGCCAAAGCAGAGGGGAAGAGGTGGA 3480
Qy 3481 AGCGGATGAGCTGATGAGGAGCGGCCCGCGGCTATGCTCCCATACAGTCCCATGTTCTG 3540
Db 3481 AGCGGATGAGCTGATGAGGAGCGGCCCGCGGCTATGCTCCCATACAGTCCCATGTTCTG 3540
Qy 3541 TTTAAGCCCCACCAACCTGCTCCGCGCTTCTGCCACTACATCGTACCATGAGGTACTT 3600
Db 3541 TTTAAGCCCCACCAACCTGCTCCGCGCTTCTGCCACTACATCGTACCATGAGGTACTT 3600
Qy 3601 CGAGGTGGTCAATCTCGTGGTCACTCGCTTGAGCAGCATCGCCCTGCTCTGAGGACCC 3660
Db 3601 CGAGGTGGTCAATCTCGTGGTCACTCGCTTGAGCAGCATCGCCCTGCTCTGAGGACCC 3660
Qy 3661 AGTGGGCAAGACTCGCCCHAGGAAACCGCTCTGAATACTCTGGATTTACATTTTCACTGG 3720
Db 3661 AGTGGGCAAGACTCGCCCHAGGAAACCGCTCTGAATACTCTGGATTTACATTTTCACTGG 3720
Qy 3721 TGTCTTTACCTTTGAGATGAGTAAAGATGATCGACTTGGGACTGCTGCTTCAACCTGG 3780
Db 3721 TGTCTTTACCTTTGAGATGAGTAAAGATGATCGACTTGGGACTGCTGCTTCAACCTGG 3780
Qy 3781 AGCCTATTTCCGGGACTTGTGGAACTTCTGGACTTCTGAGTCACTGAGTGGCGCCCTGGT 3840
Db 3781 AGCCTATTTCCGGGACTTGTGGAACTTCTGGACTTCTGAGTCACTGAGTGGCGCCCTGGT 3840
Qy 3841 GGGCTTTGCTTTCTCGAGCTTCTGGGAGGATCCAAAGGGGAAAGACATCAATACCATCAA 3900
Db 3841 GGGCTTTGCTTTCTC-----AGGATCCAAAGGGGAAAGACATCAATACCATCAA 3888
Qy 3901 GTCTCTGAGAGTCTTGTGTCCTGCGGCCCTCAAGACCATCAAGCGGCTGCCCAAGCT 3960
Db 3889 GTCTCTGAGAGTCTTGTGTCCTGCGGCCCTCAAGACCATCAAGCGGCTGCCCAAGCT 3948
Qy 3961 CAAGGCTGTGTTTGAATGTTGGTGAATCCCTGGAAGAAATGTCTCAACATCTTGATTGT 4020
Db 3949 CAAGGCTGTGTTTGAATGTTGGTGAATCCCTGGAAGAAATGTCTCAACATCTTGATTGT 4008
Qy 4021 CTACATGCTCTTCAATGTTCAATTTGCGTCAATTTGGTGCAGCTCTTTCAAGAGGAAGTT 4080
Db 4009 CTACATGCTCTTCAATGTTCAATTTGCGTCAATTTGGTGCAGCTCTTTCAAGAGGAAGTT 4068
Qy 4081 TTTTCTACTGCACAGATGAAATCCAAAGGCTGGAGAGGACTGCGAGGGTTCAGTATTGGA 4140
Db 4069 TTTTCTACTGCACAGATGAAATCCAAAGGCTGGAGAGGACTGCGAGGGTTCAGTATTGGA 4128
Qy 4141 TTATGAGAGGAGGAAGTGAAGCTCAGCCAGGCAAGTGAAGAAATAACGACTTTTCACTA 4200
Db 4129 TTATGAGAGGAGGAAGTGAAGCTCAGCCAGGCAAGTGAAGAAATAACGACTTTTCACTA 4188
Qy 4201 CGACAATGCTCTGGGCTCTGTGACGCTGTTTCAAGTGTCCAAGGAGAAAGGCTGGCC 4260
Db 4189 CGACAATGCTCTGGGCTCTGTGACGCTGTTTCAAGTGTCCAAGGAGAAAGGCTGGCC 4248
Qy 4261 CATGGTCTGAAACACTCCGTGGATGCCACTATGAGGAGCAGGCTCCAGCCCTGGGTA 4320
Db 4249 CATGGTCTGAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4308

QY	4321	CCGATGAGCTGCTCCATCTTCTACGNGCTACTTTGTGGTCTTTCCCTTCTTCTCGT	4380
Db	4309	CCGATGAGCTGCTCCATCTTCTACGNGCTACTTTGTGGTCTTTCCCTTCTTCTCGT	4368
QY	4381	CAACATCTTTGTGGCTTTGATCATCATACCTTCCAGGAGCGGGGACAAGTGATGTC	4440
Db	4369	CAACATCTTTGTGGCTTTGATCATCATACCTTCCAGGAGCGGGGACAAGTGATGTC	4428
QY	4441	TGAATGAGCTGAGAGAACGAGGGCTTGATGATCTTCCGATCAGCGCCAAACC	4500
Db	4429	TGAATGAGCTGAGAGAACGAGGGCTTGATGATCTTCCGATCAGCGCCAAACC	4488
QY	4501	CCTGACACGGTACATGCCCCCAAAACCGGCAAGTCTTCCAGTAAAGACGTGGACATTTGT	4560
Db	4489	CCTGACACGGTACATGCCCCCAAAACCGGCAAGTCTTCCAGTAAAGACGTGGACATTTGT	4548
QY	4561	GGTCTCCCCCGCTTTGAATACATTCATGAGCCATGATAGCCCTCAACACTGTGGTGT	4620
Db	4549	GGTCTCCCCCGCTTTGAATACATTCATGAGCCATGATAGCCCTCAACACTGTGGTGT	4608
QY	4621	GATGATGAAGTCTTATGATGACACCTATGAGTACGAGCTGATGCTGAATGCTGAACAT	4680
Db	4609	GATGATGAAGTCTTATGATGACACCTATGAGTACGAGCTGATGCTGAATGCTGAACAT	4668
QY	4681	CGTGTTCACATCCATGTTCTCCAATGGAATGCGTGTGAAAGATCATCGCCTTTGGGGTGT	4740
Db	4669	CGTGTTCACATCCATGTTCTCCAATGGAATGCGTGTGAAAGATCATCGCCTTTGGGGTGT	4728
QY	4741	GAACATTTTCAGAGATGCTCGAATGCTTTGACTTTGTACATGTTGGGAAGTATTAC	4800
Db	4729	GAACATTTTCAGAGATGCTCGAATGCTTTGACTTTGTACATGTTGGGAAGTATTAC	4788
QY	4801	TGATATTTTAGTAAACAGAGATTGCGGAAACGAACAAATTTTCATCAACCTCAGCTTCTCCG	4860
Db	4789	TGATATTTTAGTAAACAGAGATTGCGGAAACGAACAAATTTTCATCAACCTCAGCTTCTCCG	4848
QY	4861	CCTCTTTTCAGCTGCGCGCTGATCAAGCTGCTCCGACGGCTACACCATCCGATCCT	4920
Db	4849	CCTCTTTTCAGCTGCGCGCTGATCAAGCTGCTCCGACGGCTACACCATCCGATCCT	4908
QY	4921	GCTGTGGACCTTTGTCAGTCTTCAAGCCCTGCTACGTTGCTGCTCATTTGCCAT	4980
Db	4909	GCTGTGGACCTTTGTCAGTCTTCAAGCCCTGCTACGTTGCTGCTCATTTGCCAT	4968
QY	4981	GCTGTCTTCTACTACGCCATCATCGCATGCAAGTGTGGGAATATTGCCCTGGATGA	5040
Db	4969	GCTGTCTTCTACTACGCCATCATCGCATGCAAGTGTGGGAATATTGCCCTGGATGA	5028
QY	5041	TGACACCAACCAACCGCCCAACAACTTCGGACGTTTTTGAAGCCCTGATGCTGT	5100
Db	5029	TGACACCAACCAACCGCCCAACAACTTCGGACGTTTTTGAAGCCCTGATGCTGT	5088
QY	5101	GTTCAGGAGCGCCACGGGGAGGCTTGGACAGATCATGCTGCTTGGGAATATTGCCCTGGATGA	5160
Db	5089	GTTCAGGAGCGCCACGGGGAGGCTTGGACAGATCATGCTGCTTGGGAATATTGCCCTGGATGA	5148
QY	5161	GGCCTGTGATGAGCAGGCCAATGCAACCGAGTGTGGAAGTACATTTGCTACTTCTACTT	5220
Db	5149	GGCCTGTGATGAGCAGGCCAATGCAACCGAGTGTGGAAGTACATTTGCTACTTCTACTT	5208
QY	5221	CGTCTCTTCTACTTCTGCTGCTTCTGATGTTGAACTCTTTGGCTGTGATCAT	5280
Db	5209	CGTCTCTTCTACTTCTGCTGCTTCTGATGTTGAACTCTTTGGCTGTGATCAT	5268
QY	5281	GGACAAATTTGAGTACCTCAGCGGAGCTCTTTCATCTTAGTCTCCTCACCATTGGATGA	5340
Db	5269	GGACAAATTTGAGTACCTCAGCGGAGCTCTTTCATCTTAGTCTCCTCACCATTGGATGA	5328
QY	5341	GTTTCAATCCGGTCTGGGCTGAATAGACCCGGCTGCTGTGGGGCAGATCAGTTACAATGA	5400
Db	5329	GTTTCAATCCGGTCTGGGCTGAATAGACCCGGCTGCTGTGGGGCAGATCAGTTACAATGA	5388

QY	5401	CATGTTTGAGATGCTGAAACAATGTCCCCCCTCTGGGGCTGGGGAAGAAATCCCTGTC	5460
Db	5389	CATGTTTGAGATGCTGAAACAATGTCCCCCCTCTGGGGCTGGGGAAGAAATCCCTGTC	5448
QY	5461	TCGAGTTCTTTACAAAGCGCTGTTCCATGAAACATGATGCCCATCTCCAAACAGAGACATGAC	5520
Db	5449	TCGAGTTCTTTACAAAGCGCTGTTCCATGAAACATGATGCCCATCTCCAAACAGAGACATGAC	5508
QY	5521	TGTTCACTTCACTGCTCAACGCTGATGGGCCCTCATCCGGACGGCATCTGAGATCAAGCTTGGC	5580
Db	5509	TGTTCACTTCACTGCTCAACGCTGATGGGCCCTCATCCGGACGGCATCTGAGATCAAGCTTGGC	5568
QY	5581	CCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGAGTTGAGGAAGAGATTTCCGTTGT	5640
Db	5569	CCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGAGTTGAGGAAGAGATTTCCGTTGT	5628
QY	5641	GTGGGCCAAATCTGCCCCAGAAAGACTTTGGACTTGTCTGTTACCAACCCCATTAAGCTGATGA	5700
Db	5629	GTGGGCCAAATCTGCCCCAGAAAGACTTTGGACTTGTCTGTTACCAACCCCATTAAGCTGATGA	5688
QY	5701	GATGACAGTGGGGAAGTTTATGAGCTCTGATGATATTTGACTTCTACAAGCAGAACAA	5760
Db	5689	GATGACAGTGGGGAAGTTTATGAGCTCTGATGATATTTGACTTCTACAAGCAGAACAA	5748
QY	5761	AACCAACAGAGACAGATGACGAGCTCTGGAGGCTCTCCAGATGGGTCTGTGTC	5820
Db	5749	AACCAACAGAGACAGATGACGAGCTCTGGAGGCTCTCCAGATGGGTCTGTGTC	5808
QY	5821	CCTGTTCCACCTCTGAAGGCCACCTGGAGCAGACACAGCCGGCTGTGCTCGAGGAGC	5880
Db	5809	CCTGTTCCACCTCTGAAGGCCACCTGGAGCAGACACAGCCGGCTGTGCTCGAGGAGC	5868
QY	5881	CCGGTTTTCTTTCGACAGAAAGTTCCACCTCCCTAGCAATGGCGGGGCTATACAAA	5940
Db	5869	CCGGTTTTCTTTCGACAGAAAGTTCCACCTCCCTAGCAATGGCGGGGCTATACAAA	5928
QY	5941	CCAAGAGATGGCATCAAAAGATCTGCTCTGGGGCACTCAAAAGACCCAGATGCAAC	6000
Db	5929	CCAAGAGATGGCATCAAAAGATCTGCTCTGGGGCACTCAAAAGACCCAGATGCAAC	5988
QY	6001	CCATGAGGCGAGGCCACCTCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGGGCGGTC	6060
Db	5989	CCATGAGGCGAGGCCACCTCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGGGCGGTC	6048
QY	6061	AGGACACTGGCTGTGGAGCTTCCAGATGACAGATCAACCCGGAGGGGCTTGTATGGGA	6120
Db	6049	AGGACACTGGCTGTGGAGCTTCCAGATGACAGATCAACCCGGAGGGGCTTGTATGGGA	6108
QY	6121	GCCCCAGCTGGGCTGGAGAGCAGGGTCCAGCGGCTCCATGCCCCGCTTTCGGGCCGA	6180
Db	6109	GCCCCAGCTGGGCTGGAGAGCAGGGTCCAGCGGCTCCATGCCCCGCTTTCGGGCCGA	6168
QY	6181	GACTAGCCCGTCAACAGATGCCAGCCCATGAAAGCGCTCCATCTCAACGCTTGGCCACGG	6240
Db	6169	GACTAGCCCGTCAACAGATGCCAGCCCATGAAAGCGCTCCATCTCAACGCTTGGCCACGG	6228
QY	6241	GCCCCGTGGGACTCTCTTTGAGCAGCACCCCGGACCCCGCCACCCCTTACGAGCGCTC	6300
Db	6229	GCCCCGTGGGACTCTCTTTGAGCAGCACCCCGGACCCCGCCACCCCTTACGAGCGCTC	6288
QY	6301	GTGCAACCAACCAACCCGCTGACCGCGCAGGAGCAGGAGCAGAGATGCTCCCTGGA	6360
Db	6289	GTGCAACCAACCAACCCGCTGACCGCGCAGGAGCAGGAGCAGAGATGCTCCCTGGA	6348
QY	6361	GAAGGGGCCAGCTCTGCGGATATGATGGGCGCACCAAGCAGTGTGTGGGGCCGGG	6420
Db	6349	GAAGGGGCCAGCTCTGCGGATATGATGGGCGCACCAAGCAGTGTGTGGGGCCGGG	6408
QY	6421	GCTGCCCGGGAGAGGGGCTTACAGGCTGCGGGGGAACAGAGCCCGCGCAGAGCG	6480
Db	6409	GCTGCCCGGGAGAGGGGCTTACAGGCTGCGGGGGAACAGAGCCCGCGCAGAGCG	6468
QY	6481	GGGCGGCTCCAGGAGCGGAGCGCCCTCATGCTCTCTCCCTCGGAGAAAGACGCGCTTCTA	6540

Db 4547 GGTCTCCCCCCTTTGAAATATCTTCATCATGGCCATGATAGCCCTCAAACATCTGGTGCT 4606
QY 4621 GATGATGAAGTTCTATGATGACCCCTATGATGACGCTCATGATGCTGAAATGCCCTGAAACAT 4680
Db 4607 GATGATGAAGTTCTATGATGACCCCTATGATGACGCTCATGATGCTGAAATGCCCTGAAACAT 4666
QY 4681 CGTGTTCACATCCCATGTTCTCCATGGAATCGGTGCTGAAGATCATCGCCCTTTGGGGTGCT 4740
Db 4667 CGTGTTCACATCCCATGTTCTCCATGGAATCGGTGCTGAAGATCATCGCCCTTTGGGGTGCT 4726
QY 4741 GAACTATTTGAGAGATGCCCTGGAGTCTTTGACTTTGTCATCTGTTGGGAAGTATTAC 4800
Db 4727 GAACTATTTGAGAGATGCCCTGGAGTCTTTGACTTTGTCATCTGTTGGGAAGTATTAC 4786
QY 4801 TGATAATTTTAAAGAGATGCGGAAACGAAATTTTCATCAACTCAGCTTCCTCCG 4860
Db 4787 TGATAATTTTAAAGAGATGCGGAAACGAAATTTTCATCAACTCAGCTTCCTCCG 4846
QY 4861 CCTCTTTGAGCTGCGGGCTGATCAAGCTGCTCCGCCAGGGCTACACCATCGCATCCT 4920
Db 4847 CCTCTTTGAGCTGCGGGCTGATCAAGCTGCTCCGCCAGGGCTACACCATCGCATCCT 4906
QY 4921 GCTGTGACCTTTGTCCAGTCTTCAAGGCCCTGCCCTAGCTGCTGCTCATTTGCCAT 4980
Db 4907 GCTGTGACCTTTGTCCAGTCTTCAAGGCCCTGCCCTAGCTGCTGCTCATTTGCCAT 4966
QY 4981 GCTGTCTTTCATCTACGCCATCATCGGCATGCGAGTGTGTTGGGAATATTGCCCTGGATGA 5040
Db 4967 GCTGTCTTTCATCTACGCCATCATCGGCATGCGAGTGTGTTGGGAATATTGCCCTGGATGA 5026
QY 5041 TGACACCGCATCAACCGGCCAACAACCTTCGGAGCTTTTTCGAAAGCCCTGATGCTGCT 5100
Db 5027 TGACACCGCATCAACCGGCCAACAACCTTCGGAGCTTTTTCGAAAGCCCTGATGCTGCT 5086
QY 5101 GTTCAGGAGCCCAACGGGGAGGCCCTGGCACAGATCATGCTGCTCGCTGAGCAACCA 5160
Db 5087 GTTCAGGAGCCCAACGGGGAGGCCCTGGCACAGATCATGCTGCTCGCTGAGCAACCA 5146
QY 5161 GGCCTGTGATGAGCAGGCCCAATGCCACCGAGTGTGGAAGTGACTTTTGCCCTACTTACTT 5220
Db 5147 GGCCTGTGATGAGCAGGCCCAATGCCACCGAGTGTGGAAGTGACTTTTGCCCTACTTACTT 5206
QY 5221 CGTCTCCTTCACTCTTCCTGCTGCTCCTTTCTGATGTTGAACTCTTTGCTGCTGATCAT 5280
Db 5207 CGTCTCCTTCACTCTTCCTGCTGCTCCTTTCTGATGTTGAACTCTTTGCTGCTGATCAT 5266
QY 5281 GGACAAATTTGAGTACCTCAACCGGACTCTTCCATCTTAGGTCTCAACCACTTGGATGA 5340
Db 5267 GGACAAATTTGAGTACCTCAACCGGACTCTTCCATCTTAGGTCTCAACCACTTGGATGA 5326
QY 5341 GTTCATCCGGGTCTGGGCTGAATAGACCCGCTCGCTGCTGGGCGCATCAGTTACAATGA 5400
Db 5327 GTTCATCCGGGTCTGGGCTGAATAGACCCGCTCGCTGCTGGGCGCATCAGTTACAATGA 5386
QY 5401 CATGTTGAGATGCTGAACACATGCTCCCGCTCTGCGGCTGAGGAGAAATGCCCTGC 5460
Db 5387 CATGTTGAGATGCTGAACACATGCTCCCGCTCTGCGGCTGAGGAGAAATGCCCTGC 5446
QY 5461 TCGAGTTGCTTACAAGCCCTGGTTGCGATGAACATGCCATCTCCAACGAGGACATGAC 5520
Db 5447 TCGAGTTGCTTACAAGCCCTGGTTGCGATGAACATGCCATCTCCAACGAGGACATGAC 5506
QY 5521 TGTTCACTTTCAGCTCCAGCTGATGGCCCTCATCCGAGCGCATCTGGAGTCAAGCTGGC 5580
Db 5507 TGTTCACTTTCAGCTCCAGCTGATGGCCCTCATCCGAGCGCATCTGGAGTCAAGCTGGC 5566
QY 5581 CCCAGCTGGGCAAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGGAGATTTCGTTGT 5640
Db 5567 CCCAGCTGGGCAAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGGAGATTTCGTTGT 5626
QY 5641 GTGGGCCAATCTGCCCGCAGAGACTTTGGACTTGTGTTACCCACCCCATTAAGCCTGATGA 5700
Db 5627 GTGGGCCAATCTGGCCCGCAGAGACTTTGGACTTGTGTTACCCACCCCATTAAGCCTGATGA 5686

QY 5701 GATGACAGTGGGAAAGGTTTATGCGAGCTCTCATGATATTTGACTTCTTACAAGCAGAACAA 5760
Db 5687 GATGACAGTGGGAAAGGTTTATGCGAGCTCTCATGATATTTGACTTCTTACAAGCAGAACAA 5746
QY 5761 AACCACACAGAGACACAGATGACAGAGGCTCTCCGAGGCTCTCCAGATGGGCTCTGTGTC 5820
Db 5747 AACCACACAGAGACACAGATGACAGAGGCTCTCCGAGGCTCTCCAGATGGGCTCTGTGTC 5806
QY 5821 CTTGTTCCACCCTCTGAAGGCCACCTTGGAGCAGACACAGCCGCTGTGCTCCGAGGAGC 5880
Db 5807 CTTGTTCCACCCTCTGAAGGCCACCTTGGAGCAGACACAGCCGCTGTGCTCCGAGGAGC 5866
QY 5881 CCGGGTTTTCTCTTCGACAGAGAGTTTCACTCTCCTCAGCAATGCGGGGCGCATACAAAA 5940
Db 5867 CCGGGTTTTCTCTTCGACAGAGAGTTTCACTCTCCTCAGCAATGCGGGGCGCATACAAAA 5926
QY 5941 CCAAGAGATGGCATCAAGAGTCTGCTCTGGGGCACTCAAGGACCCAGGATGCACC 6000
Db 5927 CCAAGAGATGGCATCAAGAGTCTGCTCTGGGGCACTCAAGGACCCAGGATGCACC 5986
QY 6001 CCATGAGGCCAGGCCACCCCTGGAGCGTGCCACTCCACAGAGATCCTCTGTGGGGCGGTC 6060
Db 5987 CCATGAGGCCAGGCCACCCCTGGAGCGTGCCACTCCACAGAGATCCTCTGTGGGGCGGTC 6046
QY 6061 AGGAGCACTGGCTGTGACGTTCAGATGACAGAGATTAACCCGAGGGGCCCTGATGGGGA 6120
Db 6047 AGGAGCACTGGCTGTGACGTTCAGATGACAGAGATTAACCCGAGGGGCCCTGATGGGGA 6106
QY 6121 GCCCAGCTGGGCTGGAGAGCCAGGGTCCAGCGGCTCCATGCCCGCTTCGCGCCGA 6180
Db 6107 GCCCAGCTGGGCTGGAGAGCCAGGGTCCAGCGGCTCCATGCCCGCTTCGCGCCGA 6166
QY 6181 GACTCAGCCCGTCACAGATGCCAGCCCATGAAGCGTCCATCTCAACGTCGCCCAGCG 6240
Db 6167 GACTCAGCCCGTCACAGATGCCAGCCCATGAAGCGTCCATCTCCACGCTGCCCCAGCG 6226
QY 6241 GCCCGTGGGACTCATCTTTGACAGCACCCCGGACCGGCCCTCCATGCCCGCTTCGCGCGTC 6300
Db 6227 GCCCGTGGGACTCATCTTTGACAGCACCCCGGACCGGCCCTCCATGCCCGCTTCGCGCGTC 6286
QY 6301 GTGCGACACACACACACCGCTGCCACCGCGCAGGGAAGCAGAGAGTCTCCCTGGA 6360
Db 6287 GTGCGACACACACACACCGCTGCCACCGCGCAGGGAAGCAGAGAGTCTCCCTGGA 6346
QY 6361 GAAGGGCCCGCAGCTCTGTCGATATGATGCGCACCAACAGCAGTGTGCTGGGGCCGG 6420
Db 6347 GAAGGGCCCGCAGCTCTGTCGATATGATGCGCACCAACAGCAGTGTGCTGGGGCCGG 6406
QY 6421 GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGCGGGGAAACGAGAGCGCCYKCGAGGCG 6480
Db 6407 GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGCGGGGAAACGAGAGCGCCYKCGAGGCG 6466
QY 6481 GGGCCCGTCCAGGAGCGGAGCGCTTCTCTCTCTCGGAGAACGAGTCTCTA 6540
Db 6467 GGGCCCGTCCAGGAGCGGAGCGCTTCTCTCTCTCGGAGAACGAGTCTCTA 6526
QY 6541 CTCTCGACCGCTTTGGGGCCGTGAGCCCGGAGCCCAAGCCCTCCCTCAGCAGCCA 6600
Db 6527 CTCTCGACCGCTTTGGGGCCGTGAGCCCGGAGCCCAAGCCCTCCCTCAGCAGCCA 6586
QY 6601 CCCAAGCTCGCCAAACAGCTGGCCAGGAGCCGGAGCCCAACCCACAGGGCAGTGGTTCGT 6660
Db 6587 CCCAAGCTCGCCAAACAGCTGGCCAGGAGCCGGAGCCCAACCCACAGGGCAGTGGTTCGT 6646
QY 6661 GAATGGGAGCCCTTGTCTCAACATCTGGTGTCTAGCAGCCCGCGCGGTGGCGGAG 6720
Db 6647 GAATGGGAGCCCTTGTCTCAACATCTGGTGTCTAGCAGCCCGCGCGGTGGCGGAG 6706
QY 6721 GCAGCTCCCCCAGAGCCCTGACTCCCGCGCCAGCATCACCTACAAGACGGCCAACTC 6780
Db 6707 GCAGCTCCCCCAGAGCCCTGACTCCCGCGCCAGCATCACCTACAAGACGGCCAACTC 6766

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Qy 6781 CTACCCATCCACTCGCCGGGGCTCAGACAGGCTCCCTGCTTCTCCCGAGCCGGCT 6840
Db 6767 CTCACCATCCACTTCGCGGGGCTCAGACAGGCTCCCTGCTTCTCCCGAGCCGGCT 6826
Qy 6841 CAGCCGTGGGCTTTCGGAACACACAGCCCTCTCAGAGAGACCCCTCAGCCAGCCCT 6900
Db 6827 CAGCCGTGGGCTTTCGGAACACACAGCCCTCTCAGAGAGACCCCTCAGCCAGCCCT 6886
Qy 6901 GGCCCTTGGCTCTCGAATTGGCTCTGACCCCTTACCTGGGGCAGCGTCTGGACAGTGAGGC 6960
Db 6887 GGCCCTTGGCTCTCGAATTGGCTCTGACCCCTTACCTGGGGCAGCGTCTGGACAGTGAGGC 6946
Qy 6961 CTCGTGTCAGCCCTGCTGAGGACAGCTCACTTTGAGAGAGCTGTGGCCACCACTC 7020
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Qy 7021 GGCCCGCTCTCCAGGACTTCTACGTGTCTCCTGACCTCCCGAGCTCAACCTCTCCG 7080
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Qy 7081 CCGCGTGCCCAACCGTTACCACTGCACCCCTGGGACTCAGCTCGGGTGCCGAGCACGGCA 7140
Db 7067 CCGCGTGCCCAACCGTTACCACTGCACCCCTGGGACTCAGCTCGGGTGCCGAGCACGGCA 7126
Qy 7141 CAGTACACACACCTGACCAAGACCACTGTGTGTAGTGACCGTCAAGCGCTCAGACGC 7200
Db 7127 CAGTACACACACCTGACCAAGACCACTGTGTGTAGTGACCGTCAAGCGCTCAGACGC 7186
Qy 7201 CTGCATCAGCAGGCGGTGTTCAGTGGATGAGTTTATCATCCACACGGGCGAGTGG 7260
Db 7187 CTGCATCAGCAGGCGGTGTTCAGTGGATGAGTTTATCATCCACACGGGCGAGTGG 7246
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Qy 7321 CCCTCTTTTACTCTAGACGAGCAATAAGCCCTGTGCTTGAGTGTACGTACGCG 7376
Db 7307 CCCTCTTTTACTCTAGACGAGCAATAAGCCCTGTGCTTGAGTGTACGTACGCG 7362

RESULT 5
AAAT1703
ID AAA171703 standard; DNA; 7362 BP.
XX
AC AAA171703;
XX
DT 22-DEC-2000 (first entry)
XX
DE Human calcium channel alphaB-1 subunit encoding DNA.
XX
KW Human; calcium channel; calcium channel subunit; diagnosis;
KW Lambert Eaton Syndrome; calcium channel subunit alphaB-1; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 144..7163
FT /tag= a
FT /product= "calcium channel alphaB-1 subunit"
XX
FN US6096514-A.
XX
PD 01-AUG-2000.
XX
PF 25-MAY-1995; 95US-00450562.
XX
PR 04-APR-1988; 88US-00176899.
PR 02-FEB-1990; 90US-00482384.
PR 08-NOV-1990; 90US-00603751.
PR 30-NOV-1990; 90US-00620250.
PR 15-AUG-1991; 91US-00745206.
PR 10-APR-1992; 92US-00868354.
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PR 13-JUL-1992; 92US-00914231.
PR 11-AUG-1993; 93US-00105536.
PR 05-NOV-1993; 93US-00149097.
PR 07-FEB-1994; 94US-00193078.
PR 04-APR-1994; 94US-00223305.
PR 11-AUG-1994; 94US-00290012.
PR 23-SEP-1994; 94US-00311363.
PR 28-SEP-1994; 94US-00314083.
PR 07-NOV-1994; 94US-00336257.
PR 13-MAR-1995; 95US-00404950.
XX
PA (SIBI-) SIBIA NEUROSCIENCES INC.
XX
XX Ellis SB, Williams ME, Mccue AF, Harpold MW;
PI P-PSDB; AAB10572.
XX
DR WPI; 2000-548230/50.
DR
XX Human calcium channel beta subunit polynucleotides, useful for producing
FT recombinant eukaryotic cells and for diagnosing Lambert Eaton Syndrome.
XX
PS Example II; Col 97-112; 153pp; English.
XX
CC This invention describes a novel isolated DNA molecule (I) comprising a
CC sequence encoding a beta3-1 subunit of a human calcium channel. Nucleic
CC acid probes comprising 14-30 contiguous nucleotides of beta 3 subunit
CC encoding DNA are useful for isolation and cloning of calcium channel
CC subunit-encoding DNA. Recombinant eukaryotic cells that express
CC heterologous calcium channel are useful for identifying compounds that
CC modulate calcium channel activity and in assays for identifying agonists
CC and antagonists of calcium channel activity in humans. Human calcium
CC channel subunit or eukaryotic cells expressing the channel are useful for
CC diagnosing Lambert Eaton Syndrome (LES) in a human. This sequence encodes
CC the human calcium channel alphaB-1 subunit which is described in the
CC method of the invention
XX
SQ Sequence 7362 BP; 1445 A; 2277 C; 2215 G; 1425 T; 0 U; 0 Other;
Query Match 99.2%; Score 7316.4; DB 3; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;
Qy 1 GCGCGCGCGCTCGCGCGTGGGCGCGGCGAGGTCCGCTGCGGTCGCGGCGGCTCCGTG 60
Db 1 GCGCGCGCGCTCGCGCGTGGGCGCGGCGAGGTCCG-TGCGGTCCCGCGGCTCCGTG 59
Qy 61 GCTGCTCCGCTCTGAGCGCTGCGCGCGCCCGCGCCCTCCCTGCGCGGCGCGCTGGGCGG 120
Db 60 GCTGCTCCGCTCTGAGCGCT-GCGCGCGCCCGCGCCCTCCCTGCGCGGCGCGCTGGGCGG 118
Qy 121 GGGATGCACGCGGGGCGCGGAGCCATGGTCCGCTTCGGGGAGCAGAGCTGGGCGCGCTA 180
Db 119 GGGATGCACGCGGGGCGCGGAGCCATGGTCCGCTTCGGGGAGCAGAGCTGGGCGCGCTA 178
Qy 181 TGGAGGCGCGCGCGGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 240
Db 179 TGGAGGCGCGCGCGCGGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 238
Qy 241 GGGTCCCGGGGCTGCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 239 GGGTCCCGGGGCTGCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 298
Qy 301 CGCGCGGACCATGGCGCTGTACAAACCCATCCCGGTCAAGAGAACTGCTTACCCTCAA 360
Db 299 CGCGCGGACCATGGCGCTGTACAAACCCATCCCGGTCAAGAGAACTGCTTACCCTCAA 358
Qy 361 CCGCTGCTCTTCTGCTTTCAGCGAGAGCAAGTGTGTCGCGCAAAATACGCGAGGCGATCAC 420
Db 359 CCGCTGCTCTTCTGCTTTCAGCGAGAGCAAGTGTGTCGCGCAAAATACGCGAGGCGATCAC 418
Qy 421 CGAGTGGCCCTCCATCGAGTATATGATCCTGGGCCACCATCATCGCCAACTGCTGCTG 480
Db 419 CGAGTGGCCCTCCATTCGAGAAATATGATCCTGGGCCACCATCATCGCCAACTGCTGCTG 478
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QY 481 GGCCCTGGAGCAGCACCTCCCTGATGGGCAAAAAAGCCCAATGTCGAGCGGCTGACGA 540
Db 479 GGCCCTGGAGCAGCACCTCCCTGATGGGCAAAAAAGCCCAATGTCGAGCGGCTGACGA 538
QY 541 CACGAGGCCCTATTTCATCGGGAATCTTTGCTTCGAGGCAAGGATCAAAATCATCGCTCT 600
Db 539 CACGAGGCCCTATTTCATCGGGAATCTTTGCTTCGAGGCAAGGATCAAAATCATCGCTCT 598
QY 601 GGGCTTTGCTTCCACAAGAGGCTCTTACCTGCGGAAAGCGGCTGAAAGCTCATGGACTTCGT 660
Db 599 GGGCTTTGCTTCCACAAGAGGCTCTTACCTGCGGAAAGCGGCTGAAAGCTCATGGACTTCGT 658
QY 661 GGTGCTCCTCACAGGATCTTTCACAGGCTGGAACTGACTTCGAACTCGCAACACTGAG 720
Db 659 GGTGCTCCTCACAGGATCTTTCACAGGCTGGAACTGACTTCGAACTCGCAACACTGAG 718
QY 721 GGTGCTGCTGCTGAGGCGGCTTGAAGCTGGTGTCTGGATTTCCAAAGTTGAGGTGT 780
Db 719 GGTGCTGCTGCTGAGGCGGCTTGAAGCTGGTGTCTGGATTTCCAAAGTTGAGGTGT 778
QY 781 GCTCAAGTCCATCATGAAGGCCATGTTCCACTTCCTGCAGATTTGGGCTGCTTCTTCTT 840
Db 779 GCTCAAGTCCATCATGAAGGCCATGTTCCACTTCCTGCAGATTTGGGCTGCTTCTTCTT 838
QY 841 TGGCATCCTCATGTTTGCATCATTTGGCTTGGATTTCTACATGGGCAAGTTCCAAAGGC 900
Db 839 TGGCATCCTCATGTTTGCATCATTTGGCTTGGATTTCTACATGGGCAAGTTCCAAAGGC 898
QY 901 CTGTTTCCCCAACAGACAGATCGGAGCGGCTGGGTGACTTCCCTGTTGGCAAGAGGC 960
Db 899 CTGTTTCCCCAACAGACAGATCGGAGCGGCTGGGTGACTTCCCTGTTGGCAAGAGGC 958
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Db 959 CCCAGCCCGGCTGTGGAGGGGACACTGAGTGCCTGGGAGTACTGGCCAGGACCCAACTT 1018
QY 1021 TGGCATCACCACTTTGACAAATATCTGTTTGGCATTTGACGGTGTCCAGTGATCAC 1080
Db 1019 TGGCATCACCACTTTGACAAATATCTGTTTGGCATTTGACGGTGTCCAGTGATCAC 1078
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QY 1621 GGCCCTGAACACACTGTGTGGCATGTGTCATTACAAACAGCCGCGGCGGCTTACCAC 1680
Db 1619 GGCCCTGAACACACTGTGTGGCATGTGTCATTACAAACAGCCGCGGCGGCTTACCAC 1678
QY 1681 GACCCGTATTTTGGAGAGTTGTTTCTCTGGGTCTCTTCTCTACAGAGATGTCCTTGAA 1740
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RESULT 6
ID AAD39955
XX AAD39955 standard; DNA; 7362 BP.
AC AAD39955;
XX
DT 22-OCT-2002 (first entry)
XX
DE Human calcium channel alpha 1B-1 protein encoding DNA.
XX
KW Human; calcium channel protein; therapeutic; autoimmune disease;
KW diagnosis; Lambert Eaton Syndrome; alpha 1B-1 protein; splice variant;
KW gene; ds.
XX
OS Homo sapiens.
XX
FH Location/Qualifiers
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FT /*tag= a
FT CDS 144..7163
FT /*tag= b
FT /product= "Human calcium channel alpha 1B-1 protein"
FT 3' UTR 7164..7362
FT /*tag= c
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XX
PF 25-MAY-1995; 95US-00450272.
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PR 04-APR-1989; 89WO-US001408.
PR 02-FEB-1990; 90US-00482384.
PR 08-NOV-1990; 90US-00603751.
PR 30-NOV-1990; 90US-00620250.
PR 15-AUG-1991; 91US-00745206.
PR 13-JUL-1992; 92US-00914231.
PR 14-AUG-1992; 92WO-US006903.
PR 11-AUG-1993; 93US-00105536.
PR 05-NOV-1993; 93US-00149097.
PR 07-FEB-1994; 94US-00193078.
PR 04-APR-1994; 94US-00223305.
PR 11-AUG-1994; 94US-00290012.
PR 23-SEP-1994; 94US-00311363.
PR 07-NOV-1994; 94US-00336257.
PR 15-FEB-1995; 95US-00404354.
XX
PA (MERI) MERCK & CO INC.
XX

PI Harpold MM, Ellis SB, Williams ME, Mccue AF;
XX WPI; 2002-470318/50.
DR P-PSDB; AAE24785.
XX
PT Eukaryotic cells expressing a functional heterologous human calcium
FT channel and encoding nucleic acid isolated from human cerebellum for drug
PT design and to diagnose Lambert Eaton Syndrome.
XX
PS Example 2; Col 97-114; 154pp; English.
XX
CC The present invention relates to novel human calcium channel proteins and
CC polynucleotides encoding such proteins. The invention also relates to
CC eukaryotic cells expressing a functional heterologous human calcium
CC channel alpha 1, alpha 2, beta and gamma subunits. The eukaryotic cells
CC are useful for screening for potential calcium channel antagonists or
CC agonists to select compounds that have potential as disease or tissue-
CC specific therapeutic agents. The subunits may be used in diagnostic
CC assays for the autoimmune disease Lambert Eaton Syndrome. The present
CC sequence is a DNA encoding human calcium channel alpha 1B subunit splice
CC variant, alpha 1B-1 protein
XX
SQ Sequence 7362 BP; 1445 A; 2277 C; 2215 G; 1425 T; 0 U; 0 Other;

Query Match 99.2%; Score 7316.4; DB 6; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

Qy 1 GCGGCGCGGCTGCGGCGTGGGGCGGCGAGGTCCGCTGCGGTCCCGGCGGCTCCGTG 60
Db 1 GCGGCGCGGCTGCGGCGTGGGGCGGCGAGGTCCG-TGCGGTCCCGGCGGCTCCGTG 59

Qy 61 GCTGCTCCGCTCTGAGCGCTTGGCGGCCCGCGGCCCTTCCCTCCCGGGCGGCTGGGCGG 120
Db 60 GCTGCTCCGCTCTGAGGCGCT-GCGGCGCCCGCGGCCCTTCCCTCCCGGGCGGCTGGGCGG 118

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Db 119 GGGATGACGCGGGGCCCGGGAGCCATGTGTCCGCTTGGGGGACGAGTGGGGCGGCGCTA 178

Qy 181 TGGAGCGCCCGCGGCGAGAGCGGGCGGCGGGCGGCGGGCGGCGGGCGGGGGGCGCC 240
Db 179 TGGAGCGCCCGCGGCGGAGAGCGGGCGGCGGGCGGCGGGCGGCGGGGGGCGCC 238

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Db 479 GGCCCTGGAGCAGCAGCCTCCCTGATGGGACAAAACGCCCATGTCCGAGCGGTGACGCA 538

Qy 541 CAGGAGCCCTATTTTCATCGGATCTTTTCTTCGAGGCGAGGATCAAAATCATCGCTCT 600
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Db 839 TGGCATCTCATGTTTGGCATCATGTTGGCTCTGAGTTCATCATGGGCAAGTTCCAAAGGC 898
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QY 1021 TGGCATCACTTGTGACAAATATCTGTTTGGCATCTTGAAGTTCAGGTTCCAGTGCATCAC 1080
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DB CGAACAATGTCTCTGGGCTCTGCTGACGCTGTTTCAAGTGTCCACGGGAGAGGCTGGGCC 4246
QY 4261 CATGGTGTGAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAGCCCTGGGTA 4320
DB CATGGTGTGAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAGCCCTGGGTA 4306
QY 4321 CCGCATGGAGCTGTCCATCTTCTAGTGTGCTACTTTGTGGTCTTTTCCCTTCTTCTTCGT 4380
DB CCGCATGGAGCTGTCCATCTTCTAGTGTGCTACTTTGTGGTCTTTTCCCTTCTTCTTCGT 4366
QY 4381 CAACATCTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGACAAGGTGATGTC 4440
DB CAACATCTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGACAAGGTGATGTC 4426
QY 4441 TGAATGAGCAGCTCGGAGAAGAAACGAGAGGGCTTGCAATTTGACTTCCGCCATCAGCGCAAAACC 4500
DB TGAATGAGCAGCTCGGAGAAGAAACGAGAGGGCTTGCAATTTGACTTCCGCCATCAGCGCAAAACC 4486
QY 4501 CCTGACACAGGTAATGCCCCAAGAACCGCGAGTGTTCAGTATGAAGTGGAGCATTTGT 4560
DB CCTGACACAGGTAATGCCCCAAGAACCGCGAGTGTTCAGTATGAAGTGGAGCATTTGT 4546
QY 4561 GGTCTCCCGCCCTTTGAAATACCTTCAATGAGTACGAGCTGATGCTGAAATGCTGGAACAT 4620
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QY 4621 GATGATGAAGTCTTATGATGACCCCTATGAGTACGAGCTGATGCTGAAATGCTGGAACAT 4680
DB GATGATGAAGTCTTATGATGACCCCTATGAGTACGAGCTGATGCTGAAATGCTGGAACAT 4666
QY 4681 CGTGTTCACATCCATGTTTCTCCATGGAAATGCGTGTCTGAAGATCATCGCCCTTTGGGGTGT 4740
DB CGTGTTCACATCCATGTTTCTCCATGGAAATGCGTGTCTGAAGATCATCGCCCTTTGGGGTGT 4726
QY 4741 GAACATTTTTCAGAGATGCGCTGGAAATGCTTTGACTTTGTGACTTTGTGCTGTTGGAAAGTATTAC 4800
DB GAACATTTTTCAGAGATGCGCTGGAAATGCTTTGACTTTGTGACTTTGTGCTGTTGGAAAGTATTAC 4786
QY 4801 TGATATTTTGTAGTAAACAGAGATTCCGGAACGAAACAAATTTTCAACCTCAGCTTCTCCCG 4860
DB TGATATTTTGTAGTAAACAGAGATTCCGGAACGAAACAAATTTTCAACCTCAGCTTCTCCCG 4846
QY 4861 CCTCTTTTCGAGCTGCGCGGCTGATCAAGCTGTCTCCGCGAGGGGCTACACCATCCGCACTCT 4920
DB CCTCTTTTCGAGCTGCGCGGCTGATCAAGCTGTCTCCGCGAGGGGCTACACCATCCGCACTCT 4906
QY 4921 GCTGTGGAACCTTTGTCCAGTCCCTTCAAGGCCCTGCGCTAGTGTGTCTCATTCGCCAT 4980
DB GCTGTGGAACCTTTGTCCAGTCCCTTCAAGGCCCTGCGCTAGTGTGTCTCATTCGCCAT 4966
QY 4981 GCTGTTTCTTTCATCTAGCCCATCATCCGCATGCAAGTGTGTTGGGAATATTTGCCCTGGATGA 5040
DB GCTGTTTCTTTCATCTAGCCCATCATCCGCATGCAAGTGTGTTGGGAATATTTGCCCTGGATGA 5026
QY 5041 TGACACGAGCATCAACCGGCAACAACTTCCGGAAGTCTTTTTCGAAAGCCCTGATGTGCT 5100

Db	5027	TGACACAGCATCAACCGCCACAACTTCGGACGTTTTTTCGAAGCCCTGATGCTGCT	5086
Qy	5101	GTTCAGAGCGCCACCGGGAGCGCTGGCAAGATCATGCTGCTGCTGCTGAGCAACCA	5160
Db	5087	GTTCAGAGCGCCACCGGGAGCGCTGGCAAGATCATGCTGCTGCTGCTGAGCAACCA	5146
Qy	5161	GGCCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGACTTTGGCTACTTCTACTTT	5220
Db	5147	GGCCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGACTTTGGCTACTTCTACTTT	5206
Qy	5221	CGTCTCCTTCATCTTCTGCTGCTCTTCTGATGTTGAAACCTTTTGTGGCTGTGATCAT	5280
Db	5207	CGTCTCCTTCATCTTCTGCTGCTCTTCTGATGTTGAAACCTTTTGTGGCTGTGATCAT	5266
Qy	5281	GGACAAATTTTGTAGTACTCATCGGGGACTCTTCCATCTAGTGTCTCACCACTTCGATGA	5340
Db	5267	GGACAAATTTTGTAGTACTCATCGGGGACTCTTCCATCTAGTGTCTCACCACTTCGATGA	5326
Qy	5341	GTTTCATCCGGGTCTGGGCTGAATPACGACCCGGCTGCTGTGGCGGCATCAGTTACAATGA	5400
Db	5327	GTTTCATCCGGGTCTGGGCTGAATPACGACCCGGCTGCTGTGGCGGCATCAGTTACAATGA	5386
Qy	5401	CATGTTTGATGCTGAAACACATGTCCTCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5460
Db	5387	CATGTTTGATGCTGAAACACATGTCCTCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5446
Qy	5461	TCGAGTTGCTTACAAGCGCTGGTTCGATGAACATGCCCCTCTCCACGAGGACATGAC	5520
Db	5447	TCGAGTTGCTTACAAGCGCTGGTTCGATGAACATGCCCCTCTCCACGAGGACATGAC	5506
Qy	5521	TGTTCACTTCCAGCTGATGCGCTCATCCGAGCGGCACTGGAGATCAAGCTGGC	5580
Db	5507	TGTTCACTTCCAGCTGATGCGCTCATCCGAGCGGCACTGGAGATCAAGCTGGC	5566
Qy	5581	CCGAGCTGGGACAAAGCAGATCAGTGTGACCGGAGTTGAGGAAGGAGATTCCGTTGT	5640
Db	5567	CCGAGCTGGGACAAAGCAGATCAGTGTGACCGGAGTTGAGGAAGGAGATTCCGTTGT	5626
Qy	5641	GTGGGCCAATCTGCCCCAGAACTTTGGACTTGCTGGTACCACCCCATAGCCCTGATGA	5700
Db	5627	GTGGGCCAATCTGCCCCAGAACTTTGGACTTGCTGGTACCACCCCATAGCCCTGATGA	5686
Qy	5701	GATGACAGTGGGGAAGTTTATGACGCTGTGANGATATTTGACTTCTACAAGCAAGACAA	5760
Db	5687	GATGACAGTGGGGAAGTTTATGACGCTGTGANGATATTTGACTTCTACAAGCAAGACAA	5746
Qy	5761	AACCAACAGAGACAGATGACAGCGCTCCTGGAGGCTCTCCAGATGGGTCTCTGTGTC	5820
Db	5747	AACCAACAGAGACAGATGACAGCGCTCCTGGAGGCTCTCCAGATGGGTCTCTGTGTC	5806
Qy	5821	CCTGTTTCAACCTCTGAAGGCCACCTTGAGCAGACACAGCCGGCTGTGCTCCGAGGAGC	5880
Db	5807	CCTGTTTCAACCTCTGAAGGCCACCTTGAGCAGACACAGCCGGCTGTGCTCCGAGGAGC	5866
Qy	5881	CGGGGTTTTCTTCACACAGAGAGTTTCAACCTCCTCAGCAATGGCGGGGCCATACAAA	5940
Db	5867	CGGGGTTTTCTTCACACAGAGAGTTTCAACCTCCTCAGCAATGGCGGGGCCATACAAA	5926
Qy	5941	CCAAGAGAGTGGCATCAAAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC	6000
Db	5927	CCAAGAGAGTGGCATCAAAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC	5986
Qy	6001	CCATGAGGCAAGGCCACCCCTGGAGCGTGGCCATCTCCACAGATGCCCTGTGGGGCGGTC	6060
Db	5987	CCATGAGGCAAGGCCACCCCTGGAGCGTGGCCATCTCCACAGATGCCCTGTGGGGCGGTC	6046
Qy	6061	AGGAGCACTGGCTGGAGCTTCAGATGCAGACATTAACCCGAGGGGCCCTGATGGGGA	6120
Db	6047	AGGAGCACTGGCTGGAGCTTCAGATGCAGACATTAACCCGAGGGGCCCTGATGGGGA	6106
Qy	6121	GCCCCAGCCTGGGTGGAGAGCCAGGTCGAGCGGCTCTCCATGCCCGCCTTGGCGCCGA	6180

Db	6107	GCCCCAGCCTGGGCTGGAGAGCCAGGGTCGAGCGGCTCTCATGCCCGCCTTGGCGGCCGA	6166
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Db	6167	GACTCAGCCCTGTACAGATGCCAGCCCATGAAAGCGTCCATCTCCACGTGTGGCCCCAGCG	6226
Qy	6241	GCCCGGTGGGACTCATCTTTTGCAGCACACCCCGGAGCGGCCACCCCTTAGCCAGGGGTC	6300
Db	6227	GCCCGGTGGGACTCATCTTTTGCAGCACACCCCGGAGCGGCCACCCCTTAGCCAGGGGTC	6286
Qy	6301	GTGCACCAACCAACCAACCAACCGCTGCCACCGCGCAGGGAAGAGGAGGTCCTCTGGA	6360
Db	6287	GTGCACCAACCAACCAACCAACCGCTGCCACCGCGCAGGGAAGAGGAGGTCCTCTGGA	6346
Qy	6361	GAAGGGGCCAGCCCTGTCTGCCGATATGATGGCGCAACAAAGCATGCTGTGTGGGGCGGG	6420
Db	6347	GAAGGGGCCAGCCCTGTCTGCCGATATGATGGCGCAACAAAGCATGCTGTGTGGGGCGGG	6406
Qy	6421	GCTGCCCGCGGAGAGGGGCTTACAGGCTCCCGCGGGAACGAGAGCGCGCGGAGGAGCG	6480
Db	6407	GCTGCCCGCGGAGAGGGGCTTACAGGCTCCCGCGGGAACGAGAGCGCGCGGAGGAGCG	6466
Qy	6481	GGGCGGTCCTCAGAGCGGAGCGGCTCATCTCTCTCGGAGAGAGCGGCTTCTA	6540
Db	6467	GGGCGGTCCTCAGAGCGGAGCGGCTCATCTCTCTCGGAGAGAGCGGCTTCTA	6526
Qy	6541	CTCTGCGACCGCTTTGGGGCGCTGAGCGCCCGAGAGCCCAAGCCCTCTCTCAGCAGCCA	6600
Db	6527	CTCTGCGACCGCTTTGGGGCGCTGAGCGCCCGAGAGCCCAAGCCCTCTCTCAGCAGCCA	6586
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Db	6587	CCCAACCTGCTCCCAACAGCTGCGCAGAGCGGGAACCCACACAGGGCACTGTTCCGT	6646
Qy	6661	GAATGGAGAGCCCTTGTGTCAAATCTGTGTGTAGAACCCCGCGCGGCTGTGGCGGAG	6720
Db	6647	GAATGGAGAGCCCTTGTGTCAAATCTGTGTGTAGAACCCCGCGCGGCTGTGGCGGAG	6706
Qy	6721	GCAGTCTCCCGCAGACGCTTCCCGCCCTGAGTCCCGCCCTGAGTCAAGATGAGCACTC	6780
Db	6707	GCAGTCTCCCGCAGACGCTTCCCGCCCTGAGTCCCGCCCTGAGTCAAGATGAGCACTC	6766
Qy	6781	CTCACCCTCCTTCCCGCGGCTCAGACCAAGCTTCTCTGCTTCTCTCCAGCGCGCT	6840
Db	6767	CTCACCCTCCTTCCCGCGGCTCAGACCAAGCTTCTCTGCTTCTCTCCAGCGCGCT	6826
Qy	6841	CAGCGCTGGGCTTTCGAAACAAACCGCTTGTGAGAGAGAGAGCCCTCAGCAGCGCT	6900
Db	6827	CAGCGCTGGGCTTTCGAAACAAACCGCTTGTGAGAGAGAGAGCCCTCAGCAGCGCT	6886
Qy	6901	GGCCCTTGGCTCTCGAATTTGGCTCTGACCTTACCTGGGGCAGCGTCTGAGAGTGGC	6960
Db	6887	GGCCCTTGGCTCTCGAATTTGGCTCTGACCTTACCTGGGGCAGCGTCTGAGAGTGGC	6946
Qy	6961	CTCTGTCCAAGCGCTTCCCTGAGGACACGCTCACTTTTCGAGGAGGCTGTGGCCACCACTC	7020
Db	6947	CTCTGTCCAAGCGCTTCCCTGAGGACACGCTCACTTTTCGAGGAGGCTGTGGCCACCACTC	7006
Qy	7021	GGGCGCTCCTCAGAGCTTCTGAGTGTCTCTCTGAGTCTCCAGTCTCACTCTCGG	7080
Db	7007	GGGCGCTCCTCAGAGCTTCTGAGTGTCTCTCTGAGTCTCCAGTCTCACTCTCGG	7066
Qy	7081	CGCGCTGCCCAACCGGTTTACACTGACCCCTGGGACTCAGCTCGGGTGGCCAGCAGGCA	7140
Db	7067	CGCGCTGCCCAACCGGTTTACACTGACCCCTGGGACTCAGCTCGGGTGGCCAGCAGGCA	7126
Qy	7141	CAGCTACCAACCACTGAGCAAGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	7200
Db	7127	CAGCTACCAACCACTGAGCAAGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	7186
Qy	7201	CTGCAATGACAGAGGCTGTGTTCCAGTGGATGAGTTTTTATCATCCACGCGGAGTGG	7260
Db	7187	CTGCAATGACAGAGGCTGTGTTCCAGTGGATGAGTTTTTATCATCCACGCGGAGTGG	7246

Qy 7261 CCCTCGGGGAGGCTTGCCACCTTGCTGAGGCTCCTGTGCGCCCTCCCTCCCTCCCTCCT 7320
Dd 7247 CCCTCGGGGAGGCTTGCCACCTTGCTGAGGCTCCTGTGCGCCCTCCCTCCCTCCCTCCT 7306
Qy 7321 CCCCTCTTTTACTCTAGACGAGCAATAAGCCCTTTGCTTGAGTGACGTACCGC 7376
Dd 7307 CCCCTCTTTTACTCTAGACGAGCAATAAGCCCTTTGCTTGAGTGACGTACCGC 7362
RESULT 7
AAQ84657
ID AAQ84657 standard; DNA; 7362 BP.
XX AC AAQ84657;
XX DT 25-MAR-2003 (revised)
XX DT 01-DEC-1995 (first entry)
XX DE Human neuronal calcium channel subunit alpha 1B-1.
XX KW Calcium channel subunit; antagonist; agonist; diagnosis;
XX KW Lambert Eaton Syndrome; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 144..7163 /*tag= a
XX FT misc_difference 6633..6819 /*tag= b
XX FT /label= additional exon wrt alpha 1B-2
XX FT misc_feature 6820..7362 /*tag= c
XX FT /note= "identical to alpha 1B-2"
XX PN W09504822-A1.
XX PD 16-FEB-1995.
XX PF 11-AUG-1994; 94WO-US009230.
XX PR 11-AUG-1993; 93US-00105536.
XX PR 05-NOV-1993; 93US-00149097.
XX PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX PI Harpold WM, Ellis SB, Williams ME, Mccue AF, Gillespie A;
XX DR WPI; 1995-090900/12.
XX DR P-PSDB; AAR71005.
XX PT DNA encoding human calcium channel sub-unit(s) - used for developing
XX PT prods. for studying calcium channels, e.g. for obtaining agonists and
XX PT antagonists.
XX PS Disclosure; Page 138-149; 285pp; English.
XX CC DNA encoding the alpha 1B subunit was isolated by screening a human basal
XX CC ganglia cDNA library with fragments of the rabbit skeletal muscle calcium
XX CC channel alpha 1 subunit-encoding cDNA. A portion of one of the positive
XX CC clones was used to screen an IMR32 cell cDNA library. Clones that
XX CC hybridised to the basal ganglia probe were used to further screen an
XX CC IMR32 cell cDNA library to identify overlapping clones that in turn were
XX CC used to screen a human hippocampus cDNA library. A series of clones to
XX CC span nearly the entire length of the nt. sequence encoding the human
XX CC alpha 1B subunit was obt'd. Nucleic acid amplification of specific regions
XX CC of the IMR32 cell alpha 1B mRNA yielded additional segments of the alpha
XX CC 1B coding sequence. A full- length alpha 1B DNA clone was constructed by
XX CC ligating portions of the partial cDNA clones. Nucleic acid amplification
XX CC analysis of IMR32 cell RNA and genomic DNA using oligo primers corresp.
XX CC to sequences located 5' and 3' of the stop codon of the DNA encoding the
XX CC alpha 1B subunit revealed an alternatively spliced alpha 1B-encoding mRNA

CC in IMR32 cells. This second mRNA product is the result of differential
CC splicing of the alpha 1B subunit transcript to include another exon that
CC is not present in the mRNA corresp. to the other 3' alpha 1B cDNA
CC sequence that was initially isolated. The alpha 1B subunit encoded by a
CC DNA sequence contg. an additional exon is referred to as alpha 1B-1 and
CC given in AAQ84657/7376, whereas the other form is referred to as alpha
CC 1B-2 and is given in AAQ84658/7376. Following the sequence of the
CC additional exon in alpha 1B-1 the alpha 1B-1 and alpha 1B-2 sequences are
CC identical. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 7362 BP; 1445 A; 2278 C; 2214 G; 1425 T; 0 U; 0 Other;
Query Match 99.2%; Score 7314.8; DB 2; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7360; Conservative 0; Mismatches 2; Indels 14; Gaps 3;
Qy 1 GCGGCGCGGCTGCGGCGGTGGGCGCGGCGGCGGCTGCGTCCCGCGCGGCTCCGTG 60
Dd 1 GCGGCGCGGCTGCGGCGGTGGGCGCGGCGGCGGCTGCGTCCCGCGGCTCCGTG 59
Qy 61 GCTGCTCCGCTCTGAGCGCTGCGGCGGCGGCGGCGGCTCCCTGCGGCGGCGGCTGGGCGG 120
Dd 60 GCTGCTCCGCTCTGAGCGCTT-GCGGCGGCGGCGGCGGCTCCCTGCGGCGGCGGCTGGGCGG 118
Qy 121 GGGATGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
Dd 119 GGGATGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 178
Qy 181 TGGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Dd 179 TGGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 238
Qy 241 GGGTCCCGGCGGCGGCTGCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Dd 239 GGGTCCCGGCGGCGGCTGCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 298
Qy 301 GCGCGGAGCCATGGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGTCTTACCGTCAA 360
Dd 299 GCGCGGAGCCATGGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGTCTTACCGTCAA 358
Qy 361 CCCTGCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 420
Dd 359 CCCTGCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 418
Qy 421 CGAGTGGCCTCCATTCGAGTATATGATCTTGGCCACCATCATGCCAACTGCTGCTGCT 480
Dd 419 CGAGTGGCCTCCATTCGAGTATATGATCTTGGCCACCATCATGCCAACTGCTGCTGCT 478
Qy 481 GGGCCTGGAGCAGCAGCTCCCTGATGGGAGCAAAAAGCCCATATGTCGAGCGGCTGGAGCA 540
Dd 479 GGGCCTGGAGCAGCAGCTCCCTGATGGGAGCAAAAAGCCCATATGTCGAGCGGCTGGAGCA 538
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Dd 539 CAGGCGCCCTATTTTCATCGGATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 598
Qy 601 GGGCTTTGTCTTCCACAAGGGCTCTTACCTGCGGAACGGGTGGAAAGTCAATGGACTTCGT 660
Dd 599 GGGCTTTGTCTTCCACAAGGGCTCTTACCTGCGGAACGGGTGGAAAGTCAATGGACTTCGT 658
Qy 661 GGTGCTCTTCAAGGAGTCCCTTCCCAAGGCTGAGAACTGACTTCCGAACTCGAACTAGAG 720
Dd 659 GGTGCTCTTCAAGGAGTCCCTTCCCAAGGCTGAGAACTGACTTCCGAACTCGAACTAGAG 718
Qy 721 GGTGCTCTTCAAGGAGTCCCTTCCCAAGGCTGAGAACTGACTTCCGAACTCGAACTAGAG 780
Dd 719 GGTGCTCTTCAAGGAGTCCCTTCCCAAGGCTGAGAACTGACTTCCGAACTCGAACTAGAG 778
Qy 781 GCTCAAGTCCATCATGAAGGCCCATGGTTCCACTCTTGCAGATTTGGGCTGCTCTTCTTCTT 840
Dd 779 GCTCAAGTCCATCATGAAGGCCCATGGTTCCACTCTTGCAGATTTGGGCTGCTCTTCTTCTT 838
Qy 841 TGCCATCTCTCATGTTTGGCCATCATTTGGCCTGGAGTTTCTTACATGGGCAAGTTCCACAAGGC 900

QY 3061 GGAGAGCCGCGCGCGGCAACGCGGCCCGGCAACAGCGCGAGCCTGCTCAACGAGGCTGT 3120
DB GGAGAGCCGCGCGCGCGGCAACGCGGCCCGGCAACAGCGCGAGCCTGCTCAACGAGGCTGT 3118
QY 3121 GGAGAGGAGACCAAGAGAGAGAGGCGCAAGAGAGAGGCTGAGATAGTGGAGCGGA 3180
DB GGAGAGGAGACCAAGAGAGAGAGGCGCAAGAGAGAGGCTGAGATAGTGGAGCGGA 3178
QY 3181 CAAGGAAAAGAGCTCCGGAACCAACAGCCCGGAGCCACATGTGCACCTGGAGACAG 3240
DB CAAGGAAAAGAGCTCCGGAACCAACAGCCCGGAGCCACATGTGCACCTGGAGACAG 3238
QY 3241 TGGGACTGTGACTGTGGGTCCCATGCAACACCTGCCAGCACTGTCTCCAGAAAGTGGG 3300
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DB TTTAAGCCCAACCAACTGTCTCCGCCCTCTGCACTACATCTGTGACCACTAGGTAATT 3598
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DB TGAACAACAGCATCAACCGGCAACAACTTCCGGAAGTGTGGAAGTGTGCTTGTCTTACTT 5086
QY 5101 GTTCAGAGCGGCAACCGGAGGAGGCTGGCACGAGATCAATGCTGCTGCTGCTGAGCAACCA 5160
DB GTTCAGAGCGGCAACCGGAGGAGGCTGGCACGAGATCAATGCTGCTGCTGCTGAGCAACCA 5146
QY 5161 GGCCTGTGATGAGCAGGCAATGCCACCGAGTGTGGAAGTGTGCTTGTCTTACTT 5220
DB GGCCTGTGATGAGCAGGCAATGCCACCGAGTGTGGAAGTGTGCTTGTCTTACTT 5206
QY 5221 CGTCTCCTTCATCTTCTGCTCTCTTTTGTGAAACCTCTTTGTGGCTGTGATCAT 5280

Db	5207		CGTCTCCTTCATCTCCTGTGTCCTTTCTGAATGTTGAACCTCTTTGTGGCTGTGATCAT	5266
Qy	5281	GGACAAATTTT	GAGTACTCTCACGGGACCTCTTCCATCTAGTCTCTACCACTTTGGATGA	5340
Db	5267	GGACAAATTTT	GAGTACTCTCACGGGGACTCTTTCATCTAGTCTCACCACTTTGGATGA	5326
Qy	5341	GTTTCATCCGGTCTGGGCTGGAATACGA	CCCGGCTCGCTGTGGGCGCATCAGTTTACAATGA	5400
Db	5327	GTTTCATCCGGGCTTGGGCTGGAATAGAC	CCCGGCTCGCTGTGGGCGCATCAGTTTACAATGA	5386
Qy	5401	CATGTTTGAGATGCTGAACACACATGCTCCCGGCTCTGGGCTGGGGAAGAAATGCCCTGC	5460	
Db	5387	CATGTTTGAGATGCTGAACACACATGCTCCCGGCTCTGGGCTGGGGAAGAAATGCCCTGC	5446	
Qy	5461	TCGAGTTGCTTACAAGCGGCTGGTTTCGATGAACATGCCATCTCCAACGAGGACATGAC	5520	
Db	5447	TCGAGTTGCTTACAAGCGGCTGGTTTCGATGAATGCAATGCCATCTCCAACGAGGACATGAC	5506	
Qy	5521	TGTTTCATCTTCAGTCCAGCTGATGAGCCCTCATCCGAGCGCATCTGGAGATCAAGCTGCG	5580	
Db	5507	TGTTTCATCTTCAGTCCAGCTGATGAGCCCTCATCCGAGCGCATCTGGAGATCAAGCTGCG	5566	
Qy	5581	CCCAGCTGGGA	CAAAAGCAGCATCAGTGTGACCGCGAGTTGAGGAAGGAGATTTCCGTTGT	5640
Db	5567	CCCAGCTGGGA	CAAAAGCAGCATCAGTGTGACCGCGAGTTGAGGAAGGAGATTTCCGTTGT	5626
Qy	5641	GTGGGCCAATCTGCCCCAGAGA	CTTTTGGACTTCTGCTGGTACCAACCCTAAGCCTCATGA	5700
Db	5627	GTGGGCCAATCTGCCCCAGAGA	CTTTTGGACTTCTGCTGGTACCAACCCTAAGCCTCATGA	5686
Qy	5701	GATGACAGTGGGGAAGTTTATGACGCTCTGATGATTTTGA	CTTCTGCTGATCAACCCCTAAGCCTCATGA	5760
Db	5687	GATGACAGTGGGGAAGTTTATGACGCTCTGATGATTTTGA	CTTCTGCTGATCAACCCCTAAGCCTCATGA	5746
Qy	5761	AACACACAGACCCNATGACAGGCTCTGAGGCTCTCCACAGATGGTCTCTGTCTC	5820	
Db	5747	AACACACAGACCCNATGACAGGCTCTGAGGCTCTCCACAGATGGTCTCTGTCTC	5806	
Qy	5821	CCTGTTCCACCCTCTGAAGGCCACCTCTGAGCAGACACACGCGCTGTCTCCAGATGGTCTCTGTCTC	5880	
Db	5807	CCTGTTCCACCCTCTGAAGGCCACCTCTGAGCAGACACACGCGCTGTCTCCAGATGGTCTCTGTCTC	5866	
Qy	5881	CGGGTTTTTCTTTCGACAGAGAGTTCCACCTCCCTCAGCAATGGCGGGCCATACAAA	5940	
Db	5867	CGGGTTTTTCTTTCGACAGAGAGTTCCACCTCCCTCAGCAATGGCGGGCCATACAAA	5926	
Qy	5941	CCAAGAGATGGCATCAAGAGTCTGCTCCTGGGCACTCAAGACCCAGGATGCACC	6000	
Db	5927	CCAAGAGATGGCATCAAGAGTCTGCTCCTGGGCACTCAAGACCCAGGATGCACC	5986	
Qy	6001	CCATGAGCCAGGCAACCCCTGGAGCGTGCCACTCCAAGAGATCCCTGTGGGCGGTC	6060	
Db	5987	CCATGAGCCAGGCAACCCCTGGAGCGTGCCACTCCAAGAGATCCCTGTGGGCGGTC	6046	
Qy	6061	AGGAGCACTGGCTGTGACGCTTCAAGTGCAGACATAACCCGGAGGGCCCTGTATGGGA	6120	
Db	6047	AGGAGCACTGGCTGTGACGCTTCAAGTGCAGACATAACCCGGAGGGCCCTGTATGGGA	6106	
Qy	6121	GCCCAAGCTGGCTGTGAGACCAAGGCTCGAGCGGCTCCATGCCCCGCTTGTGGGCCGA	6180	
Db	6107	GCCCAAGCTGGCTGTGAGACCAAGGCTCGAGCGGCTCCATGCCCCGCTTGTGGGCCGA	6166	
Qy	6181	GACTCAGCCGTCACAGATGCCAGCCCATGAAAGCGCTCCATCTCOAGCTGGGCCAGCG	6240	
Db	6167	GACTCAGCCGTCACAGATGCCAGCCCATGAAAGCGCTCCATCTCOAGCTGGGCCAGCG	6226	
Qy	6241	GCCCGTGGGACTCATCTTTTGAGACACCAACCCCGGACGCCCAACCCCTGACGAGGCTC	6300	
Db	6227	GCCCGTGGGACTCATCTTTTGAGACACCAACCCCGGACGCCCAACCCCTGACGAGGCTC	6286	
Qy	6301	GTGCAACCAACCAACCAACCGCTGCCACCGCCGACAGGACAGGATCCCTGGA	6360	

ID AAQ37817 standard; cDNA; 7362 BP.
XX
AC AAQ37817;
XX
DT 25-MAR-2003 (revised)
DT 30-JUN-1993 (first entry)
XX
XX Sequence encoding the alpha 1B-1 human calcium channel subunit.
DE
XX
XX Human calcium channel subunit; diagnosis; agonist; antagonist;
KW Lambert Eaton syndrome; ss.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 144..7163
FT /*tag= a
XX
XX W09304083-A1.
XX
XX 04-MAR-1993.
XX
XX 14-AUG-1992; 92WO-US006903.
XX
XX 15-AUG-1991; 91US-00745206.
PR 10-APR-1992; 92US-00868354.
XX
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
XX Harpold MM, Ellis SB, Williams ME, Feldman DH, Mecue AF;
PI Brenner R;
XX
XX WPI; 1993-093936/11.
DR P-PSDB; AAR33549.
XX
XX DNA encoding specific human calcium channel sub-units - used for
PT identifying calcium channel agonists and antagonists and diagnosing
PT Lambert Eaton syndrome.
XX
PS Disclosure; Page 111-120; 150pp; English.
XX
CC DNA encoding the alpha 1B subunit was isolated by screening a human basal
CC ganglia cDNA library with fragments of the rabbit skeletal muscle calcium
CC channel alpha 1 subunit-encoding cDNA. A portion of one of the positive
CC clones was used to screen an IMR32 cell cDNA library. Clones that
CC hybridized to the basal ganglia DNA prove were used to further screen an
CC IMR32 cell cDNA library to identify overlapping clones that in turn were
CC used to screen a human hippocampus cDNA library. In this way, a
CC sufficient series of clones to span nearly the entire length of the
CC nucleotide sequence encoding the human alpha 1B subunit was obtained. PCR
CC amplification of specific regions of the IMR32 cell alpha 1B mRNA yielded
CC additional segments of the alpha 1B coding sequence. A full-length alpha
CC 1B DNA clone was constructed by ligating portions of the partial cDNA
CC clones (see AAQ37817, AAQ37818). Alpha 1B-1 and alpha 1B-2 are derived by
CC alternative splicing of the alpha 1B subunit transcript. (Updated on 25-
XX MAR-2003 to correct PN field.)
XX
SQ Sequence 7362 BP; 1446 A; 2276 C; 2214 G; 1426 T; 0 U; 0 Other;

Query Match 99.1%; Score 7313.2; DB 2; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7359; Conservative 0; Mismatches 3; Indels 14; Gaps 3;

QY 1 GCGGCGGGCTGCGGGTGGGCGCGGAGGTCCGCTGCGTCCGGGGCTCCGTG 60
DB 1 GCGGCGGGCTGCGGGTGGGCGCGGAGGTCCG-TCGGGTCCGGGGCTCCGTG 59

QY 61 GCTGCTCGGCTCTGAGCGCTTGGGCGCGCCGCCCTCCCTGCGGCGCGCTGGGCGG 120
DB 60 GCTGCTCGGCTCTGAGCGCTT-GCGGCGCGCGGCCCTCCCTGCGGCGCGCTGGGCGG 118

QY 121 GGGATGACGCGGGCGCGGAGCCATGTCGCTTGCGGGAACAGCTGGGCGCGCGCTA 180
|||||

DB 119 GGGATGACGCGGGGCGCGGAGCCATGTCGCTTCGGGAGCAGCTGGGCGCGCGCTA 178
QY 181 TGGAGCCCCCGCGCGGAGAGCGGCCCCGGGCGCGGCGCGGCGCGGCGCGCGCC 240
|||||
DB 179 TGGAGGCCCGCGCGGAGAGCGGCCCCGGGCGCGGCGCGGCGCGGCGCGCGCC 238
|||||
QY 241 GGGTCCGGGGGGCTGCAGCCCGGCGGAGGGTCTCTACAAGCAATCGATCGGCGAGCG 300
|||||
DB 239 GGGTCCGGGGGGCTGCAGCCCGGCGGAGGGTCTCTACAAGCAATCGATCGGCGAGCG 298
|||||
QY 301 CGGCGGACCATGGCGCTGTACAAACCCCTCCCGGTCAAGCAGAACTGCTTCAACCGTCAA 360
|||||
DB 299 CGGCGGACCATGGCGCTGTACAAACCCCTCCCGGTCAAGCAGAACTGCTTCAACCGTCAA 358
|||||
QY 361 CGGCTCGCTTTCGTCTTCAGCGAGGACAAAGTGTGTCGCAACATCGCCAACTGCTGCT 480
|||||
DB 359 CGGCTCGCTTTCGTCTTCAGCGAGGACAAAGTGTGTCGCAACATCGCCAACTGCTGCT 478
|||||
QY 421 CGAGTGGCTCCATTCGAGTATATGATCTGGGCCACCATCATCGCCAACTGCTGCTGCT 480
|||||
DB 419 CGAGTGGCTCCATTCGAGTATATGATCTGGGCCACCATCATCGCCAACTGCTGCTGCT 478
|||||
QY 481 GGGCTTGGAGCAGCACTCCCTGATGGGACAAAAAGCCCATCTTCGAGCGGCTGGACGA 540
|||||
DB 479 GGGCTTGGAGCAGCACTCCCTGATGGGACAAAAAGCCCATCTTCGAGCGGCTGGACGA 538
|||||
QY 541 CACGAGCCCTATTTTCATCGGGATCTTTTGTCTTCGAGGCGAGGATCAAAATCATCGCTCT 600
|||||
DB 539 CACGAGCCCTATTTTCATCGGGATCTTTTGTCTTCGAGGCGAGGATCAAAATCATCGCTCT 598
|||||
QY 601 GGGCTTGTCTTCACAAAGGCTCTTACCTGCGGAACGGCTGGAACGTATGACATTCGT 660
|||||
DB 599 GGGCTTGTCTTCACAAAGGCTCTTACCTGCGGAACGGCTGGAACGTATGACATTCGT 658
|||||
QY 661 GGTCTGCTTCCACAGGATCTTCCACGGCTGGAACGTACTTCGACTCGGAAACACTGAG 720
|||||
DB 659 GGTCTGCTTCCACAGGATCTTCCACGGCTGGAACGTACTTCGACTCGGAAACACTGAG 718
|||||
QY 721 GGTCTGCTGCTGCTGAGGCGCTGAAAGTGTGTCTGGGATTCGAAGTTTCAGGTTGCT 780
|||||
DB 719 GGTCTGCTGCTGCTGAGGCGCTGAAAGTGTGTCTGGGATTCGAAGTTTCAGGTTGCT 778
|||||
QY 781 GCTCAAGTCCATCATGAAGCCATGTTCCACTCTTCGAGATTTGGGCTGCTCTTCTTCTT 840
|||||
DB 779 GCTCAAGTCCATCATGAAGCCATGTTCCACTCTTCGAGATTTGGGCTGCTCTTCTTCTT 838
|||||
QY 841 TGCATCTCTCATGTTTGCATCATTTGCGCTGGAAGTCTACATGGCAAGTTTCCAAAGGC 900
|||||
DB 839 TGCATCTCTCATGTTTGCATCATTTGCGCTGGAAGTCTACATGGCAAGTTTCCAAAGGC 898
|||||
QY 901 CTGTTTTCCCCAACAGCACAGATCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC 960
|||||
DB 899 CTGTTTTCCCCAACAGCACAGATCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC 958
|||||
QY 961 CCAGCCCGGCTGTGAGGCGGACACTGAGTCCCGGAGTACTGGCAGGACCCAACTT 1020
|||||
DB 959 CCAGCCCGGCTGTGAGGCGGACACTGAGTCCCGGAGTACTGGCAGGACCCAACTT 1018
|||||
QY 1021 TGGCATCCCAACTTTGACAATATCTGTTTGGCCATCTTTCAGCGTGTTCAGATGCAATCAC 1080
|||||
DB 1019 TGGCATCCCAACTTTGACAATATCTGTTTGGCCATCTTTCAGCGTGTTCAGATGCAATCAC 1078
|||||
QY 1081 CATGGAGGGCTGGAATGACATCTCTATAATAAAACAGATGCGGCGCGGCAACACCTGGAA 1140
|||||
DB 1079 CATGGAGGGCTGGAATGACATCTCTATAATAAAACAGATGCGGCGCGGCAACACCTGGAA 1138
|||||
QY 1141 CTGGCTCTACTTCATCCCTCATCATCATCGGCTCTTCTTTCATGCTCAACCTGGTCT 1200
|||||
DB 1139 CTGGCTCTACTTCATCCCTCATCATCATCGGCTCTTCTTTCATGCTCAACCTGGTCT 1198
|||||
QY 1201 GGGCGTCTCTCGGGGAGTTTCCAAAGGAGCGAGAGGGTGGAGAACCGCCCGCGCTT 1260
|||||
DB 1199 GGGCGTCTCTCGGGGAGTTTTCGCAAGGAGCGAGAGGGTGGAGAACCGCCCGCGCTT 1258
|||||

QY	1261	CCTGAAGCTCGCGGAGCAGCAGATCGAGCGAGCTCAACGCGGTACTCGAGTGGAT	1320
Db	1259	CCTGAAGCTCGCGGAGCAGCAGATCGAGCGAGCTCAACGGGTACTCGAGTGGAT	1318
QY	1321	CTTCAAGCGGAGGAAGTCACTGTGCGCGAGGAGGACAGGAATGCAGAGGAGAAGTCCCC	1380
Db	1319	CTTCAAGCGGAGGAAGTCACTGTGCGCGAGGAGGACAGGAATGCAGAGGAGAAGTCCCC	1378
QY	1381	TTTGGAGCTCTAGAGAGCGGCCACCAAGAGAGCAGAAATGACCTGATCCAGCAGA	1440
Db	1379	TTTGGAGCTCTAGAGAGCGGCCACCAAGAGAGCAGAAATGACCTGATCCAGCAGA	1438
QY	1441	GGAGGAGAGGACCGGTTTGACATCTCTGTGTGTTGGATCCCCCTTCGCGCGGCCAG	1500
Db	1439	GGAGGAGAGGACCGGTTTGACATCTCTGTGTGTTGGATCCCCCTTCGCGCGGCCAG	1498
QY	1501	CCTCAAGCGGGAAGACAGAGAGCTCGTCACTATCTTCGAGGAAGGAGAAGATGTTCCG	1560
Db	1499	CCTCAAGCGGGAAGACAGAGAGCTCGTCACTATCTTCGAGGAAGGAGAAGATGTTCCG	1558
QY	1561	GTTTTTTATCCGCGCATGTGTGAAGCTCAGAGCTTCTACTGGGTGCTGTGTGTGT	1620
Db	1559	GTTTTTTATCCGCGCATGTGTGAAGCTCAGAGCTTCTACTGGGTGCTGTGTGTGT	1618
QY	1621	GGCCCTGAACACACTGTGTGTGSCCATGTGTGCAATTAACAACGCGCGCGGCTTACCAC	1680
Db	1619	GGCCCTGAACACACTGTGTGTGSCCATGTGTGCAATTAACAACGCGCGCGGCTTACCAC	1678
QY	1681	GACCTGTATTTTCAGAGTTGTTTCTCGGTCTCTTCCTCA CAGAGATGTCCTGAA	1740
Db	1679	GACCTGTATTTTTCAGAGTTGTTTCTCGGTCTCTTCCTCA CAGAGATGTCCTGAA	1738
QY	1741	GATGTATGCTTGGGCGCCAGAGCTACTTTCGCTCTCTCTCAACTGCTTCGACTTTGG	1800
Db	1739	GATGTATGCTTGGGCGCCAGAGCTACTTTCGCTCTCTCTCAACTGCTTCGACTTTGG	1798
QY	1801	GGTCACTGTGGGAGCGCTTTTGAAGTGTCTGGGCGGCATCAAGCCGGGAAGTCCCTT	1860
Db	1799	GGTCACTGTGGGAGCGCTTTTGAAGTGTCTGGGCGGCATCAAGCCGGGAAGTCCCTT	1858
QY	1861	TGGGATCAAGTGTCTGGGCGGCTCGGCTGTGAGGATCTTCAAGTCA CAGAGTACTG	1920
Db	1859	TGGGATCAAGTGTCTGGGCGGCTCGGCTGTGAGGATCTTCAAGTCA CAGAGTACTG	1918
QY	1921	GAGCTCCCTGCGGAACCTGGTGTGTCTGCTGAACTCCATGAAGTCCATCATCAGCT	1980
Db	1919	GAGCTCCCTGCGGAACCTGGTGTGTCTGCTGAACTCCATGAAGTCCATCATCAGCT	1978
QY	1981	GCTCTTCTGCTCTTCTGTTCAATTGTGGTCTTGGCTCTGCTGGGATGCAAGCTTTGG	2040
Db	1979	GCTCTTCTGCTCTTCTGTTCAATTGTGGTCTTGGCTCTGCTGGGATGCAAGCTTTGG	2038
QY	2041	GGGACAGTTCAACTTCCAGGATGAGCTCCACAAACCAACTTCGACACCTTCCCTGGCG	2100
Db	2039	GGGACAGTTCAACTTCCAGGATGAGCTCCACAAACCAACTTCGACACCTTCCCTGGCG	2098
QY	2101	CATCTCTACTGTTCTCCAGATCTGACGCGGAGGACTGGAAATGCAAGTATGATCAAGG	2160
Db	2099	CATCTCTACTGTTCTCCAGATCTGACGCGGAGGACTGGAAATGCAAGTATGATCAAGG	2158
QY	2161	GATCAAAATCGMACGGCGGTGAGAAAGGATGTTCTGCTCTTTTACTTTCTATGTCCT	2220
Db	2159	GATCAAAATCGMACGGCGGTGAGAAAGGATGTTCTGCTCTTTTACTTTCTATGTCCT	2218
QY	2221	GACACTGTTCCGAAACTACTCTGCTGAATGCTTTCTGGCCATCGCTGTGGACACCT	2280
Db	2219	GACACTGTTCCGAAACTACTCTGCTGAATGCTTTCTGGCCATCGCTGTGGACACCT	2278
QY	2281	GGCCAAACCCCAAGAGCTGA CCAAGGATGAAGAGGAGATGAAGAGCAGCCCAATCAGAA	2340
Db	2279	GGCCAAACCCCAAGAGCTGA CCAAGGATGAAGAGGAGATGAAGAGCAGCCCAATCAGAA	2338

QY	2341	GCTTGCTCTGCAAAAGGCCAAAGTGGCTGAAGTCAAGCCCCCATGTCTGCCGGAACAT	2400
Db	2339	GCTTGCTCTGCAAAAGGCCAAAGTGGCTGAAGTCAAGCCCCCATGTCTGCCGGAACAT	2398
QY	2401	CTCCATCGCCCCCAGGAGCAGAACTCGGCCCAAGCGCGCTCGGTGTGGAGCAGACGGGC	2460
Db	2399	CTCCATCGCCCCCAGGAGCAGAACTCGGCCCAAGCGCGCTCGGTGTGGAGCAGACGGGC	2458
QY	2461	CAGCAGCTACGGCTGCAGAACTTCGCGGCGCAGCTGCGAGGCGCTGTACAGCAGATGGA	2520
Db	2459	CAGCAGCTACGGCTGCAGAACTTCGCGGCGCAGCTGCGAGGCGCTGTACAGCAGATGGA	2518
QY	2521	CCCCGAGGAGCGCTCGCTTCGCCACTACGCGCCACCTTGGGCCCCCACHATGAAGAGCCA	2580
Db	2519	CCCCGAGGAGCGCTCGCTTCGCCACTACGCGCCACCTTGGGCCCCCACHATGAAGAGCCA	2578
QY	2581	CCTGGAACCGGCGCTGTGTGTGGAGCTTGGGCGCGCAGCGCGCGGGGCGCGTGGGAGG	2640
Db	2579	CCTGGAACCGGCGCTGTGTGTGGAGCTTGGGCGCGCAGCGCGGGGCGCGTGGGAGG	2638
QY	2641	CAAAAGCCGACCTGAGGCTCGGAGGCCCCCGAGGGCGTCAACCTTCGCGCAGGACCA	2700
Db	2639	CAAAAGCCGACCTGAGGCTCGGAGGCCCCCGAGGGCGTCAACCTTCGCGCAGGACCA	2698
QY	2701	CGGCAACCGCACAAGGACAAGACCCCGCGCGGGGACCAAGACCCGAGAGGCCCC	2760
Db	2699	CGGCAACCGCACAAGGACAAGACCCCGCGCGGGGACCAAGACCCGAGAGGCCCC	2758
QY	2761	GAAAGCGAGAGCGGGAGCCCGGTGCCCCGGGAGGAGCGGCGCGCGCCACCGCAGCCA	2820
Db	2759	GAAAGCGAGAGCGGGAGCCCGGTGCCCCGGGAGGAGCGGCGCGCGCCACCGCAGCCA	2818
QY	2821	CAGCAGGAGCGCGGGGCGCCCCCGAGGCGCGAGCGAGCGCGCGCGAGGCGGCGG	2880
Db	2819	CAGCAGGAGCGCGGGGCGCCCCCGAGGCGCGAGCGAGCGCGCGCGAGGCGGCGG	2878
QY	2881	CGAGGCGGCGCGCGGCGCCACCAACCGCGCGGCTCCCCGGAGGAGGCGCGCGGAGGCG	2940
Db	2879	CGAGGCGGCGCGCGGCGCCACCAACCGCGCGGCTCCCCGGAGGAGGCGCGCGGAGGCG	2938
QY	2941	CCGACGCGACCGCGCGCAACCGGCACAGGATCCGAGCAAGGAGTGCCTCGCCCAAGGG	3000
Db	2939	CCGACGCGACCGCGCGCAACCGGCACAGGATCCGAGCAAGGAGTGCCTCGCCCAAGGG	2998
QY	3001	CGAGCGCGCGCGCGCAGCGCGGCGGCCCCCGAGCGGGGCGCGCGGAGGCGAGAGCGG	3060
Db	2999	CGAGCGCGCGCGCGCAGCGCGGCGGCCCCCGAGCGGGGCGCGCGGAGGCGAGAGCGG	3058
QY	3061	GGAGGAGCGCGCGCGCGCAACCGGCGCGGCGCACAAAGCGCGAGCCTGCTCAACGAGGCTGT	3120
Db	3059	GGAGGAGCGCGCGCGCGCAACCGGCGCGGCGCACAAAGCGCGAGCCTGCTCAACGAGGCTGT	3118
QY	3121	GGAGAGGAGACCAACCGGAGAGGAGGCGCAACGAGAGAGGAGGCTGAGATAGTGGAAAGCGGA	3180
Db	3119	GGAGAGGAGACCAACCGGAGAGGAGGCGCAACGAGAGAGGAGGCTGAGATAGTGGAAAGCGGA	3178
QY	3181	CAAGGAAAAGGAGCTCCGGAAACCAACGAGCGCGGAGCCACACTGTGACCTGGAGACCAAG	3240
Db	3179	CAAGGAAAAGGAGCTCCGGAAACCAACGAGCGCGGAGCCACACTGTGACCTGGAGACCAAG	3238
QY	3241	TGGAGCTGTGACTGTGGTCCCATGCACTTGCCCGAGCAGCCTGTCTCCAGAGGAGTGA	3300
Db	3239	TGGAGCTGTGACTGTGGTCCCATGCACTTGCCCGAGCAGCCTGTCTCCAGAGGAGTGA	3298
QY	3301	GGAAACGCGCAGAGGATGAGCAAAATCAGCGGAAAGTCACTCGCATGGGCACTCAGGCCCC	3360
Db	3299	GGAAACGCGCAGAGGATGAGCAAAATCAGCGGAAAGTCACTCGCATGGGCACTCAGGCCCC	3358
QY	3361	AGACCCGGAACACTATTTGTATCATATCCCACTGATGCTGAGCGGCGCTCTTTGGGGAGGCCAC	3420
Db	3359	AGACCCGGAACACTATTTGTATCATATCCCACTGATGCTGAGCGGCGCTCTTTGGGGAGGCCAC	3418
QY	3421	GGTGTGTTCCAGTGTAAAGTGGACCTGGAAAGCAAGCAAGGAGGAGGAGGAGGAGTGA	3480

Db 3419 GGTCTCCAGTGGTAAACGTGGACCTTGGAAAGCCAAAGCAGAGGGGAAGAGGTGGA 3478
Qy
Db 3481 AGCGGATGAAGTGAATGAGGAGCGGCCCGCCGCTATCGTCCCATACACAGCTCCATGTTCTG 3540
Db 3479 AGCGGATGAAGTGAATGAGGAGCGGCCCGCCGCTATCGTCCCATACACAGCTCCATGTTCTG 3538
Qy 3541 TTTAAGGCCCAACCAACTGCTCCCGCGCTTCTGCACTACATCATGTGACCAATGAGGTACTT 3600
Db 3539 TTTAAGGCCCAACCAACCTGCTCCCGCGCTTCTGCACTACATCATGTGACCAATGAGGTACTT 3598
Qy 3601 CGAGGTGCTCATCTCGTGGTTCATCGCTTGAGCAGCATCGCCCTGCTGAGGACCC 3660
Db 3599 CGAGGTGCTCATCTCGTGGTTCATCGCTTGAGCAGCATCGCCCTGCTGAGGACCC 3658
Qy 3661 AGTGCGCACAGACTCGCCCGCAGAAACAAAGCTCTGAAATACCTGGAATACATTTTCACTGG 3720
Db 3659 AGTGCGCACAGACTCGCCCGCAGAAACAAAGCTCTGAAATACCTGGAATACATTTTCACTGG 3718
Qy 3721 TGTCTTTACCTTTGAGATGGTGAATAAGATGATCGACTTGGGACTGTGCTTCAACCTGG 3780
Db 3719 TGTCTTTACCTTTGAGATGGTGAATAAGATGATCGACTTGGGACTGTGCTTCAACCTGG 3778
Qy 3781 AGCCTATTTCCGGACCTTGTGGACATTTCTGACTTCAATTTGCTGAGTGGCCCTGGT 3840
Db 3779 AGCCTATTTCCGGACCTTGTGGACATTTCTGACTTCAATTTGCTGAGTGGCCCTGGT 3838
Qy 3841 GGCCTTTGCTTTCTCGAGCTTCGTGGGAGATCCAAAGGGGAAGACATCAATACCAACAA 3900
Db 3839 GGCCTTTGCTTTCTC-----AGATCCAAAGGGGAAGACATCAATACCAACAA 3886
Qy 3901 GTCTCTGAGAGTCTTCTGCTGCTCGCGCCCTCAAGACCATCAACCGCTGCCCAAGCT 3960
Db 3887 GTCTCTGAGAGTCTTCTGCTGCTCGCGCCCTCAAGACCATCAACCGCTGCCCAAGCT 3946
Qy 3961 CAAGGCTGTGTTGACTGTGTGGTGAATCCCTGGAAGAAATGTCTCAACATCTTGATGT 4020
Db 3947 CAAGGCTGTGTTGACTGTGTGGTGAATCCCTGGAAGAAATGTCTCAACATCTTGATGT 4006
Qy 4021 CTACATGCTCTTCAATGTTTCAATTTGCGCTCATTTGCGGTGCAGCTCTTCAAGGGGAAGTT 4080
Db 4007 CTACATGCTCTTCAATGTTTCAATTTGCGCTCATTTGCGGTGCAGCTCTTCAAGGGGAAGTT 4066
Qy 4081 TTTCTACTGCACAGATGAATCCAAAGGAGCTGGAGAGGACTGCAAGGGTCAAGTATTTGGA 4140
Db 4067 TTTCTACTGCACAGATGAATCCAAAGGAGCTGGAGAGGACTGCAAGGGTCAAGTATTTGGA 4126
Qy 4141 TTATGAGAGGAGGAAGTGGAGCTCAGCCAGCAGTGGAGAAATACGACTTTCACTA 4200
Db 4127 TTATGAGAGGAGGAAGTGGAGCTCAGCCAGCAGTGGAGAAATACGACTTTCACTA 4186
Qy 4201 CGACAAATGTCTCTGGGCTCTGCTGAGCTGTTCACAGTGTCCACGGGAGAGGCTGGCC 4260
Db 4187 CGACAAATGTCTCTGGGCTCTGCTGAGCTGTTCACAGTGTCCACGGGAGAGGCTGGCC 4246
Qy 4261 CATGGTCTGAAACACTCCGTTGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4320
Db 4247 CATGGTCTGAAACACTCCGTTGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4306
Qy 4321 CCGCATGAGGCTGTCCATCTTCACTGAGTGTCTACTTTGTGCTCTTCCCTTCTTCTTCGT 4380
Db 4307 CCGCATGAGGCTGTCCATCTTCACTGAGTGTCTACTTTGTGCTCTTCCCTTCTTCTTCGT 4366
Qy 4381 CAACATCTTTGTGCTTTTGAATCATCATCACTTCCAGGAGCAGGGGACAAAGGTGATGTC 4440
Db 4367 CAACATCTTTGTGCTTTTGAATCATCATCACTTCCAGGAGCAGGGGACAAAGGTGATGTC 4426
Qy 4441 TGAATGAGGCTGTGAGAGAAACGAGAGGGCTTGCAATTTGACTTCCGCAATCAGCGCCAAACC 4500
Db 4427 TGAATGAGGCTGTGAGAGAAACGAGAGGGCTTGCAATTTGACTTCCGCAATCAGCGCCAAACC 4486
Qy 4501 CCTGACACGGTACATGCCCCAAACCGGCGAGTGTTCAGTATTAAGACGTGGACATTTGT 4560

Db 4487 CCTGACACGGTACATGCCCCAAACCGCGAGTGTCTCCAGATATAAGACGTGGACATTTGT 4546
Qy 4561 GGTCTCCCCCGCCCTTTGAATACCTTTCATCATGGCCATGATAGCCCTCAACACTGTGTGCT 4620
Db 4547 GGTCTCCCCCGCCCTTTGAATACCTTTCATCATGGCCATGATAGCCCTCAACACTGTGTGCT 4606
Qy 4621 GATGATGAAGTCTTATGATGACCCCTATAGATGACGAGCTGATGCTGGAATGCTGGAACAT 4680
Db 4607 GATGATGAAGTCTTATGATGACCCCTATGATGACGAGCTGATGCTGGAATGCTGGAACAT 4666
Qy 4681 CGTGTTCACATCATGTTCTCCATGGAATGCGTGTGAAGATCATCGCCCTTTCGGGTGCT 4740
Db 4667 CGTGTTCACATCATGTTCTCCATGGAATGCGTGTGAAGATCATCGCCCTTTCGGGTGCT 4726
Qy 4741 GAACTATTTTCAGAGATGCTTGGAAATGTCTTTGACTTTGTCACTGTGTGGAAAGTATTAC 4800
Db 4727 GAACTATTTTCAGAGATGCTTGGAAATGTCTTTGACTTTGTCACTGTGTGGAAAGTATTAC 4786
Qy 4801 TGATATTTTAGTAACAGAGATTTGGGAAACGAACAAATTTTCATCAACCTCAGCTTCCCTCG 4860
Db 4787 TGATATTTTAGTAACAGAGATTTGGGAAACGAACAAATTTTCATCAACCTCAGCTTCCCTCG 4846
Qy 4861 CCTCTTTTCGAGCTGCGCGCTGATCAAGCTGTCCGCCAGGGCTACACCATCCGCAATCCT 4920
Db 4847 CCTCTTTTCGAGCTGCGCGCTGATCAAGCTGTCCGCCAGGGCTACACCATCCGCAATCCT 4906
Qy 4921 GCTGTGGACCTTTGTCCAGTCTTTCAAGGCCCTTCCCTACGTGTGTCTCATTTGCCAT 4980
Db 4907 GCTGTGGACCTTTGTCCAGTCTTTCAAGGCCCTTCCCTACGTGTGTCTCATTTGCCAT 4966
Qy 4981 GCTGTCTTCATCTACGCCATCATTCGCCATGCGCATGCGAGTGTGTTGGGAATATTGCCCTGATGA 5040
Db 4967 GCTGTCTTCATCTACGCCATCATTCGCCATGCGCATGCGAGTGTGTTGGGAATATTGCCCTGATGA 5026
Qy 5041 TGAACAACGATCAACCGCCACAACTTCCCGAGCTTTTTCGAAGCCCTGATGCTGCT 5100
Db 5027 TGAACAACGATCAACCGCCACAACTTCCCGAGCTTTTTCGAAGCCCTGATGCTGCT 5086
Qy 5101 GTTCAGAGCGCCCAACCGGGGAGGCTTGGCAACGAGATCATGCTGTCTCTGCTGAGCAACCA 5160
Db 5087 GTTCAGAGCGCCCAACCGGGGAGGCTTGGCAACGAGATCATGCTGTCTCTGCTGAGCAACCA 5146
Qy 5161 GGCTGTGATGAGCAGGCGCAATGCCACCGAGTGTGGAAATGACTTTTGCTTACTTCTTACTT 5220
Db 5147 GGCTGTGATGAGCAGGCGCAATGCCACCGAGTGTGGAAATGACTTTTGCTTACTTCTTACTT 5206
Qy 5221 CGTCTCTTCATCTTCTGTGCTTCTTCTGATGTTGAACTCTTGTGCTGCTGATCAT 5280
Db 5207 CGTCTCTTCATCTTCTGTGCTTCTTCTGATGTTGAACTCTTGTGCTGCTGATCAT 5266
Qy 5281 GGAACAATTTTGAATACCTCAACCGGGAGCTTTCATCTCTAGGTCCTCAACAATTGGATGA 5340
Db 5267 GGAACAATTTTGAATACCTCAACCGGGAGCTTTCATCTCTAGGTCCTCAACAATTGGATGA 5326
Qy 5341 GTTCATCCGGGTCTGGGCTGAATAACGACCGGCTGGGTGGGCGCATCAGTTTACAATGA 5400
Db 5327 GTTCATCCGGGTCTGGGCTGAATAACGACCGGCTGGGTGGGCGCATCAGTTTACAATGA 5386
Qy 5401 CATGTTTGAATGCTGAAACACATGTCCCGCTCTGGGCTGGGGAAGAAATGCCCTGC 5460
Db 5387 CATGTTTGAATGCTGAAACACATGTCCCGCTCTGGGCTGGGGAAGAAATGCCCTGC 5446
Qy 5461 TCCAGTGTCTTACAAGCGCTGGTTCGCATGAAATGCGCATCTCCAAACGAGGACATGAC 5520
Db 5447 TCCAGTGTCTTACAAGCGCTGGTTCGCATGAAATGCGCATCTCCAAACGAGGACATGAC 5506
Qy 5521 TGTTCATCTTCAGCTCAACGCTGATGCCCTCATTCGGAACGCGCATCTGGAATCAAGCTGGC 5580
Db 5507 TGTTCATCTTCAGCTCAACGCTGATGCCCTCATTCGGAACGCGCATCTGGAATCAAGCTGGC 5566
Qy 5581 CCCAGCTGGGACAAACAGCATCAGTGTGACCGGAGTTGAGGAAGAGATTTTCGCTGT 5640
Db 5567 CCCAGCTGGGACAAACAGCATCAGTGTGACCGGAGTTGAGGAAGAGATTTTCGCTGT 5626

QY	5641	GTGGCCCAATCTGCCCCAGAGACTTTGGAGCTTGTTGATACCCACCCCATAAAGCCTGATGA	5700
Db	5627	GTGGCCCAATCTGCCCCAGAGACTTTGGAGCTTGTTGATACCCACCCCATAAAGCCTGATGA	5686
QY	5701	GATGACAGTGGGGAAGTTTATGAGCTCTGATGATATTTGACTTTACAAAGCAGAACAA	5760
Db	5687	TATGACAGTGGGGAAGTTTATGAGCTCTGATGATATTTGACTTTACAAAGCAGAACAA	5746
QY	5761	AACCAACAGAGACAGAGATGAGCAGGCTCTGAGAGCCTCTCCAGATGGGTCTGTGTTC	5820
Db	5747	AACCAACAGAGACAGAGATGAGCAGGCTCTGAGAGCCTCTCCAGATGGGTCTGTGTTC	5806
QY	5821	CTGTTCACCCCTGTAAGGCCACCTTGAGCAGACACAGCCGCTGTGTCTCCAGAGAGC	5880
Db	5807	CCTGTTCACCCCTGTAAGGCCACCTTGAGCAGACACAGCCGCTGTGTCTCCAGAGAGC	5866
QY	5881	CCGGTTCCTTCGACAGAGAGTTCCACCTCCAGAGATGCGGGGCGCATACAAA	5940
Db	5867	CCGGTTCCTTCGACAGAGAGTTCCACCTCCAGAGATGCGGGGCGCATACAAA	5926
QY	5941	CCAAGAGAGTGGCATCAAGAGTCTGTCTCTGGGCACTCAAGGACCCAGATGCACC	6000
Db	5927	CCAAGAGAGTGGCATCAAGAGTCTGTCTCTGGGCACTCAAGGACCCAGATGCACC	5986
QY	6001	CCATGAGGCCAGGCCACCCCTGAGCGTGGCCACTCCACAGAGATCCCTGTGGGGCGGTC	6060
Db	5987	CCATGAGGCCAGGCCACCCCTGAGCGTGGCCACTCCACAGAGATCCCTGTGGGGCGGTC	6046
QY	6061	AGGACACTGGCTGTGGAGTTTCAGATGACAGAGCATTAACCCGAGGGGCTGTATGGGA	6120
Db	6047	AGGACACTGGCTGTGGAGTTTCAGATGACAGAGCATTAACCCGAGGGGCTGTATGGGA	6106
QY	6121	GCCCCAGCTGGCTGGAGAGCCAGGGTCGAGGGCTCCATGCCCGCTTGGGGCCGA	6180
Db	6107	GCCCCAGCTGGCTGGAGAGCCAGGGTCGAGGGCTCCATGCCCGCTTGGGGCCGA	6166
QY	6181	GACTGAGCCGCTCAGATGACAGCCCATGAAGCGCTCCATCTCCAGCTGGGCCAGCG	6240
Db	6167	GACTGAGCCGCTCAGATGACAGCCCATGAAGCGCTCCATCTCCAGCTGGGCCAGCG	6226
QY	6241	GCCCCGTGGGACTCATCTTTGACAGACACCCCGGACCGCCACCCCTAGCCAGGGCTC	6300
Db	6227	GCCCCGTGGGACTCATCTTTGACAGACACCCCGGACCGCCACCCCTAGCCAGGGCTC	6286
QY	6301	GTGCAACCAACACACACCGCTGCAACCGCCGAGGACAGGAAGCAGAGGTCCCTGGA	6360
Db	6287	GTGCAACCAACACACACCGCTGCAACCGCCGAGGACAGGAAGCAGAGGTCCCTGGA	6346
QY	6361	GAAGGGCCAGCCTGTCTGCCGATATGATGGCGCACCAAGCAGTGTGTGGGGCCGGG	6420
Db	6347	GAAGGGCCAGCCTGTCTGCCGATATGATGGCGCACCAAGCAGTGTGTGGGGCCGGG	6406
QY	6421	GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGCGGGGAACGAGAGCCCGGAGGAGCG	6480
Db	6407	GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGCGGGGAACGAGAGCCCGGAGGAGCG	6466
QY	6481	GGGCGGTCCAGAGAGCGAGAGCCCTCATCTCTCTCGAGAGAGCAGCGCTTCTA	6540
Db	6467	GGGCGGTCCAGAGAGCGAGAGCCCTCATCTCTCTCGAGAGAGCAGCGCTTCTA	6526
QY	6541	CTCTGCGACCGCTTTGGGGCCGTTGAGCCCGGAGCCCAAGCCCTCCCTCAGACCCA	6600
Db	6527	CTCTGCGACCGCTTTGGGGCCGTTGAGCCCGGAGCCCAAGCCCTCCCTCAGACCCA	6586
QY	6601	CCCAACGTGGCCAAACAGTGGCCAGGAGCCGGAGCCCAACCAAGGGCAGTGTTCCTG	6660
Db	6587	CCCAACGTGGCCAAACAGTGGCCAGGAGCCGGAGCCCAACCAAGGGCAGTGTTCCTG	6646
QY	6661	GAATGGGAGCCCTTGTCTCAACATCTGGTGCTAGCACCCCGCGCGGTGGGGGAG	6720
Db	6647	GAATGGGAGCCCTTGTCTCAACATCTGGTGCTAGCACCCCGCGCGGTGGGGGAG	6706

QY	6721	GCAGTCCCCAGAGCCCTTGACTCCCGCCCGAGCATACCTTACAAGACGGGCAACTC	6780
Db	6707	GCAGTCCCCAGAGCCCTTGACTCCCGCCCGAGCATACCTTACAAGACGGGCAACTC	6766
QY	6781	CTACCCCATCCACTTTGCGCGGGGCTCAGAACAGAGCTCCCTGCTCTCTCCAGGCGGGCT	6840
Db	6767	CTACCCCATCCACTTTGCGCGGGGCTCAGAACAGAGCTCCCTGCTCTCTCCAGGCGGGCT	6826
QY	6841	CAGCGTGGGCTTTCCGAAACAAACGCGCTGCTCAGAGAGACCCCTCAGCCAGCCCTC	6900
Db	6827	CAGCGTGGGCTTTCCGAAACAAACGCGCTGCTCAGAGAGACCCCTCAGCCAGCCCTC	6886
QY	6901	GCCCCCTGGCTCTCGAATTGCTGACCTTACCTGGGCGAGGCTGTGACAGTGAAGC	6960
Db	6887	GCCCCCTGGCTCTCGAATTGCTGACCTTACCTGGGCGAGGCTGTGACAGTGAAGC	6946
QY	6961	CTCTGTCCAGCCCTGCTGAGGACAGCTCACTTTTCGAGAGAGCTGTGCGCACCAACTC	7020
Db	6947	CTCTGTCCAGCCCTGCTGAGGACAGCTCACTTTTCGAGAGAGCTGTGCGCACCAACTC	7006
QY	7021	GGGCGGCTCTCCAGAGACTTCTACGTGCTCTCCCTGACCTCCAGTCTCACCTCTCCG	7080
Db	7007	GGGCGGCTCTCCAGAGACTTCTACGTGCTCTCCCTGACCTCCAGTCTCACCTCTCCG	7066
QY	7081	CCGGTGGCCAAACGGTTTACCACTGCACCTGGGACTCAGCTCGGGTGGCGAGACGGCA	7140
Db	7067	CCGGTGGCCAAACGGTTTACCACTGCACCTGGGACTCAGCTCGGGTGGCGAGACGGCA	7126
QY	7141	CAGTACCAACCCCTGACCAAGACCACTGGTGTCTAGCTGCACCGTGACCCCTCAGACGC	7200
Db	7127	CAGTACCAACCCCTGACCAAGACCACTGGTGTCTAGCTGCACCGTGACCCCTCAGACGC	7186
QY	7201	CTGCATGACAGCAGCGCTGTGCTCCAGTGGATGATGATTTTATCATCCACAGCGAGTCGG	7260
Db	7187	CTGCATGACAGCAGCGCTGTGCTCCAGTGGATGATGATTTTATCATCCACAGCGAGTCGG	7246
QY	7261	CCCTCGGGGAGGCTTTGCCACCTTTGGTGAGGCTCCTGTGGCCCTCCCTTCCCCCTCT	7320
Db	7247	CCCTCGGGGAGGCTTTGCCACCTTTGGTGAGGCTCCTGTGGCCCTCCCTTCCCCCTCT	7306
QY	7321	CCCTCTTTTACTCTAGACGACGAATAAAGCCCTGTGTGCTGTGAGTGTAGTACCGC	7376
Db	7307	CCCTCTTTTACTCTAGACGACGAATAAAGCCCTGTGTGCTGTGAGTGTAGTACCGC	7362

RESULT 9
AAV29059

ID AAV29059 standard; cDNA; 7266 BP.

XX AAV29059;

AC AAV29059;

XX 28-AUG-1998 (first entry)

DT 28-AUG-1998 (first entry)

XX Human calcium channel a1B subunit cDNA.

DE Calcium channel; human; central nervous system disorder;

XX Lambert-Eaton syndrome; diagnosis; therapy; ds.

OS Homo sapiens.

XX Key

PH CDS Location/Qualifiers

FT 92..7105

FT /*tag= a

XX WO9811131-A2.

PN 19-MAR-1998.

XX 11-SEP-1997; 97WO-US016146.

XX 16-SEP-1996; 96US-00713118.

XX (AMHP) AMERICAN HOME PROD CORP.

XX Franco R, Chen ARS, Shuey DJ;
XX WPI; 1998-207325/18.
XX P-PSDB; AAW37878.
XX DNA encoding human neuronal calcium channel subunit(s) - useful for
XX diagnosis of and treatment of central nervous system disorders, e.g.
XX Lambert-Eaton syndrome.
XX Claim 18; Fig 1; 89pp; English.
XX This cDNA clone codes for the $\alpha 1B$ subunit (see AAW37878) of the human
XX neuronal calcium channel. cDNA clones encoding the $\alpha 1B$ subunit, the $\alpha 2D$
XX subunit (see AAV29060) and a $\beta 3$ subunit (see AAV29061) have been
XX isolated. These have been inserted into expression vectors and are stably
XX expressed in transformed cell lines. The transformed cells show omega-
XX conotoxin GVIA binding activity, and omega-conotoxin GVIA toxin sensitive
XX potassium-stimulated calcium uptake, indicating that the proteins
XX expressed by the clones are capable of forming a functioning calcium
XX channel. Nucleic acids encoding the 3 subunits, as well as vectors, host
XX cells and methods of isolating nucleic acids encoding related calcium
XX channels are disclosed. Subunit proteins (see AAW37878-60), fusion
XX proteins, antibodies, as well as assays to identify agents that modulate
XX calcium channel activity are also provided. Such agents can be used to
XX treat certain central nervous system disorders by altering calcium
XX channel activity. Methods of diagnosing diseases associated with
XX particular calcium channels, such as Lambert-Eaton syndrome, are
XX disclosed
SQ Sequence 7266 BP; 1433 A; 2249 C; 2173 G; 1411 T; 0 U; 0 Other;
Query Match 99.7%; Score 7223.2; DB 2; Length 7266;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7263; Conservative 0; Mismatches 3; Indels 18; Gaps 2;
55 TCCGTGCTGCTCCGCTCTGAGCGCTTGGCGCGCCCGCGCGCTTCCCTGCGGGGCGCT 114
Db 1 TCCGTGCTGCTCCGCTCTGAGCGCTTGGCGCGCCCGCGCGCTTCCCTGCGGGGCGCT 60
115 GGGCGGGGATGACCGGGGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 174
Db 61 GGGCGGGGATGACCGGGGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 120
175 CCGCTATGAGCGCGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 234
Db 121 CCGCTATGAGCGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 180
235 GGGCGCGGCTCCGGGGGCTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 294
Db 181 GGGCGCGGCTCCGGGGGCTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 240
295 GCAGCGCGCGGACCGCGCGCTGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 354
Db 241 GCAGCGCGCGGACCGCGCGCTGACACCGCGCGCGCGCGCGCGCGCGCGCGCGG 300
355 CGTCAACCGCTCGCTCTTCTGCTTTCAGCGAGCAACGCTCGTCCGCAAAATACGGAAGCG 414
Db 301 CGTCAACCGCTCGCTCTTCTGCTTTCAGCGAGCAACGCTCGTCCGCAAAATACGGAAGCG 360
415 CATCACCGAGTGGCTCCATTCGAGTATATGATCTTGCGCAACCATCATTCGCGCAACTGCAT 474
Db 361 CATCACCGAGTGGCTCCATTCGAGTATATGATCTTGCGCAACCATCATTCGCGCAACTGCAT 420
475 GGTCTGCGCTTGGAGCGACCTCCCTGATGGGACAAACCGCGCGCGCGCGCGCGCT 534
Db 421 GGTCTGCGCTTGGAGCGACCTCCCTGATGGGACAAACCGCGCGCGCGCGCGCGCT 480
535 GGACGACACGAGCGCTATTTTCATCGGGATCTTTTGTCTTCAGGCGAGGATCAAAATCAT 594
Db 481 GGACGACACGAGCGCTATTTTCATCGGGATCTTTTGTCTTCAGGCGAGGATCAAAATCAT 540
595 CGCTCTGGGCTTGTCTTCCCAAGGGCTCTTACCTCGGAAACGGGCTGGAAACGTATGGA 654

Db 541 CGCTCTGGGCTTGTCTTCCAAAGGGCTTACCTGCGGAAACGGCTGGAAACGTATGGA 600
QY 655 CTTCTGTTGGTCTGCTCTCAAGGATCTTGTCCACGGGCTGGAATCTGACTTCCAGCTTGGCAAC 714
Db 601 CTTCTGTTGGTCTGCTCTCAAGGATCTTGTCCACGGGCTGGAATCTGACTTCCAGCTTGGCAAC 660
QY 715 ACTGAGGGCTGTGCGTGTGCTGAGGGCCCTGGAAGCTGTGCTGCGGATTCGAAGTTTGGCA 774
Db 661 ACTGAGGGCTGTGCGTGTGCTGAGGGCCCTGGAAGCTGTGCTGCGGATTCGAAGTTTGGCA 720
QY 775 GGTGTTGCTCAAGTCCATCATGAGGCCATGTTCCACTCTCTCAGATTTGGGCTGCTTCT 834
Db 721 GGTGTTGCTCAAGTCCATCATGAGGCCATGTTTCCACTCTCTCAGATTTGGGCTGCTTCT 780
QY 835 CTTCTTTTGGCATCTCATGTTTCCCATCATTTGCGCTGGAGTTCTACATGGCGCAAGTTCCA 894
Db 781 CTTCTTTTGGCATCTCATGTTTCCCATCATTTGCGCTGGAGTTCTACATGGCGCAAGTTCCA 840
QY 895 CAAGGCTGTTTCCCAACAGCAACAGATCGGAGCCGCTGGGTGACTTCCCTTGTGGCA 954
Db 841 CAAGGCTGTTTCCCAACAGCAACAGATCGGAGCCGCTGGGTGACTTCCCTTGTGGCA 900
QY 955 GAGGCGCCAGCGCGCTGTGCGAGGCGACACTGAGTCCGGGAGTACTGGCCAGGACC 1014
Db 901 GAGGCGCCAGCGCGCTGTGCGAGGCGACACTGAGTCCGGGAGTACTGGCCAGGACC 960
QY 1015 CAATTTTGGCATCAACAACTTTTGAACAATATCTTGTGTTGCCATCTTGACGCTGTTTCCAAGT 1074
Db 961 CAATTTTGGCATCAACAACTTTTGAACAATATCTTGTGTTGCCATCTTGACGCTGTTTCCAAGT 1020
QY 1075 CATCACCATGAGGGCTGGAATGACATCTCTATAATAACAGATGCGCGCGCGCAACAC 1134
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Db 1441 CGCCAGCTCAAGAGCGGAGAGCAGAGAGCTGCTATCTTCCGGGAGGAGGAGAT 1500
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QY 1675 TACACGACCTGTATTTTTCAGAGTTTGTTCCTGGGTCTTCTTCTTCAAGATGTC 1734

QY 3895 CATCAAGTCTCTGAGAGTCCTTCTGTCCTCGCGGCCCTCAAGACCATCAAAACGGCTGCC 3954
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QY 3955 CAAGCTCAAGGCTGTGTTGAGCTGTGTGAGTCACTCCCTGAAGAAATGTCCTCAACATCTT 4014
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DB GAAGTTTTTCTACTGACAGATGAATCCAAAGGAGCTGAGAGGACCTGACGGGTGAGTA 4068
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QY 4555 ATTGTGGTCTCCCCGGCTTTGAATACTTCATCATGGCCATGATAGCCCTCAACACTGT 4614
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QY 4615 GGTGCTGATGATGAAGTCTATGATGCACTTATGATGCACTTATGATGCTGAAATGCTT 4674
DB GGTGCTGATGATGAAGTCTTATGATGCACTTATGATGCACTTATGATGCTGAAATGCTT 4608
QY 4675 GAACATCGTGTTCATCATCTTCTCCATGGAATGCTGGAAGATCATCGCTTTGG 4734
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QY 4735 GGTGCTGAACTATTTCAGAGATGCTGGAATGCTTGTGACTTTGTGACTGTGTGGAAG 4794
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QY 5395 CAATGACATGTTTGAATGCTGAAACACATGTCCTCGGCTCTGGGGCTGGGGGAAGAAATG 5454
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QY 5575 GCTGGCCCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGGAGATTTT 5634
DB GCTGGCCCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGGAGATTTT 5562
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QY 5755 GAACAAAACCAACAGAGACAGATGACAGGCTCTCGGAGGCTCTCCACAGATGGGTCC 5814
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DB TGTGTCCTCTTCCACCTCTGAAGGCCACCTCGGAGCAGACACAGCCGGCTGTGCTCG 5802
QY 5875 AGAGCCCGGGTTTTCTTCGACAGAGATTTCCACTCCCTCAGCAATGGCGGGGCCAT 5934
DB AGAGCCCGGGTTTTCTTCGACAGAGATTTCCACTCCCTCAGCAATGGCGGGGCCAT 5862
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DB TGACCCCATGAGGCCAGGCCACCTCGAGGCGTGCCACTCCACAGAGATCCTGTGGG 5982
QY 6055 GCGGTACGAGGCACTGGCTGTGACGTTGATGACAGGATAAACCCGAGGGGCCCTGA 6114

Db 5983 GCGGT CAGGAGCACTGGCTGTGGACGTTTCAGATGCAGAGCATAAACCCGAGGGGCCCTGA 6042
QY 6115 TGGGGAGCCCGAGCTGGGCTGGAGAGCCAGAGTGCAGGGCTCATGCCCGGCTTGC 6174
Db 6043 TGGGGAGCCCGAGCTGGGCTGGAGAGCCAGAGTGCAGGGCTCATGCCCGGCTTGC 6102
QY 6175 GCGGAGACTCAGCCCGTCAAGATGCCAGCCCATGAAGCGCTCCATCTCCACGCTGCG 6234
Db 6103 GCGGAGACTCAGCCCGTCAAGATGCCAGCCCATGAAGCGCTCCATCTCCACGCTGCG 6162
QY 6235 CAGCGGCGCGCTGGAGCTCATCTTTGAGACACACCCCGGAGCCGCGCTAGCCA 6294
Db 6163 CAGCGGCGCGCTGGAGCTCATCTTTGAGACACACCCCGGAGCCGCGCTAGCCA 6222
QY 6295 GCGCTCGTCGACACACACACCGCTGCCACCGCGCCGCGGAGCAGGAACAGAGTC 6354
Db 6223 GCGCTCGTCGACACACACACCGCTGCCACCGCGCCGCGGAGCAGGAACAGAGTC 6282
QY 6355 CTGGAGAAAGGGGCCAGCGCTGTCTGCCGATATGATGCGCGCAACCAAGCAGTGTGTGG 6414
Db 6283 CTGGAGAAAGGGGCCAGCGCTGTCTGCCGATATGATGCGCGCAACCAAGCAGTGTGTGG 6342
QY 6415 GCGGGGCTGCCCCGGGAGAGGGGCTACAGGCTGCGCGCGGAAACGAGAGCGCGCA 6474
Db 6343 GCGGGGCTGCCCCGGGAGAGGGGCTACAGGCTGCGCGCGGAAACGAGAGCGCGCA 6402
QY 6475 GGAGCGGGCGCGTCCAGAGCGGAGCGAGCGCTCATCTCTCTCGAGAGACAGCG 6534
Db 6403 GGAGCGAGCGGTCAGGAGCGGAGCGGAGCGCTCATCTCTCTCGAGAGACAGCG 6462
QY 6535 CTCTACTCTCGACCGCTTTGGGGCGGTGAGCCCGCAAGCCCAAGCCCTCCCTCAG 6594
Db 6463 CTCTACTCTCGACCGCTTTGGGGCGGTGAGCCCGCAAGCCCAAGCCCTCCCTCAG 6522
QY 6595 CAGCCACCAACGTCGCCAACAGCTGGCCAGAGCGGAGCGGAGCCCAACCCAGAGGAGTGG 6654
Db 6523 CAGCCACCAACGTCGCCAACAGCTGGCCAGAGCGGAGCGGAGCCCAACCCAGAGGAGTGG 6582
QY 6655 TTCCGTGAATGGAGCGCCCTTCTCTCAACATCTGGTGTAGCACCCCGCGCGGTGG 6714
Db 6583 TTCCGTGAATGGAGCGCCCTTCTCTCAACATCTGGTGTAGCACCCCGCGCGGTGG 6642
QY 6715 GCGGAGGAGCTCCCGCAGACGCCCTGACTCCCGCCAGCATCACTCAAGAGCGC 6774
Db 6643 GCGGAGGAGCTCCCGCAGACGCCCTGACTCCCGCCAGCATCACTCAAGAGCGC 6702
QY 6775 CAACTCTCACCACATCCACTTCGCGCGGSGCTCAGACAGCGCTCCCTGCTTCTCCCGAG 6834
Db 6703 CAACTCTCACCACATCCACTTCGCGCGGSGCTCAGACAGCGCTCCCTGCTTCTCCCGAG 6762
QY 6835 CCGGCTCAGCCGTGGGCTTTCGAAACAAACGCGCTGCTGAGAGAGAGCCCGCTCAGCCA 6894
Db 6763 CCGGCTCAGCCGTGGGCTTTCGAAACAAACGCGCTGCTGAGAGAGAGCCCGCTCAGCCA 6822
QY 6895 GCCCTGCGCCCTGCTCTCGAATTTGGCTCTGAACCTTACCTGGGCGAGCGCTGTGACAG 6954
Db 6823 GCCCTGCGCCCTGCTCTCGAATTTGGCTCTGAACCTTACCTGGGCGAGCGCTGTGACAG 6882
QY 6955 TGAGGCGCTCTGTCACGCGCTGCTGAGGACACGCTCTACTTTGAGGAGGCTGTGGCCAC 7014
Db 6883 TGAGGCGCTCTGTCACGCGCTGCTGAGGACACGCTCTACTTTGAGGAGGCTGTGGCCAC 6942
QY 7015 CAACTCGGGCGCTCTCAGGACTTCTAGTGCTCTCTCTGCTCCAGCTCCCAAGTCTCACC 7074
Db 6943 CAACTCGGGCGCTCTCAGGACTTCTAGTGCTCTCTCTGCTCCAGCTCCCAAGTCTCACC 7002
QY 7075 TCTCGCGCGCTGCGACAGGTTACCACTGACCCCTGGGACTCAGCTCGGTTGCCAGC 7134
Db 7003 TCTCGCGCGCTGCGACAGGTTACCACTGACCCCTGGGACTCAGCTCGGTTGCCAGC 7062
QY 7135 ACGGACAGCTACCAACACCCCTGACCAAGACACACTGGTGTAGTGTGACCGTGCCTC 7194
Db 7063 ACGGACAGCTACCAACACCCCTGACCAAGACACACTGGTGTAGTGTGACCGTGCCTC 7122

QY 7195 AGACGCTGCATGCAGCAGCGGTGTTCCAGTGCATGAGTTTATCATTCACACGCGGC 7254
Db 7123 AGACGCTGCATGCAGCAGCGGTGTTCCAGTGCATGAGTTTATCATTCACACGCGGC 7182
QY 7255 AGTCGGCCCTCGGGGAGGCGCTTGCCCACTTGGTGAGGCTCCTGTGGCCCTCCCTCCC 7314
Db 7183 AGTCGGCCCTCGGGGAGGCGCTTGCCCACTTGGTGAGGCTCCTGTGGCCCTCCCTCCC 7242
QY 7315 CTTCTCCCTCTTTTACTCTAGA 7338
Db 7243 CTTCTCCCTCTTTTACTCTAGA 7266
RESULT 10
ABZ58367
ID ABZ58367 standard; cDNA; 7177 BP.
XX
AC ABZ58367;
XX
DT 28-APR-2003 (first entry)
XX
DE Human N-type calcium channel alpha-1B subunit coding sequence.
XX
KW Human; calcium channel; voltage-gated ion channel; splice variant; gene;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 146..6859
FT /*tag= a
FT /product= "Human calcium channel, alpha-1B subunit"
XX
DN WO2003006103-A2.
XX
PD 23-JAN-2003.
XX
PF 12-JUL-2002; 2002WO-US022161.
XX
PR 12-JUL-2001; 2001US-0304955P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Augustine PR, Bennett PB, Bugianesi RM, Garyantes TA, Imredy JP;
PI Kath GS, Mcmanus OB;
XX
XX WPI; 2003-221676/21.
DR P-PSDB; ABP72256.
XX
PT Identifying modulators of the activity of a voltage-gated ion channel,
PT comprises altering the transmembrane potential of a portion of the cell
PT membrane expressing the voltage-gated ion channel by electric field
PT stimulation.
XX
PS Disclosure; Fig 21A-C; 188pp; English.
XX
CC The present sequence is the coding sequence for a splice variant of the
CC alpha-1B subunit of the human T-type calcium channel. The invention
CC provides methods of identifying activators and inhibitors of voltage-
CC gated ion channels (VC). The methods use electrical field stimulation of
CC cells via extracellular electrodes to manipulate the open/close state
CC transitions of the VCs. This allows for more convenient, more precise
CC manipulation of these transitions and, coupled with efficient methods of
CC detecting ion flux or membrane potential, results in methods that are
CC especially suitable for high-throughput screening of compounds as
CC potential activators and inhibitors of VCs. The VC may be a sodium,
CC potassium calcium channel. The cells are e.g. HEK293 (ATCC 1573) cells
CC transfected with DNA encoding the VC, and may contain a fluorescent
CC indicator compound. Defective sodium, calcium and potassium VCs have been
CC implicated in a variety of disorders including long QT syndrome, ataxia,
CC migraine, muscle paralysis, deafness, and cardiac conduction
CC diseases

XX	SQ	Sequence	7177 BP; 1414 A; 2198 C; 2169 G; 1396 T; 0 U; 0 Other;
		Query Match	94.3%; Score 6958; DB 7; Length 7177;
		Best Local Similarity	97.3%; Pred. No. 0;
		Matches 7177; Conservative	0; Mismatches 0; Indels 199; Gaps 2;
Qy	1	CGCGCGCGGTGCGGCGTGGGCGGCGGCGAGGTCGCGTCCGGCGGCTCCGTTG	60
Db	1	CGCGCGCGGTGCGGCGTGGGCGGCGGCGAGGTCGCGTCCGGCGGCTCCGTTG	60
Qy	61	GCTGCTCGCTCTCAGCGCCTGCGGCGGCGGCGGCGGCTCCGTCGCGGCGGCGGCGG	120
Db	61	GCTGCTCGCTCTCAGCGCCTGCGGCGGCGGCGGCGGCTCCGTCGCGGCGGCGGCGG	120
Qy	121	GGGATGCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	180
Db	121	GGGATGCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	180
Qy	181	TGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	240
Db	181	TGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	240
Qy	241	GGGTCCCGGGGCTGACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	300
Db	241	GGGTCCCGGGGCTGACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	300
Qy	301	CGCGCGACCATGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA	360
Db	301	CGCGCGACCATGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA	360
Qy	361	CCGCTCGCTCTTCTGCTTTCAGCGAGGCAACGCTCGTCGCGAAATACGCGAAGCGCATC	420
Db	361	CCGCTCGCTCTTCTGCTTTCAGCGAGGCAACGCTCGTCGCGAAATACGCGAAGCGCATC	420
Qy	421	CGAGTGGCCTCCATTCGAGTATATGATCTGGCCACCATCATCGCCAACTGCATCGTCT	480
Db	421	CGAGTGGCCTCCATTCGAGTATATGATCTGGCCACCATCATCGCCAACTGCATCGTCT	480
Qy	481	GGCCCTGGAGCAGCACTCCCTGATGGGCAAAACCGCCCATGTCGAGCGGCTGGACGA	540
Db	481	GGCCCTGGAGCAGCACTCCCTGATGGGCAAAACCGCCCATGTCGAGCGGCTGGACGA	540
Qy	541	CACGAGCCCTATTTCATCGGATCTTTTGTCTCGAGCGAGGATCAAAATCATCGCTCT	600
Db	541	CACGAGCCCTATTTCATCGGATCTTTTGTCTCGAGCGAGGATCAAAATCATCGCTCT	600
Qy	601	GGGCTTTGTCTTCCACAAAGGCTCTTACCTCGGAAACGCGCTGGAACGTCATGGACTTC	660
Db	601	GGGCTTTGTCTTCCACAAAGGCTCTTACCTCGGAAACGCGCTGGAACGTCATGGACTTC	660
Qy	661	GGTCTCTCTCACAGGATCCTTTGCGAGCTGGAACCTGACCTTCCACCTGCGAACACTGAG	720
Db	661	GGTCTCTCTCACAGGATCCTTTGCGAGCTGGAACCTGACCTTCCACCTGCGAACACTGAG	720
Qy	721	GGCTGTGGGTGTGTCGAGGCGGCTTGAAGCTGGTGTCTGGGATTCGAAGTTTTCAGAGTGG	780
Db	721	GGCTGTGGGTGTGTCGAGGCGGCTTGAAGCTGGTGTCTGGGATTCGAAGTTTTCAGAGTGG	780
Qy	781	GCTCAAGTCCATCATGAAGGCCATGGTTCACCTCTCGAGATTTGGGCTGCTTCTTCTT	840
Db	781	GCTCAAGTCCATCATGAAGGCCATGGTTCACCTCTCGAGATTTGGGCTGCTTCTTCTT	840
Qy	841	TGCCATCTCATGTTTGGCATATTGGCTTGGAGTTCTACATGGGCAAGTTTCCAAAGGC	900
Db	841	TGCCATCTCATGTTTGGCATATTGGCTTGGAGTTCTACATGGGCAAGTTTCCAAAGGC	900
Qy	901	CTGTTTCCCAACACACAGATGCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC	960
Db	901	CTGTTTCCCAACACACAGATGCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC	960
Qy	961	CCGAGCCGCTGTGCGAGGCGGACACTGAGTGCAGGAGTACTGGCGCAGGACCCAACTT	1020
Db	961	CCGAGCTTCAACTTCAGGATGAGACTCCCAACCAACCTTCGACACCTTCCTTCGCGC	1020

Db	961	CCGAGCCGCTGTGCGAGGCGGACACTGAGTCCGGGAGTACTGGCGCAGGACCCAACTT	1020
Qy	1021	TGGCATCACCAACTTTTGACAAATATCTGTGTTGCCATCTTGACGGTGTTCAGTGCATCAC	1080
Db	1021	TGGCATCACCAACTTTTGACAAATATCTGTGTTGCCATCTTGACGGTGTTCAGTGCATCAC	1080
Qy	1081	CATGGAGGCTGGAATGACATCTCTATATAAACAAGATGCGGCCCGGCAACACTGGAA	1140
Db	1081	CATGGAGGCTGGAATGACATCTCTATATAAACAAGATGCGGCCCGGCAACACTGGAA	1140
Qy	1141	CTGCTCTACTTCTATCCCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTGCT	1200
Db	1141	CTGCTCTACTTCTATCCCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTGCT	1200
Qy	1201	GGGCGTGTCTCTCGGGGAGTTTCCAAAGAGCGAGAGAGGTGGAGAACCGCGCGCTT	1260
Db	1201	GGGCGTGTCTCTCGGGGAGTTTCCAAAGAGCGAGAGAGGTGGAGAACCGCGCGCTT	1260
Qy	1261	CCTGAAGCTCGGCCGCGCAGCAGATCGAGCGAGAGCTCAAAGGTACCTGGAGTGAT	1320
Db	1261	CCTGAAGCTCGGCCGCGCAGCAGATCGAGCGAGAGCTCAAAGGTACCTGGAGTGAT	1320
Qy	1321	CTTCAAGCGCGAGAGTCAATGCTGGCCGAGGAGCAGGAATGCGAGGAGAGTCCCC	1380
Db	1321	CTTCAAGCGCGAGAGTCAATGCTGGCCGAGGAGCAGGAATGCGAGGAGAGTCCCC	1380
Qy	1381	TTTGGAGCTGCTCAAGAGAGCGGCCCAAGAGAGCAGAAATGACTGATCCACGCAGA	1440
Db	1381	TTTGGAGCTGCTCAAGAGAGCGGCCCAAGAGAGCAGAAATGACTGATCCACGCAGA	1440
Qy	1441	GGAGGAGAGGACCGGTTTGCAGATCTGTCTGTGTTGGATTCGCCCTTCCGCCGCGCAG	1500
Db	1441	GGAGGAGAGGACCGGTTTGCAGATCTGTCTGTGTTGGATTCGCCCTTCCGCCGCGCAG	1500
Qy	1501	CCTCAAGAGCGGGAAGACAGAGAGCTGCTCATCTTCCGAGGAAGAGAGATGTTCCG	1560
Db	1501	CCTCAAGAGCGGGAAGACAGAGAGCTGCTCATCTTCCGAGGAAGAGAGATGTTCCG	1560
Qy	1561	GTTTTTTATCCGGCGCATGTTGTAAGGCTCAGAGCTTCTACTGGGTGGTGTGCTGCGTGGT	1620
Db	1561	GTTTTTTATCCGGCGCATGTTGTAAGGCTCAGAGCTTCTACTGGGTGGTGTGCTGCGTGGT	1620
Qy	1621	GGCCCTGAAACACTGTGTGTGCGCATGTTGTAAGGCTTCAACACGCGCGCGGCTTACAC	1680
Db	1621	GGCCCTGAAACACTGTGTGTGCGCATGTTGTAAGGCTTCAACACGCGCGCGGCTTACAC	1680
Qy	1681	GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTCTTCTCACAGAGATGCCCTGAA	1740
Db	1681	GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTCTTCTCACAGAGATGCCCTGAA	1740
Qy	1741	GATGTATGGCTCGGGCCCAAGAGCTACTTCCGCTCCTCCTTCAACTGCTTCCACTTTGG	1800
Db	1741	GATGTATGGCTCGGGCCCAAGAGCTACTTCCGCTCCTCCTTCAACTGCTTCCACTTTGG	1800
Qy	1801	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCATCAAGCCCGGGAAGCTCCTT	1860
Db	1801	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCATCAAGCCCGGGAAGCTCCTT	1860
Qy	1861	TGGGATCAGTGTCTGGGCGGCTTCCGCTGCTGAGGATCTTCAAGTCAAGTCAAGTACTG	1920
Db	1861	TGGGATCAGTGTCTGGGCGGCTTCCGCTGCTGAGGATCTTCAAGTCAAGTCAAGTACTG	1920
Qy	1921	GAGCTCCCTCGGAAACCTGGTGTGTCTTCCCTGCTGAACTCCATGAAGTCCATCATAGCCT	1980
Db	1921	GAGCTCCCTCGGAAACCTGGTGTGTCTTCCCTGCTGAACTCCATGAAGTCCATCATAGCCT	1980
Qy	1981	GCTCTTCTGCTCTTCTGTTCATGTTGCTTTCGCCCTGCTGGGAGTGCAGCTGTTGG	2040
Db	1981	GCTCTTCTGCTCTTCTGTTCATGTTGCTTTCGCCCTGCTGGGAGTGCAGCTGTTGG	2040
Qy	2041	GGGACAGTTTCACTTCAGGATGAGACTCCCAACCAACTTCGACACCTTCCTTCGCGC	2100
Db	2041	GGGACAGTTTCACTTCAGGATGAGACTCCCAACCAACTTCGACACCTTCCTTCGCGC	2100

QY	2101	CATCCTCACTGTCTTCCAGATCCTGACGGGAGAGACTGGAATGCGAGTGTATCACGG	2160
Db	2101	CATCCTCACTGTCTTCCAGATCCTGACGGGAGAGACTGGAATGCGAGTGTATCACGG	2160
QY	2161	GATCGAATCGCAAGCGCGCGTCAGCAAAAGGCATGTTCTCGTCTCTTTACTTTCAATGTCTCT	2220
Db	2161	GATCGAATCGCAAGCGCGCGTCAGCAAAAGGCATGTTCTCGTCTCTTTACTTTCAATGTCTCT	2220
QY	2221	GACACTGTTTGGAAACTTACACTCTGCTGAAATGTTCTTTTGCCCATCGCTGTGGACAACCT	2280
Db	2221	GACACTGTTTGGAAACTTACACTCTGCTGAAATGTTCTTTTGCCCATCGCTGTGGACAACCT	2280
QY	2281	GGCCAAACGCCCAAGAGCTGACCAAGATGAAGAGGAGATGGAAAGCAGACCAATCAGAA	2340
Db	2281	GGCCAAACGCCCAAGAGCTGACCAAGATGAAGAGGAGATGGAAAGCAGACCAATCAGAA	2340
QY	2341	GCTTGCTCTGCAAAAGGCCAAAGAGTGGCTGAAGTCAGCCCCATGTCTGCCGCAACAT	2400
Db	2341	GCTTGCTCTGCAAAAGGCCAAAGAGTGGCTGAAGTCAGCCCCATGTCTGCCGCAACAT	2400
QY	2401	CTCCATCGCCGACGACAGCAACTCGGCCAAGGCGCGCTCGGTGTGGACAGCGGCG	2460
Db	2401	CTCCATCGCCGACGACAGCAACTCGGCCAAGGCGCGCTCGGTGTGGACAGCGGCG	2460
QY	2461	CAGCCAGCTACGGCTCGAGAACTCGCGGGCCAGCTCGAGGGCGCTGTACAGCGAGATGGA	2520
Db	2461	CAGCCAGCTACGGCTCGAGAACTCGCGGGCCAGCTCGAGGGCGCTGTACAGCGAGATGGA	2520
QY	2521	CCCGAGGAGCGGCTCGCTTGCCTAAGCGGCGCACTCGCGGCCCGCATGAAAGACGCA	2580
Db	2521	CCCGAGGAGCGGCTCGCTTGCCTAAGCGGCGCACTCGCGGCCCGCATGAAAGACGCA	2580
QY	2581	CCTGGACCGCGCGCTGGTGGAGCTGGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCG	2640
Db	2581	CCTGGACCGCGCGCTGGTGGAGCTGGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCG	2640
QY	2641	CAAAGCCCGACCTGAGGCTGCGGAGGCGCCCGCGAGGCGCTCGACCTCGCGCGAGGCA	2700
Db	2641	CAAAGCCCGACCTGAGGCTGCGGAGGCGCCCGCGAGGCGCTCGACCTCGCGCGAGGCA	2700
QY	2701	CCGGACCCGACACAGGACACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2760
Db	2701	CCGGACCCGACACAGGACACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2760
QY	2761	GAAGCGGAGAGCGGGGAGCCCGGTGCCCGGAGGAGCGCGCGCGCGCGCGCGCGCGCG	2820
Db	2761	GAAGCGGAGAGCGGGGAGCCCGGTGCCCGGAGGAGCGCGCGCGCGCGCGCGCGCGCG	2820
QY	2821	CAGCAGGAGGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2880
Db	2821	CAGCAGGAGGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2880
QY	2881	CGAGGCGCGCGCGCGCGCACACCGGCGCGGTCCCGGAGGAGCGCGCGCGCGCGCGCG	2940
Db	2881	CGAGGCGCGCGCGCGCGCACACCGGCGCGGTCCCGGAGGAGCGCGCGCGCGCGCGCG	2940
QY	2941	CCGACCGCACCGCGCGCACCGGCACTAGATCCGAGCAAGAGTGCAGCGCGCGCGCGCG	3000
Db	2941	CCGACCGCACCGCGCGCACCGGCACTAGATCCGAGCAAGAGTGCAGCGCGCGCGCGCG	3000
QY	3001	CGAGCGGCGCGCGCGCACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	3060
Db	3001	CGAGCGGCGCGCGCGCACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	3060
QY	3061	GGAGAGCGCGCGCGCGCACCGGCGCGCGCGCACAGGCGCGCGCTCTCTCAGCGGCTGT	3120
Db	3061	GGAGAGCGCGCGCGCGCACCGGCGCGCGCGCACAGGCGCGCGCTCTCTCAGCGGCTGT	3120
QY	3121	GGAGAGGAGACCAAGGAGAGGAGGCGCACCGGAGAGGAGGCTGAGATAGTGAAGCCGA	3180
Db	3121	GGAGAGGAGACCAAGGAGAGGAGGCGCACCGGAGAGGAGGCTGAGATAGTGAAGCCGA	3180

QY	3181	CAAGGAAAAGAGGCTCCGGAACCAACAGCCCCGGGAGCCACACTGTGTGACTTGGAGACCAG	3240
Db	3181	CAAGGAAAAGAGGCTCCGGAACCAACAGCCCCGGGAGCCACACTGTGTGACTTGGAGACCAG	3240
QY	3241	TGGGACTGTGACTGTGGGTCCCATGTCACACTGCCCCAGCACCTGTCTCAGAAAGGTGGA	3300
Db	3241	TGGGACTGTGACTGTGGGTCCCATGTCACACTGCCCCAGCACCTGTCTCAGAAAGGTGGA	3300
QY	3301	GGAAACAGCAGAGGATGCAGACAATCAGCGGAAACGTCTCGCATGGGAGTCAAGCCCC	3360
Db	3301	GGAAACAGCAGAGGATGCAGACAATCAGCGGAAACGTCTCGCATGGGAGTCAAGCCCC	3360
QY	3361	AGACCCGAAACTATTGTTACATATCCAGTGTACTGACGGGCCCTTTGGGGAGGCCAC	3420
Db	3361	AGACCCGAAACTATTGTTACATATCCAGTGTACTGACGGGCCCTTTGGGGAGGCCAC	3420
QY	3421	GCTCGTTCCCAAGTGGTAAACGTGGAAAGCCAGAGAGGAGGAGGAGGAGGAGGAGG	3480
Db	3421	GCTCGTTCCCAAGTGGTAAACGTGGAAAGCCAGAGAGGAGGAGGAGGAGGAGGAGG	3480
QY	3481	AGCGGATGACGTGATGAGGAGCGCGGCCCTATCGTCCCATACAGCTCCATGTTCTG	3540
Db	3481	AGCGGATGACGTGATGAGGAGCGCGGCCCTATCGTCCCATACAGCTCCATGTTCTG	3540
QY	3541	TTTAAAGCCCCACCAACCTGCTCCCGGCTTCTGCCACTACATCGTGACCAATGAGGTACTT	3600
Db	3541	TTTAAAGCCCCACCAACCTGCTCCCGGCTTCTGCCACTACATCGTGACCAATGAGGTACTT	3600
QY	3601	CGAGGTGGTCAATTCCTGCTGATCGCTTGGAGCAGCATCGCCCTGGCTGCTGAGGACCC	3660
Db	3601	CGAGGTGGTCAATTCCTGCTGATCGCTTGGAGCAGCATCGCCCTGGCTGCTGAGGACCC	3660
QY	3661	AGTGCGGACAGACTCGCCAGGAAACAAAGCTCTGAAATACCTGGAATTAATTTCACTGG	3720
Db	3661	AGTGCGGACAGACTCGCCAGGAAACAAAGCTCTGAAATACCTGGAATTAATTTCACTGG	3720
QY	3721	TGTCTTTACCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	3780
Db	3721	TGTCTTTACCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	3780
QY	3781	AGCCTATTTCCGGGACTTTGGGAAACATTCCTGGAATTCATTTGGTCACTGCTGCTGCT	3840
Db	3781	AGCCTATTTCCGGGACTTTGGGAAACATTCCTGGAATTCATTTGGTCACTGCTGCTGCT	3840
QY	3841	GGCGTTTGTCTTCTCGAGCTTGGGAGGATCCAAAGGAAAGACATCAATACCAATCAA	3900
Db	3841	GGCGTTTGTCTTCTCGAGCTTGGGAGGATCCAAAGGAAAGACATCAATACCAATCAA	3900
QY	3901	GTCTCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3960
Db	3901	GTCTCTGAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3960
QY	3961	CAAGGCTGTGTTGACTGTGTGTGAACTCCCTGGAAGAAATGCTCTCAACAATTTGATTT	4020
Db	3961	CAAGGCTGTGTTGACTGTGTGTGAACTCCCTGGAAGAAATGCTCTCAACAATTTGATTT	4020
QY	4021	CTACATGCTCTTCACTGTTTCAATTTGCGGTCAATGCGGTGAGCTCTTCAAGGAGGTT	4080
Db	4021	CTACATGCTCTTCACTGTTTCAATTTGCGGTCAATGCGGTGAGCTCTTCAAGGAGGTT	4080
QY	4081	TTTCTACTGCAAGATGAATCCAGGAGCTGGAGAGGAGCTGAGGGGTCTGATTTTGA	4140
Db	4081	TTTCTACTGCAAGATGAATCCAGGAGCTGGAGAGGAGCTGAGGGGTCTGATTTTGA	4140
QY	4141	TTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	4200
Db	4141	TTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	4200
QY	4201	CGCAAAATGTGCTCTGGGCTCTGCTGACGCTGTTTCACTGCTCCAGCGGAGAGGCTGGCC	4260
Db	4201	CGCAAAATGTGCTCTGGGCTCTGCTGACGCTGTTTCACTGCTCCAGCGGAGAGGCTGGCC	4260
QY	4261	CATGCTGTGTAACACTCGGTGGATGCCACCTATGAGGAGGAGGAGGAGGAGGAGGAGG	4320
Db	4261	CATGCTGTGTAACACTCGGTGGATGCCACCTATGAGGAGGAGGAGGAGGAGGAGGAGG	4320

[illegible]

QY 6481 GGCCTGCTCCAGAGCGAGGAGCCCTCATCTCTCTCGGAGAACGCGCTTCTA 6540
DB 6469 GGGCCGGTCCAGAGCGGAGGAGCCCTCATCTCTCTCGGAGAACGCGCTTCTA 6528
QY 6541 CTCTGCGACCGCTTTGGGGCCGCTGAGCCCGGAGAGCCCGCTCTCTCAGCAGCCA 6600
DB 6529 CTCTGCGACCGCTTTGGGGCCGCTGAGCCCGGAGAGCCCGCTCTCTCAGCAGCCA 6588
QY 6601 CCCAAGTTCGCGCAACAGCTGCGCAGAGCGGAGCCCGCAACAGAGGAGTGGTTCGCT 6660
DB 6589 CCCAAGTTCGCGCAACAGCTGCGCAGAGCGGAGCCCGCAACAGAGGAGTGGTTCGCT 6631
QY 6661 GAATGGAGCCCTTGTGTCAACATCTGTGTGCTAGCACCCCGCGCGGTGGGCGGAG 6720
DB 6632 ----- 6631
QY 6721 GCAGCTCCCCAGACGCCCTGACTCCCGCCGCCAGCATCACCTACAGACGGCAACTC 6780
DB 6632 ----- 6631
QY 6781 CTCACCCATCCACTTCGCGGGGCTCAGACAGCCCTCCCTGCTTCTCCCGAGCGCGCT 6840
DB 6632 -----CAGGCGCGCT 6641
QY 6841 CAGCGTGGGCTTTCCGAACACAAACGCGCTGCTGAGAGAGACCCCTCAGCCAGCCCT 6900
DB 6642 CAGCGTGGGCTTTCCGAACACAAACGCGCTGCTGAGAGAGACCCCTCAGCCAGCCCT 6701
QY 6901 GGGCCCTGGCTCTCGAATTTGGCTTGACCCCTTACCTGGGCGAGCTGTGGACAGTGGGC 6960
DB 6702 GGGCCCTGGCTCTCGAATTTGGCTTGACCCCTTACCTGGGCGAGCTGTGGACAGTGGGC 6761
QY 6961 CTCTGTCACGCGCTGCTGAGAGACGCTCACTTTCGAGGAGGCTGTGGCCACCACTC 7020
DB 6762 CTCTGTCACGCGCTGCTGAGAGACGCTCACTTTCGAGGAGGCTGTGGCCACCACTC 6821
QY 7021 GGGCGCTCTCTCAGGACTTCTTACGCTGCTCTCTGCTGACCTCCAGTCTCACCCCTCTCCG 7080
DB 6822 GGGCGCTCTCTCAGGACTTCTTACGCTGCTCTCTGCTGACCTCCAGTCTCACCCCTCTCCG 6881
QY 7081 CGCGTGGCCAGCGTTTACCTGACGCTGCTGAGAGTCTGAGTGGGTCGCGAGACGCA 7140
DB 6882 CGCGTGGCCAGCGTTTACCTGACGCTGCTGAGAGTCTGAGTGGGTCGCGAGACGCA 6941
QY 7141 CAGCTACCAACACCTGACCAAGACACTGTGTGCTAGCTGCACCGTGCAGCGCTCAGACGC 7200
DB 6942 CAGCTACCAACACCTGACCAAGACACTGTGTGCTAGCTGCACCGTGCAGCGCTCAGACGC 7001
QY 7201 CTGCAATGACAGCGCTGTGTTCCAGTGGATGAGTATCATCCACACGGGGCAGTCCG 7260
DB 7002 CTGCAATGACAGCGCTGTGTTCCAGTGGATGAGTATCATCCACACGGGGCAGTCCG 7061
QY 7261 CCCTGGGGGAGGCTTGGCCACCTTGTGAGGCTCTGTGGCCCTCCCTCCCTCCCTCTCT 7320
DB 7062 CCCTGGGGGAGGCTTGGCCACCTTGTGAGGCTCTGTGGCCCTCCCTCCCTCCCTCTCT 7121
QY 7321 CCCCTCTTTTACTCTAGACGAGCAATAAGCCCTGCTGCTTGTGAGTGTACGTACGCG 7376
DB 7122 CCCCTCTTTTACTCTAGACGAGCAATAAGCCCTGCTGCTTGTGAGTGTACGTACGCG 7177

RESULT 11
ID AAQ84658
XX AAQ84658 standard; DNA; 7175 BP.
AC AAQ84658;
XX
XX
DT 25-MAR-2003 (revised)
TT 01-DEC-1995 (first entry)
XX
DE Human neuronal calcium channel subunit alpha 1B-2.
XX

KW Calcium channel subunit; antagonist; agonist; diagnosis;
KW Lambert Eaton Syndrome; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 144..6857
FT /*tag= a
FT 6633..7175
FT misc_feature /*tag= b
FT /note= "identical to alpha 1B-1"
XX
XX WO9504822-A1.
PD 16-FEB-1995.
XX
PF 11-AUG-1994; 94WO-US009230.
XX
PR 11-AUG-1993; 93US-00105536.
PR 05-NOV-1993; 93US-00149097.
XX
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
PA Harpold MW, Ellis SB, Williams ME, Mccue AF, Gillespie A;
PI
XX WPI; 1995-090900/12.
DR P-PSDB; AAR71006.
XX
PT DNA encoding human calcium channel sub-unit(s) - used for developing
PT prods. for studying calcium channels, e.g. for obtaining agonists and
PT antagonists.
XX
PS Disclosure; Page 149-160; 285pp; English.
XX
CC DNA encoding the alpha 1B subunit was isolated by screening a human basal
CC ganglia cDNA library with fragments of the rabbit skeletal muscle calcium
CC channel alpha 1 subunit-encoding cDNA. A portion of one of the positive
CC clones was used to screen an IMR32 cell cDNA library. Clones that
CC hybridised to the basal ganglia probe were used to further screen an
CC IMR32 cell cDNA library to identify overlapping clones that in turn were
CC used to screen a human hippocampus cDNA library. A series of clones to
CC span nearly the entire length of the nt. sequence encoding the human
CC alpha 1B subunit was obt'd. Nucleic acid amplification of specific regions
CC of the IMR32 cell alpha 1B mRNA yielded additional segments of the alpha
CC 1B coding sequence. A full-length alpha 1B DNA clone was constructed by
CC ligating portions of the partial cDNA clones. Nucleic acid amplification
CC analysis of IMR32 cell RNA and genomic DNA using oligo primers corresp.
CC to sequences located 5' and 3' of the stop codon of the DNA encoding the
CC alpha 1B subunit revealed an alternatively spliced alpha 1B-encoding mRNA
CC in IMR32 cells. This second mRNA product is the result of differential
CC splicing of the alpha 1B subunit transcript to include another exon that
CC is not present in the mRNA corresp. to the other 3' alpha 1B cDNA
CC sequence that was initially isolated. The alpha 1B subunit encoded by a
CC DNA sequence contg. an additional exon is referred to as alpha 1B-1 and
CC given in AAQ84657/R71005, whereas the other form is referred to as alpha
CC 1B-2 and is given in AAQ84658/R71006. Following the sequence of the
CC additional exon in alpha 1B-1 the alpha 1B-1 and alpha 1B-2 sequences are
CC identical. (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 U; 0 Other;

Query Match 94.0%; Score 6932.4; DB 2; Length 7175;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 7174; Conservative 0; Mismatches 1; Indels 201; Gaps 4;
QY 1 GCGGCGCGGCTGCGCGGCTGCGGCGCGGCGGAGTCCGCTCGGTCCTCCGCTCCGTCG 60
DB 1 GCGGCGCGGCTGCGCGGCTGCGGCGCGGCGGAGTCCG-TGCGGTCCCGGCTCCGTCG 59
QY 61 GCTGCTCCGCTCTGAGCGCTGCGGCGCGGCGGCTCCCTGCGGCGGCTGCTGGGCG 120
DB 60 GCTGCTCCGCTCTGAGCGCT -GCGGCGCGGCGGCTCCCTGCGGCGGCTGCTGGGCG 118

Qy 121 GGGATGACCGGGGGCCGGAGGCCATGGTCCGCTTCGGGGACGAGCTGGCGGCGCCGCTA 180
Db 119 GGGATGACCGGGGGCCGGAGGCCATGGTCCGCTTCGGGGACGAGCTGGCGGCGCCGCTA 178
Qy 181 TGGAGGCCCGGGCGGAGAGCGGGCCCGGGGGCGGGGCGGGGCGGGGGGGCC 240
Db 179 TGGAGGCCCGGGCGGAGAGCGGGCCCGGGGGCGGGGCGGGGCGGGGGGGCC 238
Qy 241 GGGTCCGGGGGGGTGACGCCCGGCCAGCGGGTCTCTTACAAGCAATCGATCGCGCAGCG 300
Db 239 GGGTCCGGGGGGGTGACGCCCGGCCAGCGGGTCTCTTACAAGCAATCGATCGCGCAGCG 298
Qy 301 CGCGCGACCATGGCGCTGTACAACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA 360
Db 299 CGCGCGACCATGGCGCTGTACAACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA 358
Qy 361 CCGCTCGCTCTTCTGCTTTCGCGAGGACAGGTGCTCGGCAATACCGAGCGCATCAC 420
Db 359 CCGCTCGCTCTTCTGCTTTCGCGAGGACAGGTGCTCGGCAATACCGAGCGCATCAC 418
Qy 421 CGAGTGGCCTCCATTCGAGTATATGATCTTGGCCACCACCATATCGCCAACTGCACTGCT 480
Db 419 CGAGTGGCCTCCATTCGAGTATATGATCTTGGCCACCACCATATCGCCAACTGCACTGCT 478
Qy 481 GGCCTCGAGCAGCACTCCCTGATGGGACAAACCGCCCATGTCGAGCGGTGGACGA 540
Db 479 GGCCTCGAGCAGCACCCTCCGTGATGGGACAAACCGCCCATGTCGAGCGGTGGACGA 538
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Db 539 CACGGAGCCTATTTTCATCGGGATCTTTGCTTCGAGCGAGGATCAAAATCATCGCTCT 598
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Db 599 GGGCTTGTCTTCCACAAGGCTCTTACCTGCGGAACGGCTGGAACTGATGCACTTCGT 658
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Db 659 GGTGCTCTCACAGGATCTTGTGACAGCGTGGAACTGACTTGAACCTGGGAACTGTGAG 718
Qy 721 GGTGCTGCTGTGAGGCGCCCTGAACTGCTGCTGGGATTCGAAGTTTGCAGGTGGT 780
Db 719 GGTGCTGCTGTGAGGCGCCCTGAACTGCTGCTGGGATTCGAAGTTTGCAGGTGGT 778
Qy 781 GCTCAAAGTCCATGAAAGCCATGTTTCCACTCCTGCAGATTGGGCTGCTTCTTCTT 840
Db 779 GCTCAAAGTCCATGAAAGCCATGTTTCCACTCCTGCAGATTGGGCTGCTTCTTCTT 838
Qy 841 TGCATCCTCATGTTTGCATCATGTCGAGTTCAGTTCATGAGGCAAGTTTCAAGGC 900
Db 839 TGCATCCTCATGTTTGCATCATGTCGAGTTCAGTTCATGAGGCAAGTTTCAAGGC 898
Qy 901 CTGTTTCCCAACAGCAGATGCGGAGCCGTTGGTGACTTCCCTGTCGCGAGGAGGC 960
Db 899 CTGTTTCCCAACAGCAGATGCGGAGCCGTTGGTGACTTCCCTGTCGCGAGGAGGC 958
Qy 961 CCCAGCCGGCTGTGCGAGGCGACACTGAGTGGCGGAGTACTTGGCCAGGACCCAACTT 1020
Db 959 CCCAGCCGGCTGTGCGAGGCGACACTGAGTGGCGGAGTACTTGGCCAGGACCCAACTT 1018
Qy 1021 TGGCATCAACCACTTTGACAAATCTCTGTTTGGCATCTTGAAGGTTTGAAGTGCATCAC 1080
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Qy 1081 CATGGGGCTGACTGACTCTCTATATACAAACGATCGGCGGCAACCTGGAA 1140
Db 1079 CATGGGGCTGACTGACTCTCTATATACAAACGATCGGCGGCAACCTGGAA 1138
Qy 1141 CTGGCTCTACTTCTCTCATCATCATCGGCTCTTCTTCAATGCTCAACCTGGTCT 1200
Db 1139 CTGGCTCTACTTCTCTCATCATCATCGGCTCTTCTTCAATGCTCAACCTGGTCT 1198
Qy 1201 GGGCGTCTCTCGGGGGAGTTTTCGAAGGACGAGAGGGTGGAGAACCGCGCGCTT 1260

Db 1199 GGGCGTCTCTCGGGGGAGTTTCCAAAGGAGCGAGAGGGTGGAGAACCGCGCGCTT 1258
Qy 1261 CTTGAAAGCTCGCGCGGAGCAGAGTTCGAGCGAGAGCTCAAAGGTTACTTGGAGTGGAT 1320
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Qy 1321 CTTCAAAGGCGGAGAAAGTCAATGCTGCGAGGAGGACAGAAATGCAAGAGAGTCCCC 1380
Db 1319 CTTCAAAGGCGGAGAAAGTCAATGCTGCGAGGAGGACAGAAATGCAAGAGAGTCCCC 1378
Qy 1381 TTTTGGAGCTGCTCAAGAGCGGCGCAACCAAGAGAGGAGAAATGCACTGATCCACGAGA 1440
Db 1379 TTTTGGAGCTGCTCAAGAGCGGCGCAACCAAGAGAGGAGAAATGCACTGATCCACGAGA 1438
Qy 1441 GGAAGGAGAGGAGCCGGTTTGCAGATCTCTGCTGTTGGATCCCTTCCCGCGCGCAG 1500
Db 1439 GGAAGGAGAGGAGCCGGTTTGCAGATCTCTGCTGTTGGATCCCTTCCCGCGCGCAG 1498
Qy 1501 CCTCAAAGCGGGAAGACAGAGAGCTCGTCATACTTCCGAGGAAGAGAGATGTTCCG 1560
Db 1499 CCTCAAAGCGGGAAGACAGAGAGCTCGTCATACTTCCGAGGAAGAGAGATGTTCCG 1558
Qy 1561 GTTTTATTCGGCGCATGCTGTAAGGCTCAGAGCTTCTACTGGGTGGTCTGCTGCTGGT 1620
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Qy 1681 GACCTGTATTTTGCAGAGTTGTTTTCTCTGGGTCTCTTCTCACAGAGATGCTCCGTAA 1740
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Db 1859 TGGGATCAGTGTCTCGGGCCCTCGCGCTGTGAGGATCTTCAAAGTCAAGAGTACTG 1918
Qy 1921 GAGCTCCCTGGGAACTGCTGCTGCTGCTGAACTCAATGAAGTCAATCATCAGCCT 1980
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Qy 2221 GACACTGTTGGAACTACACTCTGCTGAATGCTTTCTTGGCCATCGCTGTGACAACT 2280
Db 2219 GACACTGTTGGAACTACACTCTGCTGAATGCTTTCTTGGCCATCGCTGTGACAACT 2278
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QY 4681 CGTGTTCACATCCATGTTCTCCATGGAATGGGTGCTGAAGATCATGTCGCCCTTTGGGGTGCT 4740
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QY 5101 GTTCAGAGCGCACGGGGAGGCTGGCAGAGATCATGCTGCTGCCCTGAGCAACCA 5160
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QY 5161 GGCCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGACTTTTGCCTACTTTCTACTT 5220
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QY 5221 CGTCTCCTTCATCTTCTGTGCTCTTTCTGATGTTGAACTCTTTGTGGCTGTGATCAT 5280
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QY 5281 GGACAAATTTGAGTACCTCAGCGGGACTCTTCCATCCTAGGTCTTCAACCACTGGATGA 5340
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QY 5701 GATGACAGTGGGAAGGTTTATGACGCTCTGATGATATTGACTTCTTACAAGCAGAACAA 5760
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Db CCATGAGGCTGAGCCACCTCGAGGTGCGCACTCCACAGAGATCCCTGTGTGGGCGGTC 6046
QY 6061 AGGAGCACTGGCTGTGGACGTTTCAGATGCAGAGCATAAACCCGAGGGGCCCTGATGGGGA 6120
Db AGGAGCACTGGCTGTGGACGTTTCAGATGCAGAGCATAAACCCGAGGGGCCCTGATGGGGA 6106
QY 6121 GCCCAGCCTGGCTGTGGACGAGCCAGGGTCAGCGGCTCCATGCTCCGCTTCGGGCCGA 6180
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QY 6481 GGGCCCGGTCTCAGGAGCGGAGCGCCTCATCTCTCTCGGAGAACGAGCGCTTCTA 6540
Db GGGCCCGGTCTCAGGAGCGGAGCGCCTCATCTCTCTCGGAGAACGAGCGCTTCTA 6526
QY 6541 CTCCTCGGACCGGTTTTGGGGGCGTGCAGCCCGGAAGCCCAAGCCCTCTCCTCAGCAGCCA 6600
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QY 6601 CCCAAGCTGCCCAACAGCTGGCCAGGAGCCGGGACCCCAACCCAGGCGAGTGGTTCCGT 6660
Db CCCAAGCTGCCCAACAGCTGGCCAGGAGCCGGGACCCCAACCCCAAGGCGAGTGGTTCCGT 6629
QY 6661 GAATGGAGGCCCTTGTCTCAACATCTGTGTGCTAGCAACCCCGCGCGGCTGGGGCGGAG 6720

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Db 6630 ----- 6629
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Qy 7081 CGCGTGCCCAAGGTTTACCACTGCAACCCCTGGGACTCAGCTCGGCTGGCCGAGCAGCA 7140
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Db 6940 CAGCTACCAACCCCTGACCAAGACACATGTGTGCTAGCTGCAACCGTGACCGCTCAGAGC 6999
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Db 7000 CTGCATGACAGAGGCTGTGTTCAGTGATGATTTTATCATCATCCAGGGGAGTGG 7059
Qy 7261 CCCTGGGGAGGCTTGGCCACCTTGCTGAGGCTCTGTGGCCCTTCCCTCCCTCTCT 7320
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Db 7120 CCCCTCTTTTACTGTAGACGAGCAATAAGCCCTCTGCTTGAGTGATGATACGC 7175

RESULT 12
AAV42686
ID AAV42686 standard; DNA; 7175 BP.
XX
AC AAV42686;
XX
XX 25-MAR-2003 (revised)
DT 12-OCT-1998 (first entry)
XX
DE DNA encoding human calcium channel alpha-1B subunit.
XX
XX Alpha-1B subunit; human; calcium channel; assay; detection;
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis; ds.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..143
FT FT /*tag= a
FT CDS 144..6857
FT FT /*tag= b
FT FT 6855..7175
FT FT /*tag= c
XX
PN US5792846-A.
XX
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PD 11-AUG-1998.
XX
PF 31-MAY-1995; 95US-00455543.
XX
PR 04-APR-1988; 88US-00176899.
PR 04-APR-1989; 89WO-US001408.
PR 20-FEB-1990; 90US-00482384.
PR 08-NOV-1990; 90US-00603751.
PR 30-NOV-1990; 90US-00620250.
PR 15-AUG-1991; 91US-00745206.
PR 04-APR-1994; 94US-00223305.
XX
PA (SIBI-) SIBIA NEUROSCIENCES INC.
XX
XX Brenner R, Ellis SB, Williams ME, Feldman DH, Mecue AF,
PI Harpold WM;
XX
XX WPI; 1998-456192/39.
XX P-PSDB; AAW63142.
XX
PT DNA encoding human calcium channel alpha 1B subunit protein - useful for
PT recombinant production of the channel for screening of its modulators,
PT and diagnosis of Lambert Eaton Syndrome.
XX
XX Claim 1; Col 91-106; 166pp; English.
XX
XX The present sequence encodes the alpha-1B subunit of a human calcium
XX channel. The present sequence is derived from alternative splicing of
XX AAV42685. Calcium channels are membrane-spanning, multi-subunit proteins
XX that allow controlled entry of calcium ions into cells. This leads to
XX depolarisation events required for muscle contraction. The recombinant
XX subunit, when expressed with nucleic acids encoding the complete calcium
XX channel, can be used in assays for the detection and characterisation of
XX compounds that modulate the channel. The DNA encoding the subunit can be
XX alternatively spliced when transcribed, giving more than one form of the
XX protein from the same transcript, each having slightly different
XX properties. In addition, the reactivity of the alpha 1 subunit with IgG
XX molecules from the serum of an individual with Lambert Eaton Syndrome
XX (LES) can be used as a diagnostic for the disease. (Updated on 25-MAR-
XX 2003 to correct PR field.)
XX
XX Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 U; 0 Other;
XX
Query Match 94.0%; Score 6932.4; DB 2; Length 7175;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 7174; Conservative 0; Mismatches 1; Indels 201; Gaps 4;
Qy 1 GCGGCGCGGCTGCGGCGTGGGCGCGGCGGCGGCGGCTGCGGCTCCCGTCCGTCGCTCCGTG 60
Db 1 GCGGCGCGGCTGCGGCGTGGGCGCGGCGGCGGCGGCTGCGGCTCCCGTCCGTCGCTCCGTG 59
Qy 61 GCTGCTCCGCTCTGAGCGCTGCGGCGCGGCGGCGGCGGCTCCCTGCGGCGGCGGCGGCGG 120
Db 60 GCTGCTCCGCTCTGAGCGCT -GCGGCGCGGCGGCGGCGGCTCCCTGCGGCGGCGGCGGCGG 118
Qy 121 GGGATCACGCGGGGCGCGGAGCCATGCTGCTTCGGGGAGCAGCTGGGCGGCGGCGGCGGCTA 180
Db 119 GGGATCACGCGGGGCGCGGAGCCATGCTGCTTCGGGGAGCAGCTGGGCGGCGGCGGCGGCTA 178
Qy 181 TGGAGCGCGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 179 TGGAGCGCGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 238
Qy 241 GGGTCCCGGGGCGGCTGCAGCGCGGCGGCGGCGGCGGCTCTTACAAGCAATCGATCGCGCAGCG 300
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Db 361 CGCTCGCTTTCGTTCTTCAGGCGAGCAACCTGCTCCGCAATACGGGAGCGGATCAC 420
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Db 959 CCCAGCCGGCTGTGCGAGGCGGACACTGAGTGCGGGAGTACTTGGCCAGGACCCAACTT 1018
Qy 1021 TGGCATCAACAACTTTGACAAATATCCTGTTTGGCCATCTTGACGGTGTTCAGTGCATCAC 1080
Db 1019 TGGCATCAACAACTTTGACAAATATCCTGTTTGGCCATCTTGACGGTGTTCAGTGCATCAC 1078
Qy 1081 CATGGGGCTGGAATGACATCCTCTATATACAAAGTGGCGCGGACACCTGGAA 1140
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Db 1139 CTGGCTCTACTTCACTCCCTCTCATCATCATCGGCTCTTCTTCACTGCTCAACCTGGTGT 1198
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Db 1199 GGGCGTGTCTCGGGGAGTTTGCAGAGCGAGAGAGGTTGAGAAACCGCCGCGCTT 1258
Qy 1261 CCTAAGCTGCGCGGAGAGAGAGTCTGAGCGAGAGCTCAACGGGTACCTGGAGTGGAT 1320
Db 1259 CCTAAGCTGCGCGGAGAGAGAGTCTGAGCGAGAGCTCAACGGGTACCTGGAGTGGAT 1318
Qy 1321 CTTCAAGCGGAGGAAGTCACTGTGCGCGAGGAGCAGGAATGCAGAGGAGAGTCCCC 1380
Db 1319 CTTCAAGCGGAGGAAGTCACTGTGCGCGAGGAGCAGGAATGCAGAGGAGAGTCCCC 1378
Qy 1381 TTTGGACGTGTGAAGAGAGCGGCCACCAAGAGCAGAAATGACCTGATCCACGCGAGA 1440
Db 1379 TTTGGACGTGTGAAGAGAGCGGCCACCAAGAGCAGAAATGACCTGATCCACGCGAGA 1438
Qy 1441 GGAGGAGAGGACCGGTTTGCAGATCTGTGCTGTTGGATCCCTTCCGCGCGCGCAG 1500
Db 1439 GGAGGAGAGGACCGGTTTGCAGATCTGTGCTGTTGGATTCCTTCCGCGCGCGCAG 1498
Qy 1501 CCTCAAGAGCGGGAAGCAGAGAGCTCGTCACTCTCCGAGGAAGAGAGATGTTCCG 1560
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Qy 1561 GTTTTTTATCCGCGCATGGTGAAGGCTCAGAGCTTCTACTGGGTGGTCTGTGCTGGT 1620
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Qy 1921 GAGTCCCTCGGGAACCTGGTGGTCTCTGCTGAAGTCCATGAATCCATCATCAGCCT 1980
Db 1919 GAGTCCCTCGGGAACCTGGTGGTCTCTGCTGAAGTCCATGAAGTCCATCATCAGCCT 1978
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DB 6630 ----- 6629
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RESULT 14
AAD39956
ID AAD39956 standard; DNA; 7175 BP.
XX
AC AAD39956;
XX
XX 22-OCT-2002 (first entry)
XX
DE Human calcium channel alpha 1B-2 protein encoding DNA.
XX
KW Human; calcium channel protein; therapeutic; autoimmune disease;
KW diagnosis; Lambert Eaton Syndrome; alpha 1B-2 protein; splice variant;
KW gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..143
FT CDS /*tag= a
FT 144..6857
FT /*tag= b
FT /*tag= c
FT 3'UTR /product= "Human calcium channel alpha 1B-2 protein"
FT 6858..7175
FT /*tag= c
XX
XX US6387696-B1.
XX
XX 14-MAY-2002.
XX
XX 25-MAY-1995; 95US-00450272.
XX
XX 04-APR-1989; 89WO-US001408.
XX 02-FEB-1990; 90US-00482384.
XX 08-NOV-1990; 90US-00603751.
XX 30-NOV-1990; 90US-00620250.
XX 15-AUG-1991; 91US-00745206.
XX 13-JUL-1992; 92US-00914231.
XX 14-AUG-1992; 92WO-US006903.
XX 11-AUG-1993; 93US-00105536.
XX 05-NOV-1993; 93US-00149097.
XX 07-FEB-1994; 94US-00193078.
XX 04-APR-1994; 94US-00223305.
XX 11-AUG-1994; 94US-00290012.
XX 23-SEP-1994; 94US-00311363.
XX 07-NOV-1994; 94US-00336257.
XX 15-FEB-1995; 95US-00404354.
XX
XX (MERI) MERCK & CO INC.
XX
XX Harpold MM, Ellis SB, Williams ME, McCue AF;
XX WPI; 2002-470318/50.
XX P-PSDB; AAE24786.
XX
XX Eukaryotic cells expressing a functional heterologous human calcium
XX channel and encoding nucleic acid isolated from human cerebellum for drug
XX design and to diagnose Lambert Eaton Syndrome.
XX
XX Example 2; Col 113-128; 154pp; English.
XX
XX The present invention relates to novel human calcium channel proteins and

CC polynucleotides encoding such proteins. The invention also relates to
CC eukaryotic cells expressing a functional heterologous human calcium
CC channel alpha 1, alpha 2, beta and gamma subunits. The eukaryotic cells
CC are useful for screening for potential calcium channel antagonists or
CC agonists to select compounds that have potential as disease or tissue-
CC specific therapeutic agents. The subunits may be used in diagnostic
CC assays for the autoimmune disease Lambert Eaton Syndrome. The present
CC sequence is a DNA encoding human calcium channel alpha 1B subunit splice
CC variant, alpha 1B-2 protein
XX
SQ Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 U; 0 Other;

Query Match 94.0%; Score 6932.4; DB 6; Length 7175;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 7174; Conservative 0; Mismatches 1; Indels 201; Gaps 4;
QY 1 GCGGCGGCGGTGCGGCGGTGGGCGCGAGGTCCGCTCGCGTCCCGGGGCGGTCCG 60
Db 1 GCGGCGGCGGTGCGGCGGTGGGCGCGAGGTCCG-TCGCGTCCCGGCGGTCCG 59
QY 61 GCTGCTCGCTCTGAGCGCTTGGCGCCCGCGGCCCTCCCTCCCGGGGCGGTGGCGCG 120
Db 60 GCTGCTCGCTCTGAGCGCT-6CGGCGCCCGCGGCCCTCCCTCCCGGGGCGGTGGCGCG 118
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Db 119 GGGATGACGCGGGGCGCGGAGCCATGTCGCTTCGCGGAGCAGTGG3CGGCGCTA 178
QY 181 TGGAGGCGCGCGCGGAGAGCGGCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 179 TGGAGGCGCGCGCGGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 238
QY 241 GGTTCGCGGGGCGGTGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
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Db 359 CGCTCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 418
QY 421 CGAGTGGCTTCCATTCGAGTATATGATCTCTGCGCACCACATCATCGCACTCATCGTCT 480
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Db 479 GGCCCTGGAGCAGCACCTCCCTGATGGGACAAACCGCCCATGTCCGAGCGCGTGGACGA 538
QY 541 CAGGAGCGCTATTTTCATCGGATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 600
Db 539 CAGGAGCGCTATTTTCATCGGATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 598
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Db 599 GGGCTTTTGTCTTCCAAAGGGCTTTTACCTGCGGAACGCGTGGACGCTCATGGCTTCT 658
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Db 659 GGTCTCTCACAGGGATCTTTGCCACCGCTGGAACTGACTTCGACCTTCGAAACACTGAG 718
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QY 781 GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCCTCTGCAGATTGGGCTGTCTCTCTT 840
Db 779 GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCCTCTGCAGATTGGGCTGTCTCTCTT 838
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Db 839 TGCCATCCTCATGTTTGGCCATCATGTCCTGGAGTTCTATCATGGCAAGTTCCACAAGGC 898
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Db 1499 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCAATCTCCGAGGGAAGAGAGATGTTCCG 1558
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Qy 2221 GACACTGTTTCGGAACCTACACTCTGCTGAATGTCTTCTGGCCATCGCTGTGACAACT 2280
Db 2219 GACACTGTTTCGGAACCTACACTCTGCTGAATGTCTTCTGGCCATCGCTGTGACAACT 2278
Qy 2281 GGCACACGCCCAAGAGCTGACCAAGATGAAGAGGAGATGGAAGAGAGAGCCCAATCAGAA 2340
Db 2279 GGCACACGCCCAAGAGCTGACCAAGATGAAGAGGAGATGGAAGAGAGAGCCCAATCAGAA 2338
Qy 2341 GCTTGTCTCTGCAAAAGGCCAAAGAGTGGCTGAAGTCAGCCCATGTCTGTCGCGCAACAT 2400
Db 2339 GCTTGTCTCTGCAAAAGGCCCAAGAGTGGCTGAAGTCAGCCCATGTCTGTCGCGCAACAT 2398
Qy 2401 CTCATCTGCGCCAGCGAGCAGAACTCGGCCAAGGCGCGCTCGGTGTGGAGGAGCGGGC 2460
Db 2399 CTCATCTGCGCCAGCGAGCAGAACTCGGCCAAGGCGCGCTCGGTGTGGAGGAGCGGGC 2458
Qy 2461 CAGCAGCTACGCTGTCAGAACCTCGCGGCCAGCTCGAGCGCTGTGTACAGCGAGATGGA 2520
Db 2459 CAGCAGCTACGCTGTCAGAACCTCGCGGCCAGCTCGAGCGCTGTGTACAGCGAGATGGA 2518
Qy 2521 CCCCGAGGAGCGCTGCGCTTCCCTACTACGCGCCACTGTCGCGCCGACATGAAGACGA 2580
Db 2519 CCCCGAGGAGCGCTGCGCTTCCCTACTACGCGCCACTGTCGCGCCGACATGAAGACGA 2578
Qy 2581 CTTGGACCGGCGCTGCTGTGTGAGCTGCGCCGAGCGCGCGCGGGGGCCCTGTGGAGG 2640
Db 2579 CTTGGACCGGCGCTGCTGTGTGAGCTGCGCCGAGCTGCGCGCGCGGGGGCCCTGTGGAGG 2638
Qy 2641 CAAGCCGACCTGAGGCTGCGAGCGCCCGGAGGCGTCACTTCCGCGAGGCGCACCA 2700
Db 2639 CAAGCCGACCTGAGGCTGCGAGGCGCCCGGAGGCGTCACTTCCGCGAGGCGCACCA 2698
Qy 2701 CCGGCAACCGCAACAGGACAAAGACCCCGCGCGGGGACAGGACCGAGCAGAGGCCCC 2760
Db 2699 CCGGCAACCGGCAACAGGACAAAGACCCCGCGCGGGGACAGGACCGAGCAGAGGCCCC 2758
Qy 2761 GAAAGCGGAGAGCGGGAGCGCCCGTGTCCCGGAGGAGCGGCGCGCGCGCACCGCAGCCA 2820
Db 2759 GAAAGCGGAGAGCGGGAGCGCCCGTGTCCCGGAGGAGCGGCGCGCGCGCACCGCAGCCA 2818
Qy 2821 CAGCAAGGAGGCGCGGGCGCCCGGAGGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 2880
Db 2819 CAGCAAGGAGGCGCGGGCGCCCGGAGGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 2878
Qy 2881 CGAGGCGCGCGGGCGCACCCACCGCGCGCTCCCGGAGGAGGCGCGCGCGCGCGCGCG 2940
Db 2879 CGAGGCGCGCGGGCGCACCCACCGCGCGCTCCCGGAGGAGGCGCGCGCGCGCGCGCG 2938
Qy 2941 CCGACCGCACCGCGCGCACCGGCAACAGATCCGAGCAAGAGTGTGCGCGCGCGCGCGCG 3000
Db 2939 CCGACCGCACCGCGCGCACCGGCAACAGATCCGAGCAAGAGTGTGCGCGCGCGCGCGCG 2998
Qy 3001 CGAGCGCGCGCGCGCGCACCGCGCGCGCCCGCGAGCGGGCGCCCGGAGCGCGAGCGG 3060
Db 2999 CGAGCGCGCGCGCGCGCACCGCGCGCGCCCGCGAGCGGGCGCCCGGAGCGCGAGCGG 3058

QY 3061 GGAGGAGCGCGCGCGGCA CCGGGCCGGCACAAGGCGCAGCCCTGCTCACGAGGCTGT 3120
Db 3059 GGAGGAGCGCGCGCGGCA CCGGGCCGGCACAAGGCGCAGCCCTGCTCACGAGGCTGT 3118
QY 3121 GGAGAGGAGACACCGAGAGGAGGAGGCCACGAGGAGAGGAGGCTGAGATAGTGAAGCCGA 3180
Db 3119 GGAGAGGAGACACCGAGAGGAGGAGGCCACGAGAGAGGAGGCTGAGATAGTGAAGCCGA 3178
QY 3181 CAAGGAAAAGGAGCTCCGNAACACAGACCCCGGGAGCCACACTGTGACTTGAGACCCAG 3240
Db 3179 CAAGGAAAAGGAGCTCCGNAACACAGACCCCGGGAGCCACACTGTGACTTGAGACCCAG 3238
QY 3241 TGGGACTGTGACTGTGGGTCCCATGCACACACTGCCCCAGACCTGTCTCCAGAAAGTGA 3300
Db 3239 TGGGACTGTGACTGTGGGTCCCATGCACACACTGCCCCAGACCTGTCTCCAGAAAGTGA 3298
QY 3301 GGAACGCCAGAGGATGCGAGCAATCAGCGGAAACGTCACTCGCATGGGCAGTCAGCCCCC 3360
Db 3299 GGAACGCCAGAGGATGCGAGCAATCAGCGGAAACGTCACTCGCATGGGCAGTCAGCCCCC 3358
QY 3361 AGACCCGAACACTATTGTATCATATCCAGTGTGATGCTGACGGGCCCTCTTGGGGAGCCAC 3420
Db 3359 AGACCCGAACACTATTGTATCATATCCAGTGTGATGCTGACGGGCCCTCTTGGGGAGCCAC 3418
QY 3421 GGTCTGTTCCAGTGTGTAACCTGTGACCTGGAAGCCAAAGCAGAGGGGAAAGAGGAGTGA 3480
Db 3419 GGTCTGTTCCAGTGTGTAACCTGTGGAAGCCAAAGCAGAGGGGAAAGAGGAGTGA 3478
QY 3481 AGCGGATGAGTATGAGAGAGGGCCCCCGGCGTATCGTCCCATACAGCTCCATGTTCTG 3540
Db 3479 AGCGGATGAGTATGAGAGAGGGCCCCCGGCGTATCGTCCCATACAGCTCCATGTTCTG 3538
QY 3541 TTTAAGCCCCACCAACTCTCGCGCTTCGCCACTACATCGGACCATGAGTACTT 3600
Db 3539 TTTAAGCCCCACCAACTCTCGCGCTTCGCCACTACATCGGACCATGAGTACTT 3598
QY 3601 CGAGTGTGCTATTCTGTGGTTCATCGCCTTGAGCAGCATCGCCCTGGCTGTGAGGACCC 3660
Db 3599 CGAGTGTGCTATTCTGTGGTTCATCGCCTTGAGCAGCATCGCCCTGGCTGTGAGGACCC 3658
QY 3661 AGTGGCAGAGACTCGCCCGAGAAACAGCTCTGAAATACCTGGATACATTTTCACTGG 3720
Db 3659 AGTGGCAGAGACTCGCCCGAGAAACAGCTCTGAAATACCTGGATACATTTTCACTGG 3718
QY 3721 TGTCTTTACCTTTGAGATGGTGATAAAGATGATCGACTTGGGACTGTGCTTCAACCCTGG 3780
Db 3719 TGTCTTTACCTTTGAGATGGTGATAAAGATGATCGACTTGGGACTGTGCTTCAACCCTGG 3778
QY 3781 AGCCTATTTCCGGGACTTGTGGAACATTTCTGACTTCAATTTGCTCAGTGGCGCCCTGGT 3840
Db 3779 AGCCTATTTCCGGGACTTGTGGAACATTTCTGACTTCAATTTGCTCAGTGGCGCCCTGGT 3838
QY 3841 GSCGTTTCTTCTCGAGCTTCTGGGAGGATCCAAAGGGAAGACATCAATACATCAA 3900
Db 3839 GSCGTTTCTTCTC-----AGGATCCAAAGGGAAGACATCAATACATCAA 3886
QY 3901 GTCTCTGAGAGCTTCTGTGTCCTCGGCCCTCAAGACCATCAAAAGGCTGCCCAAGCT 3960
Db 3887 GTCTCTGAGAGCTTCTGTGTCCTCGGCCCTCAAGACCATCAAAAGGCTGCCCAAGCT 3946
QY 3961 CAAGGCTGTGTTGACTGTGTGGAATCTCGCTGAAGAAATGTCCTCAACATCTTTGATGT 4020
Db 3947 CAAGGCTGTGTTGACTGTGTGGAATCTCGCTGAAGAAATGTCCTCAACATCTTTGATGT 4006
QY 4021 CTACATGCTCTTCATGTTTCAATATTGTCGTCATTTGCGGTGAGCTCTTCAAGGGGAAGTT 4080
Db 4007 CTACATGCTCTTCATGTTTCAATATTGTCGTCATTTGCGGTGAGCTCTTCAAGGGGAAGTT 4066
QY 4081 TTTCTATGCGACAGATGAATCCAAAGGAGCTGAGAGGGAGCTGCAAGGGGTCAAGTATTTGGA 4140
Db 4067 TTTCTACTGCAAGATGAATCCAAAGGAGCTGAGAGGGAGCTGCAAGGGGTCAAGTATTTGGA 4126

QY 4141 TTATGAGAGGAGGAGTGGAGGCTCAGCCAGGAGCTGGAGAGAAATACGACTTTTCACTA 4200
Db 4127 TTATGAGAGGAGGAGTGGAGGCTCAGCCAGGAGCTGGAGAGAAATACGACTTTTCACTA 4186
QY 4201 CGACAAATGTCTCTGTGGGCTCTGCTGACGCTGTTCACAGTGTCCACGGGAGAGGCTGGCC 4260
Db 4187 CGACAAATGTCTCTGTGGGCTCTGCTGACGCTGTTCACAGTGTCCACGGGAGAGGCTGGCC 4246
QY 4261 CATGGTGTGMAAACATCTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4320
Db 4247 CATGGTGTGMAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4306
QY 4321 CCGCATGAGGTGTCATCTCTACGTGTCTACTTTTGGTCTTTTCCCTCTCTTCTTCTGT 4380
Db 4307 CCGCATGAGGTGTCATCTCTACGTGTCTACTTTTGGTCTTTTCCCTCTCTTCTTCTGT 4366
QY 4381 CAACATCTTTTGGCTTTTGATCATCATCTTCCAGGAGCAGGGGACAAAGTGTATGTC 4440
Db 4367 CAACATCTTTTGGCTTTTGATCATCATCTTCCAGGAGCAGGGGACAAAGTGTATGTC 4426
QY 4441 TGANTGAGCCTGGAGAGAAACGAGAGGGCTTGATTTGACTTCGCCATCAGCGCCAAACC 4500
Db 4427 TGAATGAGCCTGGAGAGAAACGAGAGGGCTTGATTTGACTTCGCCATCAGCGCCAAACC 4486
QY 4501 CCTGACACGGTACATGCCCCCAAAACCGGCAGTCGTTCCAGTATAAGACGTGACATTTGT 4560
Db 4487 CCTGACACGGTACATGCCCCCAAAACCGGCAGTCGTTCCAGTATAAGACGTGACATTTGT 4546
QY 4561 GGTCTCCCCGCCCTTTGAATACATTCATGCGCATGATAGCCCTCAACACTGTGTGTCT 4620
Db 4547 GGTCTCCCCGCCCTTTGAATACATTCATGCGCATGATAGCCCTCAACACTGTGTGTCT 4606
QY 4621 GATGATGAAGTCTTATGATGACACCTATGATGAGTACGAGCTGATCTGAAATCTGTAACAT 4680
Db 4607 GATGATGAAGTCTTATGATGACACCTATGATGAGTACGAGCTGATCTGAAATCTGTAACAT 4666
QY 4681 CGTGTTCACATCCATGTTCTCCATGGAATGCGTGTCTGAAGATCATCGCCTTTGGGGTGTCT 4740
Db 4667 CGTGTTCACATCCATGTTCTCCATGGAATGCGTGTCTGAAGATCATCGCCTTTGGGGTGTCT 4726
QY 4741 GAACATATTCAGAGATGCGCTGGAAATGCTTTGACTTTGTCTGCTGTTGGGAAAGTATTAC 4800
Db 4727 GAACATATTCAGAGATGCGCTGGAAATGCTTTGACTTTGTCTGCTGTTGGGAAAGTATTAC 4786
QY 4801 TGATATTTTAAACAGAGATTCGCGAAACGAAACAAATTTTCACTCAAGCTCAGCTTCCTCCG 4860
Db 4787 TGATATTTTAAACAGAGATTCGCGAAACGAAACAAATTTTCACTCAAGCTCAGCTTCCTCCG 4846
QY 4861 CCTCTTTTCGAGCTGCGCGCTGATCAAGCTGTCTCCGCGAGGCTACACCATCCGATCCT 4920
Db 4847 CCTCTTTTCGAGCTGCGCGCTGATCAAGCTGTCTCCGCGAGGCTACACCATCCGATCCT 4906
QY 4921 GCTGTGACCTTTGTCAGTCTCTTCAAGGCCCTGCCCTACGTTGTGTCTGCTCATTTGCCAT 4980
Db 4907 GCTGTGACCTTTGTCAGTCTCTTCAAGGCCCTGCCCTACGTTGTGTCTGCTCATTTGCCAT 4966
QY 4981 GCTGTTTCTTCATCTAGCCCATCATCGGCATGCAAGTGTTTGGGAAATTTGCGCTGATGA 5040
Db 4967 GCTGTTTCTTCATCTAGCCCATCATCGGCATGCAAGTGTTTGGGAAATTTGCGCTGATGA 5026
QY 5041 TGACACAGATCAACCGCCCAACAACTTCCGGACGTTTTTTCGAAGCCCTGATGCTGTCT 5100
Db 5027 TGACACAGATCAACCGCCCAACAACTTCCGGACGTTTTTTCGAAGCCCTGATGCTGTCT 5086
QY 5101 GTTCAGGAGGCCACGGGGAGGCTGGCACGAGATCATGCTGTCTGTCTGCTGAGCAACCA 5160
Db 5087 GTTCAGGAGGCCACGGGGAGGCTGGCACGAGATCATGCTGTCTGTCTGCTGAGCAACCA 5146
QY 5161 GGCCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTACTTTGCGCTACTTCTACTTT 5220
Db 5147 GGCCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTACTTTGCGCTACTTCTACTTT 5206
QY 5221 CGTCTCCTTCATCTTCTGTGTCTCTTTCTGATGTTGAACCTCTTTGTGTGGCTGTGATCAT 5280

Db	5207		CGTCTCCTTCAATCTTCTCTGTGTCCTTCTTCTGATGTTGAACCTCTTGTGGCTGTGATCAT	5266
Qy	5281		GGACAAATTTTGGTACCTTCACGGGGACTCTTTCATCTAGTCTCTCACACATTTGGATGA	5340
Db	5267		GGACAAATTTTGGTACCTTCACGGGGACTCTTTCATCTAGTCTCTCACACATTTGGATGA	5326
Qy	5341		GTTTCATCCGGTCTGGGCTGAATACGACCCTGGCTGGTGGTGGGCGCATCAGTTACAATGA	5400
Db	5327		GTTTCATCCGGTCTGGGCTGAATACGACCCTGGCTGGTGGTGGGCGCATCAGTTACAATGA	5386
Qy	5401		CATGTTTGAATGCTGAAACACATGTCCTGGCTCTGGGGCTGGGGAGAAATGCCCTGC	5460
Db	5387		CATGTTTGAATGCTGAAACACATGTCCTGGCTCTGGGGCTGGGGAGAAATGCCCTGC	5446
Qy	5461		TCGAGTTGCTTACAAGCGCTGGTTTCGATGAACATGCCATCTCCAAACGAGGACATGCAC	5520
Db	5447		TCGAGTTGCTTACAAGCGCTGGTTTCGATGAACATGCCATCTCCAAACGAGGACATGCAC	5506
Qy	5521		TGTTCACTTCACTGCTCAGCTGATGGCCCTCATCCGACCGGCACTGGAGATCAAGCTGGC	5580
Db	5507		TGTTCACTTCACTGCTCAGCTGATGGCCCTCATCCGACCGGCACTGGAGATCAAGCTGGC	5566
Qy	5581		CCGAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGGATTTCCGTTGT	5640
Db	5567		CCGAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGGATTTCCGTTGT	5626
Qy	5641		GTGGGCCAATCTGCCCCAGAAAGACTTTTGGACTTCTGTGATCCACCCCATAGCCCTGATGA	5700
Db	5627		GTGGGCCAATCTGCCCCAGAAAGACTTTTGGACTTCTGTGATCCACCCCATAGCCCTGATGA	5686
Qy	5701		GATGACAGTGGGGAAGTTTATGAGCTCTGATGATATTTGACTTCTACAAGCAGAAACAA	5760
Db	5687		GATGACAGTGGGGAAGTTTATGAGCTCTGATGATATTTGACTTCTACAAGCAGAAACAA	5746
Qy	5761		AACACACAGACACAGATGACGAGGCTCCTGGAGGCTCTCCAGATGGTCTGTGTGC	5820
Db	5747		AACACACAGACACAGATGACGAGGCTCCTGGAGGCTCTCCAGATGGTCTGTGTGC	5806
Qy	5821		CCTGTTCCACCCTCTGAAGGCCACCTTGAGCAGACACAGCCGCTGTCTCCAGGAGGC	5880
Db	5807		CCTGTTCCACCCTCTGAAGGCCACCTTGAGCAGACACAGCCGCTGTCTCCAGGAGGC	5866
Qy	5881		CCGGGTTTCTTTCGACAGAAAGTTTCACTCTCCTCAGCAATCGCGGGCCCATACAAA	5940
Db	5867		CCGGGTTTCTTTCGACAGAAAGTTTCCACCCTCCTCAGCAATCGCGGGCCCATACAAA	5926
Qy	5941		CCAAGAGATGGCATCAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC	6000
Db	5927		CCAAGAGATGGCATCAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC	5986
Qy	6001		CCATGAGGCCAGGCCACCTTGGAGCGTGGCCACTTCCACAGAGATCCTGTGGGGCGGTC	6060
Db	5987		CCATGAGGCCAGGCCACCTTGGAGCGTGGCCACTTCCACAGAGATCCTGTGGGGCGGTC	6046
Qy	6061		AGGAGCACTGGCTGTGACGTTTCAAGTGCAGAGCATAAACCGAGGGGCCCTGTATGGGGA	6120
Db	6047		AGGAGCACTGGCTGTGACGTTTCAAGTGCAGAGCATAAACCGAGGGGCCCTGTATGGGGA	6106
Qy	6121		GGCCAGCCTGGCTGTGAGACCCAGGTCGAGCGGCTCTCATGCCCGGCTTGGCGCCGA	6180
Db	6107		GGCCAGCCTGGCTGTGAGACCCAGGTCGAGCGGCTCTCATGCCCGGCTTGGCGCCGA	6166
Qy	6181		GACTCAGCCCTGCACAGATGCCAGCCCATCAAGCGTCTCCATCTCCAGCTGGGCCAGCG	6240
Db	6167		GACTCAGCCCTGCACAGATGCCAGCCCATCAAGCGTCTCCATCTCCAGCTGGGCCAGCG	6226
Qy	6241		GCCCGTGGGACTCATCTTTGACGACCAACCCCGGACCGCCACCCCTAGCCAGGCGTC	6300
Db	6227		GCCCGTGGGACTCATCTTTGACGACCAACCCCGGACCGCCACCCCTAGCCAGGCGTC	6286
Qy	6301		GTCCGACCAACCAACCAACCCCTGCGCACCGCGGACAGGAGCGAGGTCCTTGGGA	6360

RESULT 15
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Qy	1261	CCTGAAGCTGCGCGGACAGCAGATCGACGAGAGCTCAACGGGTACTTGAGTGGAT	1320
Db	1259	CCTGAAGCTGCGCGGACAGCAGATCGACGAGAGCTCAACGGGTACTTGAGTGGAT	1318
Qy	1321	CTTCAAGCGGAGGAGTCACTGCTGGCGGAGGAGCAGGAAATCGACGAGGAGTCCCC	1380
Db	1319	CTTCAAGCGGAGGAGTCACTGCTGGCGGAGGAGCAGGAAATCGACGAGGAGTCCCC	1378
Qy	1381	TTTGGACGTGTGAAGAGAGCGGCCACCAAGAGAGCAGAAATGACCTGATCCACGCAGA	1440
Db	1379	TTTGGACGTGTGAAGAGAGCGGCCACCAAGAGAGCAGAAATGACCTGATCCACGCAGA	1438
Qy	1441	GGAGGAGAGAACCGGTTTGAGATCTCTGTGCTGTGGATGCCCTTGGCCCGCGCAG	1500
Db	1439	GGAGGAGAGAACCGGTTTGAGATCTCTGTGCTGTGGATGCCCTTGGCCCGCGCAG	1498
Qy	1501	CCTCAAGAGCGGAGAGCAGAGAGCTCGTCATACTTCGGAGGAGAGAGATGTTCCG	1560
Db	1499	CCTCAAGAGCGGAGAGCAGAGAGCTCGTCATACTTCGGAGGAGAGAGATGTTCCG	1558
Qy	1561	GTTTTATCCGGCGCATGTGTAAAGGCTCAGAGCTTCTACTGGGTGTGCTGTGCTGGT	1620
Db	1559	GTTTTATCCGGCGCATGTGTAAAGGCTCAGAGCTTCTACTGGGTGTGCTGTGCTGGT	1618
Qy	1621	GGCCTGAACACACTGTGTGTGGCCATGGTGCATTTACAACAGCCGCGGGGCTTACCAC	1680
Db	1619	GGCCTGAACACACTGTGTGTGGCCATGGTGCATTTACAACAGCCGCGGGGCTTACCAC	1678
Qy	1681	GACCTGTATTTTCAGAGTTTGTTCCTGGGTCTCTCTCACAGAGATGCCCTGAA	1740
Db	1679	GACCTGTATTTTCAGAGTTTGTTCCTGGGTCTCTCTCACAGAGATGCCCTGAA	1738
Qy	1741	GATGTATGGCTGCGGCCACGAAGCTACTTCCGCTCTCTTCAACTGCTTCGACTTTGG	1800
Db	1739	GATGTATGGCTGCGGCCACGAAGCTACTTCCGCTCTCTTCAACTGCTTCGACTTTGG	1798
Qy	1801	GGTCATCGTGGGAGCGTCTTTGAAGTGGTCTGGCGGCCATCAAGCCGGGAAGCTCCTT	1860
Db	1799	GGTCATCGTGGGAGCGTCTTTGAAGTGGTCTGGCGGCCATCAAGCCGGGAAGCTCCTT	1858
Qy	1861	TGGGATCAGTGTGCTGGGGCCCTCCGCTCTCAGGATCTTCAAGTCAAGAGTACTG	1920
Db	1859	TGGGATCAGTGTGCTGGGGCCCTCCGCTCTCAGGATCTTCAAGTCAAGAGTACTG	1918
Qy	1921	GAGCTCCTCGGAACTGTGTGTGCTCCTGCTGAACTTCAATGAAGTCCATCATCAGCT	1980
Db	1919	GAGCTCCTCGGAACTGTGTGTGCTCCTGCTGAACTTCAATGAAGTCCATCATCAGCT	1978
Qy	1981	GCTCTTCTGCTCTTCTGTTTCATTTGTGGTCTTCGCCCTGCTGGGGATGAGCTGTTGG	2040
Db	1979	GCTCTTCTGCTCTTCTGTTTCATTTGTGGTCTTCGCCCTGCTGGGGATGAGCTGTTGG	2038
Qy	2041	GGGACAGTTCAACTTCCAGATGAGATCCCAACAACTTCGACACCTTCCCTGCCGC	2100
Db	2039	GGGACAGTTCAACTTCCAGATGAGATCCCAACAACTTCGACACCTTCCCTGCCGC	2098
Qy	2101	CATCCTCACTGTCTTCCAGATCTCGAGGGAGGACTTGAATCGAGTGATATCACGG	2160
Db	2099	CATCCTCACTGTCTTCCAGATCTCGAGGGAGGACTTGAATCGAGTGATATCACGG	2158
Qy	2161	GATCGAATTCGAAGCGGCGTCAGCAAGGCAATGTTCTCGTCTCTTTTACTTCAATGTCT	2220
Db	2159	GATCGAATTCGAAGCGGCGTCAGCAAGGCAATGTTCTCGTCTCTTTTACTTCAATGTCT	2218
Qy	2221	GACACTGTTCCGAACTACACTCTGCTGAATGTCTTTCTGGCCATCGCTGTGGCAACCT	2280
Db	2219	GACACTGTTCCGAACTACACTCTGCTGAATGTCTTTCTGGCCATCGCTGTGGCAACCT	2278
Qy	2281	GGCCAAACCGCCAGAGCTGACCAAGGATGAAGAGAGATGGAAGACGACCAATCAGAA	2340
Db	2279	GGCCAAACCGCCAGAGCTGACCAAGGATGAAGAGAGATGGAAGACGACCAATCAGAA	2338

Qy	2341	GCTTGTCTTCGAAAAAGCCAAAGAGTGGCTGAAGTCAGCCCCATGTCTGCGCGGAACAT	2400
Db	2339	GCTTGTCTTCGAAAAAGCCAAAGAGTGGCTGAAGTCAGCCCCATGTCTGCGCGGAACAT	2398
Qy	2401	CTCCATCGCGCGCAGGACAGCAACTCGGCCAAAGCGCGCTCGGTGTGGAGACGCGGGC	2460
Db	2399	CTCCATCGCGCGCAGGACAGCAACTCGGCCAAAGCGCGCTCGGTGTGGAGACGCGGGC	2458
Qy	2461	CAGCCAGTACGGCTGCAGAACTTCGGGGCCAGCTTCGAGGCGCTGTATCAGCGAGATGGA	2520
Db	2459	CAGCCAGTACGGCTGCAGAACTTCGGGGCCAGCTTCGAGGCGCTGTATCAGCGAGATGGA	2518
Qy	2521	CCCGAGGAGCGCTGGCTTCGCCACTACGCGCACCTCTCGGCGCCGACATGAAGACGCA	2580
Db	2519	CCCGAGGAGCGCTGGCTTCGCCACTACGCGCACCTCTCGGCGCCGACATGAAGACGCA	2578
Qy	2581	CCTGGACCGGCGCTGTGTGTGGAGCTGGGCGCGAGCGCGCGGGGCGCGTGGGAGG	2640
Db	2579	CCTGGACCGGCGCTGTGTGTGGAGCTGGGCGCGAGCGCGCGGGGCGCGTGGGAGG	2638
Qy	2641	CAAAAGCCCGACCTGAGGCTTCGGAGGCGCCCGGAGGCGTTCGACCTCTCGCGCAGGACCA	2700
Db	2639	CAAAAGCCCGACCTGAGGCTTCGGAGGCGCCCGGAGGCGTTCGACCTCTCGCGCAGGACCA	2698
Qy	2701	CCGCGACCGCGCAAAAGCAAAAGACCCCGCGCGGGGACACAGAACCGAGAGAGGCCCC	2760
Db	2699	CCGCGACCGCGCAAAAGCAAAAGACCCCGCGCGGGGACACAGAACCGAGAGAGGCCCC	2758
Qy	2761	GAAGGCGGAGAGCGGGAGCGCCGCTGCGCGGAGGAGCGCGCGCGCGCACCGCAGCACA	2820
Db	2759	GAAGGCGGAGAGCGGGAGCGCCGCTGCGCGGAGGAGCGCGCGCGCGCACCGCAGCACA	2818
Qy	2821	CAGCAAGAGAGCGCGGGCGCCCGGAGGCGCGAGCGAGCGCGCGCGCCAGGCCCC	2880
Db	2819	CAGCAAGAGAGCGCGGGCGCCCGGAGGCGCGAGCGAGCGCGCGCGCCAGGCCCC	2878
Qy	2881	CGAGGCGCGCGCGCGGCAACAACCGCGCGGCTCCCGGAGGAGCGCGCGCGCGGAGCC	2940
Db	2879	CGAGGCGCGCGCGCGGCAACAACCGCGCGGCTCCCGGAGGAGCGCGCGCGCGGAGCC	2938
Qy	2941	CCGACGCCACCGCGCGCACCGCGCACCAAGGATCCGAGCAAGAGTGTGCGCGCGCGCAGGG	3000
Db	2939	CCGACGCCACCGCGCGCACCGCGCACCAAGGATCCGAGCAAGAGTGTGCGCGCGCGCAGGG	2998
Qy	3001	CGAGCGCGCGCGCGGCAACAACCGCGCGGCGCCCGGAGGCGCGCGCGCGCGGAGCGG	3060
Db	2999	CGAGCGCGCGCGCGGCAACAACCGCGCGGCGCCCGGAGGCGCGCGCGCGGAGCGG	3058
Qy	3061	GGAGGAGCGCGCGCGGCAACAACCGCGCGGCGCAACAAGCGCAGCTGCTCACGAGGCTGT	3120
Db	3059	GGAGGAGCGCGCGCGGCAACAACCGCGCGGCGCAACAAGCGCAGCTGCTCACGAGGCTGT	3118
Qy	3121	GGAGAGGAGACCAACCGAGAGGAGGAGCCACGAGAGAGGAGGCTGAGATAGTGGAGCCGA	3180
Db	3119	GGAGAGGAGACCAACCGAGAGAGGAGGAGCCACGAGAGAGGAGGCTGAGATAGTGGAGCCGA	3178
Qy	3181	CAAGGAAAAGAGAGCTCCGGAAACCAACAGCGCCCGGAGGCCACACTGTGACCTCGAGACCG	3240
Db	3179	CAAGGAAAAGAGAGCTCCGGAAACCAACAGCGCCCGGAGGCCACACTGTGACCTCGAGACCG	3238
Qy	3241	TGGGACTGTGACTGTGGGTCCCATGCAACAATGCCCCAGCACTGTCTCCAGAAAGTGGGA	3300
Db	3239	TGGGACTGTGACTGTGGGTCCCATGCAACAATGCCCCAGCACTGTCTCCAGAAAGTGGGA	3298
Qy	3301	GGAAACCGCAGAGATGACAGCAATCAGCGGAACGTCATCGCATGGGAGTCCAGGCCCC	3360
Db	3299	GGAAACCGCAGAGATGACAGCAATCAGCGGAACGTCATCGCATGGGAGTCCAGGCCCC	3358
Qy	3361	AGACCCCGAACACTATTGTATCATATCCAGTGTGAGCGGGCCCTCTTGGGGAAGCCAC	3420
Db	3359	AGACCCCGAACACTATTGTATCATATCCAGTGTGAGCGGGCCCTCTTGGGGAAGCCAC	3418
Qy	3421	GGTCTTCCAGTGGTAAAGTGGACCTGGGAAAGCCAAAGCAGAGGGGGAAGAGGTTGGA	3480

Db 3419 GGTCTGTTCCAGTGTAAAGTGGAGCTGGAAGAGCGGTGGA 3478
QY 3481 AGCGGATGACGTGATGAGAGGGGCCCCGGGCTATCGTCCCATACAGCTCCATGTTCTG 3540
Db 3479 AGCGGATGACGTGATGAGAGGGGCCCCGGGCTATCGTCCCATACAGCTCCATGTTCTG 3538
QY 3541 TTTAAGCCCAACCAACTGCTCGCGCGCTTCTGCCACTACATCGTGACCATGAGGTACTT 3600
Db 3539 TTTAAGCCCAACCAACTGCTCGCGCGCTTCTGCCACTACATCGTGACCATGAGGTACTT 3598
QY 3601 CGAGGTGTCATTTCTCGTGGTCAATGCGCTTGAGAGAGCATGCGCCCTGGCTGCTGAGGAGCC 3660
Db 3599 CGAGGTGTCATTTCTCGTGGTCAATGCGCTTGAGAGAGCATGCGCCCTGGCTGCTGAGGAGCC 3658
QY 3661 AGTGGSCACAGACTCGCCCAAGAACAAAGCTCTGAAATACCTGGATTAATTTTCACTGG 3720
Db 3659 AGTGGSCACAGACTCGCCCAAGAACAAAGCTCTGAAATACCTGGATTAATTTTCACTGG 3718
QY 3721 TGTCTTTTACCTTTGAGATGGTGAATAAGATGATCGACTTTGGGACTGCTGCTTCAACCCTGG 3780
Db 3719 TGTCTTTTACCTTTGAGATGGTGAATAAGATGATCGACTTTGGGACTGCTGCTTCAACCCTGG 3778
QY 3781 AGCCTATTTCCGGGACTTGTGGAACATTTCTGAGCTTTCATTTGCTGAGTGGCGCCCTGGT 3840
Db 3779 AGCCTATTTCCGGGACTTGTGGAACATTTCTGAGCTTTCATTTGCTGAGTGGCGCCCTGGT 3838
QY 3841 GCGCTTTGCTTCTCGAGCTTCGTGGGAGATCCAAAGGGAAGACATCAATACCATCAA 3900
Db 3839 GCGCTTTGCTTCTC-----AGGATCCAAAGGGAAGACATCAATACCATCAA 3886
QY 3901 GTCTCTGAGAGTCCCTTGTGCTCGGGCCCCCTCAAGACCATCAACGGCTGCCCAAGCT 3960
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QY 3961 CAAAGCTGTGTTGACTGTGCTGGAACATTCCTCTGAAGAAATGTCCTCAACATCTTGATTTGT 4020
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OM nucleic - nucleic search, using sw model

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	7342	99.5	7364	4	US-09-268-163-5
3	7316.4	99.2	7362	1	US-08-455-543A-7
4	7316.4	99.2	7362	2	US-08-193-078B-7
5	7316.4	99.2	7362	2	US-08-223-305C-7
6	7316.4	99.2	7362	2	US-08-149-097D-7
7	7316.4	99.2	7362	3	US-08-949-386-7
8	7316.4	99.2	7362	3	US-08-450-562-7
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ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 60/077,901
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7376
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..7174
US-09-268-163-3

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Matches 7376;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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RESULT 2
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; Sequence 5, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER FILING DATE: 1998-03-12
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 7364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..7162
US-09-268-163-5

Query Match          99.5%; Score 7342; DB 4; Length 7364;
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Matches 7364; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

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RESULT 3

US-08-455-543A-7
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; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6362-52517
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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US-08-455-543A-7

Query Match 99.2%; Score 7316.4; DB 1; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

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Db 599 GGCCTTTGCTCTTCCAAAGGGCTCTTACTGCGGAAACGGCTGGAAAGTTCATGAGCTTCGT 658
Qy |||||
Db 661 GGTGCTCTCACAGGGATCTTCGCGAGCTGGAACCTGACTTCGACTCGACTCGGAACTGAG 720
Qy |||||
Db 659 GGTGCTCTCACAGGGATCTTCGCGAGCTGGAACCTGACTTCGACTCGGAACTGAG 718
Qy |||||
Db 721 GGTGCTGCGTGTCTGAGGCGCTTGAAGCTGTGTCTGGGATTCGAAGTTTGAGGTTGTT 780
Qy |||||
Db 719 GGTGCTGCGTGTCTGAGGCGCTTGAAGCTGTGTCTGGGATTCGAAGTTTGAGGTTGTT 778
Qy |||||
Db 781 GCTCAAGTCCATCATGAAGGCCATGGTTCCATCTCTCGAGATTTGGGCTGCTTCTTCTTT 840
Qy |||||
Db 779 GCTCAAGTCCATCATGAAGGCCATGGTTCCATCTCTCGAGATTTGGGCTGCTTCTTCTTT 838
Qy |||||
Db 841 TGCATCTCTCATGTTTGGCATCATTTGGCTGGAGTTCTACATGGGCAAGTTCCACAGGC 900
Qy |||||
Db 839 TGCATCTCTCATGTTTGGCATCATTTGGCTGGAGTTCTACATGGGCAAGTTCCACAGGC 898
Qy |||||
Db 901 CTGTTTCCCCAACAGCACAGATCGGAGCCCTGGGTGACTTCCCTCTGGCAGGAGGC 960
Qy |||||
Db 899 CTGTTTCCCCAACAGCACAGATCGGAGCCCTGGGTGACTTCCCTCTGGCAGGAGGC 958
Qy |||||
Db 961 CCAGCCCGGCTGTCGAGGGCGACACTGAGTCCCGGAGTACTGCGCAGGACCCAACTT 1020
Qy |||||
Db 959 CCAGCCCGGCTGTCGAGGGCGACACTGAGTCCCGGAGTACTGCGCAGGACCCAACTT 1018
Qy |||||
Db 1021 TGGCATCAACCACTTTGACAAATCTCTGTTTGGCATCTTTCAGCGTGTTCAGTGCATCAC 1080
Qy |||||
Db 1019 TGGCATCAACCACTTTGACAAATCTCTGTTTGGCATCTTTCAGCGTGTTCAGTGCATCAC 1078
Qy |||||
Db 1081 CATGGAGGGCTGACTGACATCTCTATATAAACAAGATCGCGCGGCAACACCTGGAA 1140
Qy |||||
Db 1079 CATGGAGGGCTGACTGACATCTCTATATAAACAAGATCGCGCGGCAACACCTGGAA 1138
Qy |||||
Db 1141 CTGGCTCTACTTCACTCTCATCATCATCGGCTCTTCTTTCATGCTCAACCTGTTGCT 1200
Qy |||||
Db 1139 CTGGCTCTACTTCACTCTCATCATCATCGGCTCTTCTTTCATGCTCAACCTGTTGCT 1198
Qy |||||
Db 1201 GGGCGTGTCTCGGGGAGTTTCCGAGGAGCGAGAGGGTGGAGAACCGCGCGCGCTT 1260
Qy |||||
Db 1199 GGGCGTGTCTCGGGGAGTTTCCGAGGAGCGAGAGGGTGGAGAACCGCGCGCGCTT 1258
Qy |||||
Db 1261 CTTGAAGCTCGCGCGCAGCAGATCGAGCGAGAGCTCAACGGGTACTCTGGAGTGGAT 1320
Qy |||||
Db 1259 CTTGAAGCTCGCGCGCAGCAGATCGAGCGAGAGCTCAACGGGTACTCTGGAGTGGAT 1318
Qy |||||
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Qy |||||
Db 1319 CTTCAAGGCGGAGAAAGTCACTGCTGCGCAGGAGGACAGAAATGCAAGAGAGAAAGTCCCC 1378
Qy |||||
Db 1381 TTTGAGAGTCTGAGAGAGCGGCGCAACAGAGAGCAGAAATGACCTGATCCACGCGAGA 1440
Qy |||||

Db 1379 TTTGGACGTCTGAAGAGAGCGGCCACCAAGAAAGACAGAAATGACCTCGATCCACGCAGA 1438
Qy 1441 GGAGGGAGAGACCGGTTTTCAGATCTCTGTGCTGTTGGATCCCTTCGCGCGCCAG 1500
Db 1439 GGAGGGAGAGACCGGTTTTCAGATCTCTGTGCTGTTGGATCCCTTCGCGCGCCAG 1498
Qy 1501 CCTCAAGAGCGGAAGAAGAGAGCTCGTCAATCTTCCGAGGAAGGAAGATGTTCCG 1560
Db 1499 CCTCAAGAGCGGAAGAAGAGAGCTCGTCAATCTTCCGAGGAAGGAAGATGTTCCG 1558
Qy 1561 GTTTTATTCGCGGATGCTGAAGCTCAGAGCTTCTAAGTGGTGGTCTGTGGTGGT 1620
Db 1559 GTTTTATTCGCGGATGCTGAAGCTCAGAGCTTCTAAGTGGTGGTCTGTGGTGGT 1618
Qy 1621 GGCCCTGAACACACTGTGTGGCCATGTGTGCAATACAAACGAGCGCGGCTTACCAAC 1680
Db 1619 GGCCCTGAACACACTGTGTGGCCATGTGTGCAATACAAACGAGCGCGGCTTACCAAC 1678
Qy 1681 GACCTGTATTTGACAGATGTTGTTTCTGGGTCTCTTCTCACAGAGATGTCCTGAA 1740
Db 1679 GACCTGTATTTGACAGATGTTGTTTCTGGGTCTCTTCTCACAGAGATGTCCTGAA 1738
Qy 1741 GATGATATGCTGGGCGCCAGAGCTACTTCCGCTCTCTTCAACTGCTTCGACTTTGG 1800
Db 1739 GATGATATGCTGGGCGCCAGAGCTACTTCCGCTCTCTTCAACTGCTTCGACTTTGG 1798
Qy 1801 GGTATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCCATCAAGCGGGAGCTCCTT 1860
Db 1799 GGTATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCCATCAAGCGGGAGCTCCTT 1858
Qy 1861 TGGGATCAGTGTCTGGGCGCCCTCGCTGTGAGGATCTTTCAAAGTCAAGAACTAG 1920
Db 1859 TGGGATCAGTGTCTGGGCGCCCTCGCTGTGAGGATCTTTCAAAGTCAAGAACTAG 1918
Qy 1921 GAGCTCCCTCGGAACCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 1919 GAGCTCCCTCGGAACCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1978
Qy 1981 GCTCTTCTGCTCTTCTGCTTCAATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Db 1979 GCTCTTCTGCTCTTCTGCTTCAATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2038
Qy 2041 GGGACAGTTCAACTTCCAGGATGAGCTCCCAACCAACCACTTCCGACCTTCCCTGCGGC 2100
Db 2039 GGGACAGTTCAACTTCCAGGATGAGCTCCCAACCAACCACTTCCGACCTTCCCTGCGGC 2098
Qy 2101 CATCTCTACTGTTCCAGATCCTGACCGGAGAGACTGGAAATGCAGTGAATGATCAAGG 2160
Db 2099 CATCTCTACTGTTCCAGATCCTGACCGGAGAGACTGGAAATGCAGTGAATGATCAAGG 2158
Qy 2161 GATCGAATCGCAAGCGGCGTCAAGAAAGGATGTTCTGCTCTTTTACTTCAATGTCCT 2220
Db 2159 GATCGAATCGCAAGCGGCGTCAAGAAAGGATGTTCTGCTCTTTTACTTCAATGTCCT 2218
Qy 2221 GACACTGTTGGAACTACACTCTGCTGAATGCTTTCTGCGCCATCGTGTGGACAACT 2280
Db 2219 GACACTGTTGGAACTACACTCTGCTGAATGCTTTCTGCGCCATCGTGTGGACAACT 2278
Qy 2281 GGCACACCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGAAGCAGCCAACTCAGAA 2340
Db 2279 GGCACACCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGAAGCAGCCAACTCAGAA 2338
Qy 2341 GCTTGTCTTGCAAAAGGCCAAGAGTGGCTGAAGTCAAGCCCAATGTTGCGCGCAACAT 2400
Db 2339 GCTTGTCTTGCAAAAGGCCAAGAGTGGCTGAAGTCAAGCCCAATGTTGCGCGCAACAT 2398
Qy 2401 CTCAATCGCGCCAGCAGCAACTCGGCCAAGCGCGCTCGGTGGGAGAGCGGCG 2460
Db 2399 CTCAATCGCGCCAGCAGCAACTCGGCCAAGCGCGCTCGGTGGGAGAGCGGCG 2458
Qy 2461 CAGCCAGCTACGGCTGCAAGAACTGCGGCGCAGCTGCGAGCGCTGTACAGCGAGATGGA 2520
Db 2459 CAGCCAGCTACGGCTGCAAGAACTGCGGCGCAGCTGCGGCGCAGCTGTACAGCGAGATGGA 2518

Qy 2521 CCCGAGGAGCGGCTGCGCTTTCGCCACTA CCGGCCA CCGTGGCGCCCGACATGAAGACGA 2580
Db 2519 CCCGAGGAGCGGCTGCGCTTTCGCCACTA CCGGCCA CCGTGGCGCCCGACATGAAGACGA 2578
Qy 2581 CCTCGACCGGCGCTGCTGTTGGAGCTGGGCGAGCGGCGCGCGGGGCCCGTGGGAGG 2640
Db 2579 CCTCGACCGGCGCTGCTGTTGGAGCTGGGCGAGCGGCGCGGGGGGCCCGTGGGAGG 2638
Qy 2641 CAAAGCCCGACCTTGAGCTCGGAGGCCCCCGAGGGCTCGACCTCCGCGAGGACCA 2700
Db 2639 CAAAGCCCGACCTTGAGCTCGGAGGCCCCCGAGGGCTCGACCTCCGCGAGGACCA 2698
Qy 2701 CCGGACCGGAGCAAGACCAAGACCCCGCGCGGGGAGCAGACCGAGAGAGGCC 2760
Db 2699 CCGGACCGGAGCAAGACCAAGACCCCGCGCGGGGAGCAGACCGAGAGGCC 2758
Qy 2761 GAAGCGGAGAGCGGAGCGCCGCTGCCCGGAGAGCGCGCGCGCCAGCAGCCA 2820
Db 2759 GAAGCGGAGAGCGGAGCGCCGCTGCCCGGAGAGCGCGCGCGCCAGCAGCCA 2818
Qy 2821 CAGCAAGAGAGCGCGGGGCCCGCGAGGCGCGAGCGCGCGCGCCAGGCCAGGCC 2880
Db 2819 CAGCAAGAGAGCGCGGGGCCCGCGAGGCGCGAGCGAGCGCGCGCCAGGCCAGGCC 2878
Qy 2881 CGAGGGCGCGCGGCGCACCGCGCACCGAGGCTCCCGAGGAGCGCGCGCGCGGCCAGGCC 2940
Db 2879 CGAGGGCGCGCGGCGCACCGCGCGCACCGAGGCTCCCGAGGAGCGCGCGCGGCCAGGCC 2938
Qy 2941 CCGACGCCACCGCGCGCACCGCGCACCGAGATCCGAGCAAGAGTGGCGCGCCCAAGGG 3000
Db 2939 CCGAGGCCACCGCGCGCACCGCGCACCGAGATCCGAGCAAGAGTGGCGCGCCCAAGGG 2998
Qy 3001 CGAGCGCGCGCGGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGCGG 3060
Db 2999 CGAGCGCGCGCGGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGCGG 3058
Qy 3061 GGAGGAGCGCGCGCGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGCGT 3120
Db 3059 GGAGGAGCGCGCGCGCGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 3118
Qy 3121 GGAGAGAGAGACCA CCGAGAGAGAGCGCCACCGAGAGAGGAGGCTGAGATAGTGAAGCCGA 3180
Db 3119 GGAGAGAGAGACCA CCGAGAGAGAGCGCCACCGAGAGAGGAGGCTGAGATAGTGAAGCCGA 3178
Qy 3181 CAAGGAAAAGGAGCTCCGGAA CCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAG 3240
Db 3179 CAAGGAAAAGGAGCTCCGGAA CCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAG 3238
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Db 3239 TGGGACTGTGACTGTGGTCCCATG CACACACTGCCCGAGCAGCTGTCTCCAGAGGTGA 3298
Qy 3301 GGNACAGCCAGAGGATG CAGACATCAGCGGAAGCTCACTCGGATGGGCAFTCAGGCCCC 3360
Db 3299 GGAACAGCCAGAGGATG CAGACATCAGCGGAAGCTCACTCGGATGGGCAFTCAGGCCCC 3358
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Db 3359 AGACCCGAAACATATTGTACATAT CCGAGTGTCTGAGCGGCGCTTCTGGGGAAGCCAC 3418
Qy 3421 GGTCTGTCCAGTGTGTAACTGTGA CCGTGGAAAGCCAAAGCAGAGGGGAAGAGAGGTGA 3480
Db 3419 GGTCTGTCCAGTGTGTAACTGTGA CCGTGGAAAGCCAAAGCAGAGGGGAAGAGAGGTGA 3478
Qy 3481 AGCGGATGAGCTGATGAGAGCGCGCGCGCGCTTCTCCCATACAGCTCATGTTCTG 3540
Db 3479 AGCGGATGAGCTGATGAGAGCGCGCGCGCGCTTCTCCCATACAGCTCATGTTCTG 3538
Qy 3541 TTTAAGCCCCCAACCTGCTCCGCGGCTTCTGCGCACTACATCGTGACCAATGAGGTACTT 3600
Db 3539 TTTAAGCCCCCAACCTGCTCCGCGGCTTCTGCGCACTACATCGTGACCAATGAGGTACTT 3598

QY 3601 CGAGGTGGTCAATTCGTGGTCAATCGCTTGAGCAGCATCGCCCTGGCTGCTGAGGAGCCC 3660
Db 3599 CGAGGTGGTCAATTCGTGGTCAATCGCTTGAGCAGCATCGCCCTGGCTGCTGAGGAGCCC 3658
QY 3661 AGTGGCAGACAGACTCGGCCAGGAACAACGCTCTCAAAATACCTGATTTACATTTTCACTGG 3720
Db 3659 AGTGGCAGACAGACTCGGCCAGGAACAACGCTCTCAAAATACCTGATTTACATTTTCACTGG 3718
QY 3721 TGTCTTTACCTTTGAGATGGTGATPAAAGATGATCGACTTGGGACTGCTGCTTCAACCTGG 3780
Db 3719 TGTCTTTACCTTTGAGATGGTGATPAAAGATGATCGACTTGGGACTGCTGCTTCAACCTGG 3778
QY 3781 AGCCTATTTCCGGACATGTGGAAACATTTGGACTTCATTTGTGTGAGTGGCGCCCTGGT 3840
Db 3779 AGCCTATTTCCGGACATTTGGAAACATTTGGACTTCATTTGTGTGAGTGGCGCCCTGGT 3838
QY 3841 GGCCTTTGCTTTTCFCGAGCTTTCGTGGAGGATCAAAGGGAAGACATCAATACCATCAA 3900
Db 3839 GGCCTTTGCTTTTCFC-----AGGATCCAAAGGGAAGACATCAATACCATCAA 3886
QY 3901 GTCTCTGAGAGTCCCTTGGTGTCTGTGCGGCCCTCAAGACCATCAAAAGGCTGCCAAAGCT 3960
Db 3887 GTCTCTGAGAGTCCCTTGGTGTCTGTGCGGCCCTCAAGACCATCAAAAGGCTGCCAAAGCT 3946
QY 3961 CAAGGCTGTGTGATCTGTGTGTGAACTCCCTGAAGAAATGTCTCAACATCTTGATTTGT 4020
Db 3947 CAAGGCTGTGTGATCTGTGTGTGAACTCCCTGAAGAAATGTCTCAACATCTTGATTTGT 4006
QY 4021 CTACATGCTCTTCAATGTTTCAATTTGCGTCAATTTGCGGTGAGCTCTTCAAAAGGGAAGTT 4080
Db 4007 CTACATGCTCTTCAATGTTTCAATTTGCGTCAATTTGCGGTGAGCTCTTCAAAAGGGAAGTT 4066
QY 4081 TTTCTACTGCAAGATGAATCAAAGGAGCTGGAGAGGAGCTGCAAGGGTCAAGTATTTTGA 4140
Db 4067 TTTCTACTGCAAGATGAATCAAAGGAGCTGGAGAGGAGCTGCAAGGGTCAAGTATTTTGA 4126
QY 4141 TTATGAGAAGGAGAAGTGGAGCTCAGCCAGCAGTGGAGAAATACAGATTTTCACTA 4200
Db 4127 TTATGAGAAGGAGAAGTGGAGCTCAGCCAGCAGTGGAGAAATACAGATTTTCACTA 4186
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Db 4187 CGACAAATGTCTGGGCTCTGTGAGCTGTGTTCAAGTGTCCACGGGAGAGGCTGGCC 4246
QY 4261 CATGGTGTGAAAACACTCCGTGGATGCCACCTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4320
Db 4247 CATGGTGTGAAAACACTCCGTGGATGCCACCTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4306
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Db 4307 CCGCATGGAGCTGTCCATCTTACGTGGTCTACTTTGTGGTCTTTCCCTTCTTCTTCGT 4366
QY 4381 CAACATCTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGACAGGTGATGTC 4440
Db 4367 CAACATCTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGACAGGTGATGTC 4426
QY 4441 TGAATGAGCTCGAGAGAAACAGAGGGCTTGCATTTGACTTCCCATCAGCGCCAAACC 4500
Db 4427 TGAATGAGCTCGAGAGAAACAGAGGGCTTGCATTTGACTTCCCATCAGCGCCAAACC 4486
QY 4501 CCTGACACGGTACATGCCAAAACCGGCACTGCTTCCAGTATTAAGACGTGGACATTTGT 4560
Db 4487 CCTGACACGGTACATGCCAAAACCGGCACTGCTTCCAGTATTAAGACGTGGACATTTGT 4546
QY 4561 GGTCTCCCGCCCTTTGAATCTTCAATGCGCCATGATGCCCTCAACCTGTGGTGTCT 4620
Db 4547 GGTCTCCCGCCCTTTGAATCTTCAATGCGCCATGATGCCCTCAACCTGTGGTGTCT 4606
QY 4621 GATGATGAAGTCTTATGATGACCCCTATGAGTACGAGCTGATGCTGAAATGCCCTGAACAT 4680
Db 4607 GATGATGAAGTCTTATGATGACCCCTATGAGTACGAGCTGATGCTGAAATGCCCTGAACAT 4666
QY 4681 CGTGTTCACATCCATGTTTCTCCATGGAAATGCGTGTGAAAGATCAATCGCCTTTGGGGTGTCT 4740

Db 4667 CGTGTTCACATCCATGTTTCTCCATGGAATCGGTGCTGGAAGATCAATCGCCCTTTGGGGTGTCT 4726
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Db 4727 GAACCTATTTTTCAGAGATGCTCGGAATGCTTTTGAATTTGTCACTGTGTGGGAAGTATTAC 4786
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QY 4861 CCTCTTTCGAGCTGCGCGCTGATCAAGCTGCTCCGCCAGGGCTACACCATCCGCACTCT 4920
Db 4847 CCTCTTTCGAGCTGCGCGCTGATCAAGCTGCTCCGCCAGGGCTACACCATCCGCACTCT 4906
QY 4921 GCTGTGGACCTTTGTCCAGTCTTCAAGGCCCTGCCCTACGTGTGTCTCATTTGTCATTTGCCAT 4980
Db 4907 GCTGTGGACCTTTGTCCAGTCTTCAAGGCCCTGCCCTACGTGTGTCTCATTTGTCATTTGCCAT 4966
QY 4981 GCTGTCTTTCATCTACGCCATCAATCGGCATGCGAGGTGTTTGGGAATATTGCCCTGAGATGA 5040
Db 4967 GCTGTCTTTCATCTACGCCATCAATCGGCATGCGAGGTGTTTGGGAATATTGCCCTGAGATGA 5026
QY 5041 TGACACAGCATCAACCGGCCACAACTTCCGGAAGTTCGAGCCCTGATGCTGTCT 5100
Db 5027 TGACACAGCATCAACCGGCCACAACTTCCGGAAGTTCGAGCCCTGATGCTGTCT 5086
QY 5101 GTTCAGGAGCGCCACCGGGGAGGCTTGGCACGAGATCATGCTGTCTGCTGAGCAACCA 5160
Db 5087 GTTCAGGAGCGCCACCGGGGAGGCTTGGCACGAGATCATGCTGTCTGCTGAGCAACCA 5146
QY 5161 GGCTGTGTATGAGCAGGCGCAATGCCACCGAGTGTGGAAGTGAATTTGCCCTACTTCTACTT 5220
Db 5147 GGCTGTGTATGAGCAGGCGCAATGCCACCGAGTGTGGAAGTGAATTTGCCCTACTTCTACTT 5206
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Db 5207 CGTCTCTTTCATCTTCTGTGCTCTTCTGTGATGTTGAACTCTTGTGTGCTGTGATCAT 5266
QY 5281 GGAACAAATTTTGAATCACTCACCGGGAAGTCTTCCATCTCTAGGTCTTCCACCATTTGGATGA 5340
Db 5267 GGAACAAATTTTGAATCACTCACCGGGAAGTCTTCCATCTCTAGGTCTTCCACCATTTGGATGA 5326
QY 5341 GTTCATCCGGCTCTGGCTGGAATACGACCGGCTGCTGTGGGCGCATAGTTACAATGA 5400
Db 5327 GTTCATCCGGCTCTGGCTGGAATACGACCGGCTGCTGTGGGCGCATAGTTACAATGA 5386
QY 5401 CATGTTTGAATGCTGAAAACAGATGTCGCGCTCTGGGCTGGGGAAGAAATGCCCTGC 5460
Db 5387 CATGTTTGAATGCTGAAAACAGATGTCGCGCTCTGGGCTGGGGAAGAAATGCCCTGC 5446
QY 5461 TCGAGTTTGTCTTACAAGCGCTGTTTCGATGAACATGCCCCATCTCCAACGAGGACATGAC 5520
Db 5447 TCGAGTTTGTCTTACAAGCGCTGTTTCGATGAACATGCCCCATCTCCAACGAGGACATGAC 5506
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Db 5507 TGTTCATCTTCACGTCCAAGTGTGCGCTTCAATCCGGAACGGCACTGAGATCAAGCTGGC 5566
QY 5581 CCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGGAGATTTCCGTTGT 5640
Db 5567 CCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGGAGATTTCCGTTGT 5626
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Db 5807 CTTGTTCCACCTCTGAAGCCACCTGGAGACAGACAGCCGGCTGTCTCCGAGGAGC 5866
Qy 5881 CCGGGTTTCTCTCGACAGAGAGTTTCCACCTCCCTCAGCAATGGGGGGCCATACAAAA 5940
Db 5867 CCGGGTTTCTCTCGACAGAGAGTTTCCACCTCCCTCAGCAATGGGGGGCCATACAAAA 5926
Qy 5941 CCAAGAGAGTGGATCAAGAGTCTGTCTCTGGGGCACTCAAGAGACCCAGAGTGCACC 6000
Db 5927 CCAAGAGAGTGGATCAAGAGTCTGTCTCTGGGGCACTCAAGAGACCCAGAGTGCACC 5986
Qy 6001 CCATGAGGCCAGGCCACCCCTGAGAGCTGGCCACTCCACAGAGATCCCTGTGGGGGGGTC 6060
Db 5987 CCATGAGGCCAGGCCACCCCTGAGAGCTGGCCACTCCACAGAGATCCCTGTGGGGGGGTC 6046
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Qy 6121 GCCCAGCCTGGCTGGAGAGCAGGGTCGAGGGCTCCATGCCCGGCTTGGCGGCCGA 6180
Db 6107 GCCCAGCCTGGCTGGAGAGCAGGGTCGAGGGCTCCATGCCCCGCTTGGCGGCCGA 6166
Qy 6181 GACTAGCCCGTCAACAGATGCCAGCCCATGAAGCGCTCCATCTCCAGCTGGCCAGCG 6240
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Db 6467 GGGCCGGTCCAGGAGCGGACCGCTCATCTCTCTCGGAGAGAGCGCTTCTA 6526
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Db 6527 CTCTGCGACCGCTTTGGGGCGGTGAGCCCGGAGCCCAAGCCCTCCCTCAGCAGCCA 6586
Qy 6601 CCCAGCTGCGCAACAGCTGGCAGAGCGGGAGCCGCCACCCACAGGCGAGTTCGT 6660
Db 6587 CCCAAGCTGCGCAACAGCTGGCAGAGCGGGAGCCGCCACCCACAGGCGAGTTCGT 6646
Qy 6661 GAATGGGAGCCCTTGTGTCAACATCTGTGTAGCACCCCGCGCGGTGGGGGAG 6720
Db 6647 GAATGGGAGCCCTTGTGTCAACATCTGTGTAGCACCCCGCGCGGTGGGGGAG 6706
Qy 6721 GCAGTCCCGCAGAGCCCTGACTCCCGCCGAGCATCACTACAAGAGCGGCAACTC 6780
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Db 6767 CTCACCATCACTTCCGCGGGGCTCAGACAGGCTCCCTGCTTCTCCAGGCGCGCT 6826
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Db 6827 CAGCGTGGGCTTTCGGAACACACAGCCGCTGCTGAGAGAGACCCCTCAGCCAGCCCT 6886

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Qy 6961 CTCTGTCCAGCCCTGCTGAGGACAGCGCTCACCTTTGAGAGAGCTGTGGCCACCACTC 7020
Db 6947 CTCTGTCCAGCCCTGCTGAGGACAGCGCTCACCTTTGAGAGAGCTGTGGCCACCACTC 7006
Qy 7021 GGGCGCTCTCTCAGGACTTCTACGTCTCTCCCTGACCTCCAGCTCTACCCCTCTCCG 7080
Db 7007 GGGCGCTCTCTCAGGACTTCTACGTCTCTCCCTGACCTCCAGCTCTACCCCTCTCCG 7066
Qy 7081 CCGCTGCGCCAAAGCTTTACCACTGAGGACTGAGCTCGGGTGGCTGAGCAGGCA 7140
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Qy 7321 CCCCTCTTTTACTCTAGACGACGAATAAGCCCTGTGTCTTGTAGTGTACGTAACGC 7376
Db 7307 CCCCTCTTTTACTCTAGACGACGAATAAGCCCTGTGTCTTGTAGTGTACGTAACGC 7362

RESULT 4
US-08-193-078B-7
; Sequence 7, Application US/08193078B
; Patent No. 5846757
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
; STREET: 1660 UNION STREET
; CITY: SAN DIEGO
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,078B
; FILING DATE: 07-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/868,354
; FILING DATE: 10-APR-1992
; PRIOR APPLICATION DATA:
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; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-53607

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INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 7362 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 144..7163

FEATURE:

NAME/KEY: 5'UTR

LOCATION: 1..143

FEATURE:

NAME/KEY: 3'UTR

LOCATION: 7161..7362

US-08-193-078B-7

Query Match 99.2%; Score 7316.4; DB 2; Length 7362;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

Qy	1	GCGCGCGCGGTGCGCGCGTGGGCGCGGCGGAGGTCCGCTGCGGTCCCGGGCGGCTCCGCTG	60
Db	1	GCGCGCGCGGTGCGCGGTGGGCGCGGCGGAGGTCCG-TGCGGTCCCGGGCGGTCCGCTG	59
Qy	61	GCTGCTCGCTCTGAGCGCTTGGCGCGCCCGCGCGCTTCCCTGCGCGGCGCGTGGGCGG	120
Db	60	GCTGCTCGCTCTGAGCGCTT-GCGCGCGCGCGCGCTTCCCTGCGCGGCGCGTGGGCGG	118
Qy	121	GGGATGCACGCGGCGCGGAGCCAGTCCGCTTCGGGACAGCTGGCGCGCGCTA	180
Db	119	GGGATGCACGCGGCGCGGAGCCAGTCCGCTTCGGGACAGCTGGCGCGCGCTA	178
Qy	181	TGGAGGCGCGCGCGGAGAGCGGCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCC	240
Db	179	TGGAGGCGCGCGCGGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC	238
Qy	241	GGGTCCCGGGGGGTGCGCGCGCGCGCGAGCGGGTCTCTA CAAAGCAATCGATCGCGAGCG	300
Db	239	GGGTCCCGGGGGGTGCGCGCGCGCGCGAGCGGGTCTCTA CAAAGCAATCGATCGCGAGCG	298
Qy	301	CGCGCGACCATGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGCTTACCGGTCAA	360
Db	299	CGCGCGACCATGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGCTTACCGGTCAA	358
Qy	361	CCGCTCGCTCTTCTTTCAGCGAGGACAAAGTCTCGCGCAATACGCGAAGCGCATCAC	420
Db	359	CCGCTCGCTCTTCTTTCAGCGAGGACAAAGTCTCGCGCAATACGCGAAGCGCATCAC	418
Qy	421	CGAGTGGCTCCATTCGAGTATATGATCTGGCCACCATCATCGCCAACTGCATCGTGT	480
Db	419	CGAGTGGCTCCATTCGAGTATATGATCTGGCCACCATCATCGCCAACTGCATCGTGT	478
Qy	481	GGCCCTGGAGCAGCACTCCCTGATGGGACAAACCGCCCATGTCGCGCGGCTGGACGA	540
Db	479	GGCCCTGGAGCAGCACTCCCTGATGGGACAAACCGCCCATGTCGCGCGGCTGGACGA	538
Qy	541	CACGAGCGCTATTTTCGCGGATCTTTTGTCTCGAGCGGGATCAAAATCATCGCTCT	600
Db	539	CACGAGCGCTATTTTCGCGGATCTTTTGTCTCGAGCGGGATCAAAATCATCGCTCT	598
Qy	601	GGGCTTTGCTTCCAAAGGCTCTTACCTCGGAAAGCGGTGGAAAGTCAATGGACTTCGT	660
Db	599	GGGCTTTGCTTCCAAAGGCTCTTACCTCGGAAAGCGGTGGAAAGTCAATGGACTTCGT	658
Qy	661	GGTGTCTTCAAGGATCTTGGCAGCGGTGGAACTGACTTCGACCTCGGAACACTGAG	720
Db	659	GGTGTCTTCAAGGATCTTGGCAGCGGTGGAACTGACTTCGACCTCGGAACACTGAG	718

Qy	721	GGCTGTGCGTGTGCTGAGGCGCCCTGAAGCTGGTGTCTGGGATTCAAAGTTTGCAAGTGGT	780
Db	719	GGCTGTGCGTGTGCTGAGGCGCCCTGAAGCTGGTGTCTGGGATTCAAAGTTTGCAAGTGGT	778
Qy	781	GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCTCGCAGATTTGGGCTGCTCTCTTCTT	840
Db	779	GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCTCGCAGATTTGGGCTGCTCTCTTCTT	838
Qy	841	TGCCATCTCATGTTTGCCATCATTTGGCCCTGGAGTTCTACATGGGCAAGTTTCCAAGGC	900
Db	839	TGCCATCTCATGTTTGCCATCATTTGGCCCTGGAGTTCTACATGGGCAAGTTTCCAAGGC	898
Qy	901	CTGTTTCCCAACAGCAGATGCGAGCCCGTGGGTGACTTCCCTGTGGCAAGAGGC	960
Db	899	CTGTTTCCCAACAGCAGATGCGAGCCCGTGGGTGACTTCCCTGTGGCAAGAGGC	958
Qy	961	CCAGCCCGGCTGTGCGAGGGCGACACTGAGTGGCGGAGTACTGGGCCAGGCCAATCTT	1020
Db	959	CCAGCCCGGCTGTGCGAGGGCGACACTGAGTGGCGGAGTACTGGGCCAGGCCAATCTT	1018
Qy	1021	TGGCATCACCAACTTTGACAAATATCCCTGTTGCCATCTTGACGCTGTTCCAGTGCATCAC	1080
Db	1019	TGGCATCACCAACTTTGACAAATATCCCTGTTGCCATCTTGACGCTGTTCCAGTGCATCAC	1078
Qy	1081	CATGGAGGGCTGGAATGACATCTCTATAATA CAAACGATGCGGCGCGGCAACACCTGGAA	1140
Db	1079	CATGGAGGGCTGGAATGACATCTCTATAATA CAAACGATGCGGCGCGGCAACACCTGGAA	1138
Qy	1141	CTGGCTCTACTTCAATCCCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTCT	1200
Db	1139	CTGGCTCTACTTCAATCCCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTCT	1198
Qy	1201	GGGCTGCTCTCGGGGAGTTTGCAGAGGAGCAGAGAGGTGGAGAACCGCGCGCTT	1260
Db	1199	GGGCTGCTCTCGGGGAGTTTGCAGAGGAGCAGAGAGGTGGAGAACCGCGCGCTT	1258
Qy	1261	CCTGAAGCTCGCGCGCAGCAGATCGAGCGAGCTCAACGGGTACCTGGAGTGGAT	1320
Db	1259	CCTGAAGCTCGCGCGCAGCAGATCGAGCGAGCTCAACGGGTACCTGGAGTGGAT	1318
Qy	1321	CTTCAAGCGGAGGAAGTCAATGCTGGCGGAGGAGGACAGGAATGCAGAGAGTCCCC	1380
Db	1319	CTTCAAGCGGAGGAAGTCAATGCTGGCGGAGGAGGACAGGAATGCAGAGAGTCCCC	1378
Qy	1381	TTTGGAGCTGCTCAAGAGAGCGGCACCAAGAGAGCAGAAATGACCTGATCCACGAGA	1440
Db	1379	TTTGGAGCTGCTCAAGAGAGCGGCACCAAGAGAGCAGAAATGACCTGATCCACGAGA	1438
Qy	1441	GGAGGAGAGGACCGGTTTCAGATCTCTGTGTTGGATCCCTTCGCCCGCGCCAG	1500
Db	1439	GGAGGAGAGGACCGGTTTCAGATCTCTGTGTTGGATCCCTTCGCCCGCGCCAG	1498
Qy	1501	CCTCAAGAGCGGGAAGACAGAGAGCTGTCATACTTCCGAGGAGAGAGAGATGTTCCG	1560
Db	1499	CCTCAAGAGCGGGAAGACAGAGAGCTGTCATACTTCCGAGGAGAGAGAGATGTTCCG	1558
Qy	1561	GTTTTTTATCCGCGCATGTTGAAGGCTCAGAGCTTCTACTGGGTGGTGTGCTGCGTGGT	1620
Db	1559	GTTTTTTATCCGCGCATGTTGAAGGCTCAGAGCTTCTACTGGGTGGTGTGCTGCGTGGT	1618
Qy	1621	GGCCCTGAAACACTGTGTGGCCATGGTGCATTACAACAGCCCGCGCGGCTTACAC	1680
Db	1619	GGCCCTGAAACACTGTGTGGCCATGGTGCATTACAACAGCCCGCGCGGCTTACAC	1678
Qy	1681	GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTTCTTCTCAAGAGATGCTCCGAA	1740
Db	1679	GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTTCTTCTCAAGAGATGCTCCGAA	1738
Qy	1741	GATGTATGGCTCGGGCCCAAGAGTACTTCCCGTCTCTCTTCAACTGCTTCCACTTTGG	1800
Db	1739	GATGTATGGCTCGGGCCCAAGAGTACTTCCCGTCTCTCTTCAACTGCTTCCACTTTGG	1798

QY 1801 GGTCACTCGTGGGAGCGCTTTTGAAGTGTCTGGCGGCATCAAGCCGGAGAGCTCCTT 1860
Db 1799 GGTCACTCGTGGGAGCGCTTTTGAAGTGTCTGGCGGCATCAAGCCGGAGAGCTCCTT 1858
QY 1861 TGGGATCAGTGTCTGGGCGCTTCGGCTGCTGAGGATCTTCAAGTACAGAGTACTG 1920
Db 1859 TGGATCAGTGTCTGGGCGCTTCGGCTGCTGAGGATCTTCAAGTACAGAGTACTG 1918
QY 1921 GAGCTCCCTCGGAACTCGTGTGTCTCCCTGCTGAACTCATGAAGTCCATCATAGCCT 1980
Db 1919 GAGCTCCCTCGGAACTCGTGTGTCTCCCTGCTGAACTCATGAAGTCCATCATAGCCT 1978
QY 1981 GCTCTTTCTGCTCTTCTGTTCAATGTGTCTTCGCTTCGCTGGGATCGAGCTGTTGG 2040
Db 1979 GCTCTTTCTGCTCTTCTGTTCAATGTGTCTTCGCTTCGCTGGGATCGAGCTGTTGG 2038
QY 2041 GGGACAGTTCAACTCCAGAGTGAAGTCCCAACCAACTTCGACACTTCCTTCCCTGCCG 2100
Db 2039 GGGACAGTTCAACTCCAGAGTGAAGTCCCAACCAACTTCGACACTTCCTTCCCTGCCG 2098
QY 2101 CAPCTCACTGTCTTCAGATCTGACGGGAGAGACTGGAATGCAAGTGAATATCAAGG 2160
Db 2099 CATCTCACTGTCTTCAGATCTGACGGGAGAGACTGGAATGCAAGTGAATATCAAGG 2158
QY 2161 GATCGAATCGAAGCGGCGTCAAGAGGCAATGTTCTCGTCTTTTACTTCATTTGCTCT 2220
Db 2159 GATCGAATCGAAGCGGCGTCAAGAGGCAATGTTCTCGTCTTTTACTTCATTTGCTCT 2218
QY 2221 GACACTGTTCCGAAATACACTCTGCTGAATGTTCTTCTGGCCATCGCTGTGGAACT 2280
Db 2219 GACACTGTTCCGAAATACACTCTGCTGAATGTTCTTCTGGCCATCGCTGTGGAACT 2278
QY 2281 GGGCAAGCCCAAGAGCTGACCAAGATGAAGAGGAGATGGAAGAGCAGCAATCAGAA 2340
Db 2279 GGGCAAGCCCAAGAGCTGACCAAGATGAAGAGGAGATGGAAGAGCAGCAATCAGAA 2338
QY 2341 GCTTCTCTGCAAAAGGCCAAAGAGTGTCTGAACTGACGCCCATGTCTGCCGCAAT 2400
Db 2339 GCTTCTCTGCAAAAGGCCAAAGAGTGTCTGAACTGACGCCCATGTCTGCCGCAAT 2398
QY 2401 CTCCATCGCGCGCAGCAGCAAACTCGGCCAAGCGGCTCGGTGTGGAGCAGCGGCG 2460
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QY 2461 CAGCAGCTACGCTGCGAGAACTCGGGGCGAGCTGCGAGGCGTGTACAGCGAGTGA 2520
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QY 2521 CCCGAGGAGCGGCTGCGCTTCGCCACTAGCGGCCACCTGCGGCCCGACATGAAGCGCA 2580
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QY 2581 CTGACCGCGCGCTGTTGTGAGCTGCGGCGGACGCGCGCGCGGCGCGCTGGGAGG 2640
Db 2579 CTGACCGCGCGCTGTTGTGAGCTGCGGCGGACGCGCGCGCGGCGCGCTGGGAGG 2638
QY 2641 CAAAGCCGACCTGAGGCTGGGAGGCCCGCGAGGCGTCAAGCTTCGCGCAGGCAACA 2700
Db 2639 CAAAGCCGACCTGAGGCTGGGAGGCCCGCGAGGCGTCAAGCTTCGCGCAGGCAACA 2698
QY 2701 CCGGCACTCGGACAGGACAAAGACCCCGCGCGGGGACAGGCGCGCGCGGCGCGAGGCC 2760
Db 2699 CCGGCACTCGGACAGGACAAAGACCCCGCGCGGGGACAGGCGCGCGCGGCGCGAGGCC 2758
QY 2761 GAAAGCGAGAGCGGGAGCCCGTGTCCCGGAGAGCGCGCGCGGCGCGACCCAGCGCA 2820
Db 2759 GAAAGCGAGAGCGGGAGCCCGTGTCCCGGAGAGCGCGCGCGGCGCGACCCAGCGCA 2818
QY 2821 CAGCAAGAGAGCGCGGGCGCCCGGAGCGCGGAGCGCGCGCGCGCGAGGCCCGAGGCC 2880
Db 2819 CAGCAAGAGAGCGCGGGCGCCCGGAGCGCGGAGCGCGCGCGCGCGAGGCCCGAGGCC 2878
QY 2881 CGAGGCGCGCGCGGCAACCAACCGCGCGGCTCCCGGAGGAGCGCGCGCGAGGCC 2940

Db 2879 CGAGGCGCGCGCGGCAACCAACCGCGCGGCTCCCGGAGAGGCGGCGCGAGCGGAGCC 2938
QY 2941 CCGAGCGCACCGCGCGCACCGGCAACAGGATCCAGCAAGAGTGCAGCGCGCAAGGG 3000
Db 2939 CCGAGCGCACCGCGCGCACCGGCAACAGGATCCAGCAAGAGTGCAGCGCGCAAGGG 2998
QY 3001 CGAGCGCGCGCGCGGACCGCGCGGCGCCCGAGCGGGGCGCGGAGCGCGGAGCGG 3060
Db 2999 CGAGCGCGCGCGCGGACCGCGCGGCGCCCGAGCGGGGCGCGGAGCGCGGAGCGG 3058
QY 3061 GGAGGAGCGCGCGCGGCGCACCGCGGCGCCCGGCAACAGCGCGAGCTGTCTACAGAGGCTGT 3120
Db 3059 GGAGGAGCGCGCGCGGCGCACCGCGGCGCCCGGCAACAGCGCGAGCTGTCTACAGAGGCTGT 3118
QY 3121 GGAGAGGAGCACAGGAGAGAGGCGCACCGAGAGGAGGCTGAGATAGTGGAGGCGCA 3180
Db 3119 GGAGAGGAGCACAGGAGAGAGGCGCACCGAGAGGAGGCTGAGATAGTGGAGGCGCA 3178
QY 3181 CAAGGAAAGGAGCTCCGGAACCAACAGCGCCCGGAGCGGCTGTCTCCAGAGGCTGA 3240
Db 3179 CAAGGAAAGGAGCTCCGGAACCAACAGCGCCCGGAGCGGCTGTCTCCAGAGGCTGA 3238
QY 3241 TGGGACTGTGTGTGGGTCCCATGCAACACTGCCAGCACCTGTCTCCAGAGGCTGA 3300
Db 3239 TGGGACTGTGTGTGGGTCCCATGCAACACTGCCAGCACCTGTCTCCAGAGGCTGA 3298
QY 3301 GGAACAGCAGAGGATGACAGCAATCAGCGGAAGCTGCTCGCATGGGCACTCAGAGGCTGA 3360
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QY 3421 GGTCTGTTCCAGTGTGTAACTGTGAACCTTGGAAACCAAGCAGAGGAGGAGGAGGCTGA 3480
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Db 3659 AGTGGCGCAGACTCGCCAGGAAACCGCTCTGAAATACCTGGATTAACATTTTCACTGG 3718
QY 3721 TGTCTTTA CTTTGAAGATGGTGAATAAGATGATCGACTTTGGGAGCTGCTGCTCACCGCTG 3780
Db 3719 TGTCTTTA CTTTGAAGATGGTGAATAAGATGATCGACTTTGGGAGCTGCTGCTCACCGCTG 3778
QY 3781 AGCTATTTTCCGGGACTTGTGAAACATTTCTGAGCTTTCATTTGGTGTGCTGCTGCTGCT 3840
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QY 3901 GTCTCTGAGAGCTTCTGCTGCTCGCGCCCTCAAGACCATCAAAAGCTGCCCAAGCT 3960
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QY 3961 CAAAGCTGTGTTGACTGTGTGTAACCTCCCTGAGAGATGCTCAACATCTGATGCT 4020

Db 3947 CAAGGCTGTGTTGACTGTGTGGTGAACCTCCCTGAAGAAATGTCCTCAACATCTTGATTGT 4006
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Qy 4021 CTACATGCTCTTCATGTTTCATATTTGCGCTCATMTGCGGTGCAGCTCTTCAAAGGAAAGTT 4080
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Db 4007 CTACATGCTCTTCATGTTTCATATTTGCGCTCATMTGCGGTGCAGCTCTTCAAAGGAAAGTT 4066
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Qy 4081 TTTTCTACTGCACAGATGAATCCAAAGGAGCTGGAGAGGACTGCAGGGGTCAAGTATTTGGGA 4140
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Db 4067 TTTTCTACTGCACAGATGAATCCAAAGGAGCTGGAGAGGACTGCAGGGGTCAAGTATTTGGGA 4126
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Qy 4141 TTATGAGAGGAGGAAGTGGGAAGCTCAGCCAGGCAAGTGGGAAGAAATACGACTTTTCACTA 4200
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Db 4127 TTATGAGAGGAGGAAGTGGGAAGCTCAGCCAGGCAAGTGGGAAGAAATACGACTTTTCACTA 4186
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Qy 4201 CGACAAATGTGCTCTGGGCTCTGCTGAGCGCTGTTTCACTAGTGTCCACGGGAGAAAGCTGGCC 4260
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Db 4187 CGACAAATGTGCTCTGGGCTCTGCTGAGCGCTGTTTCACTAGTGTCCACGGGAGAAAGCTGGCC 4246
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Qy 4261 CATGGTGTGAAACACTCCGTGGATGGCACTATGAGAGGACAGGGTCCAAAGCCCTGGGTA 4320
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Qy 4321 CCGCATGAGCTGTCCATCTTCTACGTGCTCTATTTGGTCTCTTCCCTTCTTCTTCGT 4380
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Db 4307 CCGCATGAGCTGTCCATCTTCTACGTGCTCTATTTGGTCTCTTCCCTTCTTCTTCGT 4366
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Qy 4621 GATGATGAAGTTCTATGATGACCCCTATGAGTAGAGCTGATGCTGAAATGCCTGGAACAT 4680
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Qy 4681 CGTGTTCAATCCATGTTCTCCATGGAATGCTGCTGAAGATCATCGCTTTGGGGTGCT 4740
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Db 4667 CGTGTTCAATCCATGTTCTCCATGGAATGCTGCTGAAGATCATCGCTTTGGGGTGCT 4726
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Db 4847 CCTCTTTTCGAGCTGCGGGCTGATCAAGCTGCTCCGCGGCTACACCATCCGCACTCCT 4906
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Db 4907 GCTGTGGAACCTTTGTCCAGTCTTTCAAGGCCCTGCCCTACGTGTGTCTGTCTCATTTGCCAT 4966
Qy
Qy 4981 GCTGTCTTTCATCTACGCCATCATCGGCATGCAAGTGTGTGGGAATATTTGCCCTTGGATGA 5040
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Db 4967 GCTGTCTTTCATCTACGCCATCATCGGCATGCAAGTGTGTGGGAATATTTGCCCTTGGATGA 5026
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Qy 5041 TGACACAGGATCAACCGGCACACACTTCCGAGCGTCTTTCGACGCCCTGTAGTCTGCT 5100
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Db 5027 TGACACAGGATCAACCGGCACACACTTCCGAGCGTCTTTCGAGCGGCTTTCATGCGCCCTGTGCTGCT 5086

Qy 5101 GTTCAGAGCGCCACCGGGGAGGCGCTGGACGAGATCATGCTGTCTCTGCTGAGCAACCA 5160
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Db
Db 5747 AACACAGAGACAGATGACGAGGCTCTCGAGGCTCTCCAGATGGGTCTCTGTGTC 5806
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Qy 5821 CCTGTTCCACCTCTGAAAGCCACCTGGAGCAGACACAGCCGGCTGTGTCGAGGAGC 5880
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Db 5807 CCTGTTCCACCTCTGAAAGCCACCTGGAGCAGACACAGCCGGCTGTGTCGAGGAGC 5866
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Qy 5881 CCGGTTTTCTTCGACAGAGAGTTCCACCTCCCTCAGCAATGGGGGCGCATACAAA 5940
Db
Db 5867 CCGGTTTTCTTCGACAGAGAGTTCCACCTCCCTCAGCAATGGGGGCGCATACAAA 5926
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Qy 5941 CCAAGAGATGGCATCAAAGAGTCTGTCTCTGGGGCACTCAAAGGACCAGGATGCACC 6000
Db
Db 5927 CCAAGAGATGGCATCAAAGAGTCTGTCTCTGGGGCACTCAAAGGACCAGGATGCACC 5986
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Qy 6001 CCATGAGGCGAGGCCACCTCTGGAGCGTGCCACTCCACAGAGATCCCTGTGGGGGGTCC 6060
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Db 5987 CCATGAGGCGAGGCCACCTCTGGAGCGTGCCACTCCACAGAGATCCCTGTGGGGGGTCC 6046
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Qy 6061 AGGAGCACTGGCTGTGGAAGTTCAGATGACAGATAAACCCGAGGGGCCCTCATGGGA 6120
Db
Db 6047 AGGAGCACTGGCTGTGGAAGTTCAGATGACAGATAAACCCGAGGGGCCCTCATGGGA 6106
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Qy 6121 GCCCAGCTGGGCTGGAGAGCCAGGCTCGAGCGGCTCTCATGCCCGCTTGGGGCCGA 6180
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Db 6107 GCCCAGCTGGGCTGGAGAGCCAGGCTCGAGCGGCTCTCATGCCCGCTTGGGGCCGA 6166

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DB	6167	GACTCAGCCCGTCACAGATGCCAGCGCCCATGAGCGCTCCATCTCCACGCTGGCGCCAGCG	6326
QY	6241	GCCCCGTGGGACTCATCTTTGACGACCAACCCCGGACCGCCACCCCTTAGCCAGCGGCTC	6300
DB	6227	GCCCCGTGGGACTCATCTTTGACGACCAACCCCGGACCGCCACCCCTTAGCCAGCGGCTC	6386
QY	6301	GTTCGACCAACCAACCAACCGCTGCCACCGCGCGAGGGAAGGAGCAGAGGTCCTCTGGA	6360
DB	6287	GTTCGACCAACCAACCAACCGCTGCCACCGCGCGAGGGAAGGAGCAGAGGTCCTCTGGA	6346
QY	6361	GAAGGGGCCACGCTGTCTGCCGATATGGATGGCGCCACCAAGCAGTGTCTGTGGGGCCGG	6420
DB	6347	GAAGGGGCCACGCTGTCTGCCGATATGGATGGCGCCACCAAGCAGTGTCTGTGGGGCCGG	6406
QY	6421	GCTGCCCGGGAGAGGGGCCCTTACAGGCTGCCGGCGGGAAACGAGAGCGCGCGCAGAGAGCG	6480
DB	6407	GCTGCCCGGGAGAGGGGCCCTTACAGGCTGCCGGCGGGAAACGAGAGCGCGCGCAGAGAGCG	6466
QY	6481	GGGGCGGTCCACGAGCGGAGCGGACGCTCATCTCTCTCTCGGAGAGCAGAGCGCTTCTTA	6540
DB	6467	GGGGCGGTCCACGAGCGGAGCGGACGCTCATCTCTCTCTCGGAGAGCAGAGCGCTTCTTA	6526
QY	6541	CTCTCTCGACCGCTTTTGGGGGCCGTGTAGCCCCCGAAGCCCAAGCCCTCCCTCAGCAGCCA	6600
DB	6527	CTCTCTCGACCGCTTTTGGGGGCCGTGTAGCCCCCGAAGCCCTCCCTCAGCAGCCA	6586
QY	6601	CCCAACGTTCGACACAGCTGGCCAGGACCGGGACCCCAACCCAGGGCAGTGGTTCCGT	6660
DB	6587	CCCAACGTTCGACACAGCTGGCCAGGACCGGGACCCCAACCCAGGGCAGTGGTTCCGT	6646
QY	6661	GAATGGGAGCCCTTTGCTGTCAAATCTGGTGTAGCAACCCGGCGCGGTGGGGCGGAG	6720
DB	6647	GAATGGGAGCCCTTTGCTGTCAAATCTGGTGTAGCAACCCGGCGCGGTGGGGCGGAG	6706
QY	6721	GGAGCTTCCCAGACGCCCCCTGACTTCCCOCGCCAGCATCACTTACAAGACGCCCAACTC	6780
DB	6707	GGAGCTTCCCAGACGCCCCCTGACTTCCCOCGCCAGCATCACTTACAAGACGCCCAACTC	6766
QY	6781	CTCACCCATCACTTCCCGGGGCTCAGACGAGCTTCCCTTCTCCCGAGCGCGCT	6840
DB	6767	CTCACCCATCACTTCCCGGGGCTCAGACGAGCTTCCCTTCTCCCGAGCGCGCT	6826
QY	6841	CAGCGTGGGCTTTCCGAACAACAAGCCCTGCTCAGAGAGACCCCTCAGCCAGCGCCCT	6900
DB	6827	CAGCGTGGGCTTTCCGAACAACAAGCCCTGCTCAGAGAGACCCCTCAGCCAGCGCCCT	6886
QY	6901	GGCCCCGTGGCTTCGAATTGGCTCTGACCTTACCTGGGGCAGCGCTTGACAGTGAGGC	6960
DB	6887	GGCCCCGTGGCTTCGAATTGGCTCTGACCTTACCTGGGGCAGCGCTTGACAGTGAGGC	6946
QY	6961	CTCTGTCCAAGCCCTGCTGAGGACAGCTTCTCATTTTCGAGGAGGCTGTGGCCACCAACTC	7020
DB	6947	CTCTGTCCAAGCCCTGCTGAGGACAGCTTCTCATTTTCGAGGAGGCTGTGGCCACCAACTC	7006
QY	7021	GGGGCGCTCCTCAGAGACTTCTACGTGTCTCTCGCTGACCTCCAGTCTCACCCCTCCG	7080
DB	7007	GGGGCGCTCCTCAGAGACTTCTACGTGTCTCTCGCTGACCTCCAGTCTCACCCCTCCG	7066
QY	7081	CCGCGTGCCCAAACGGTTTACCACTGACCCCTGGGACTCAGCTCGGGTGGCCGAGCAGGCA	7140
DB	7067	CCGCGTGCCCAAACGGTTTACCACTGACCCCTGGGACTCAGCTCGGGTGGCCGAGCAGGCA	7126
QY	7141	CAGTACCAACCAACCTGACCAAGACCACTGGTGTCTAGCTGCAACCGGTACCGTTCAGAGC	7200
DB	7127	CAGTACCAACCAACCTGACCAAGACCACTGGTGTCTAGCTGCAACCGGTACCGTTCAGAGC	7186
QY	7201	CTGCATCAGCAGCGGTGTCTCAGTGGATGATTTTATCTCCACACGGGGCAGTCCG	7260
DB	7187	CTGCATCAGCAGCGGTGTGTTCAGTGGATGATTTTATCTCCACACGGGGCAGTCCG	7246
QY	7261	CCCTCGGGGAGGCCCTTGGCCCACTTGTGGTAGGCTCTCTGTGGCCCTCTCCCTCCCTCTCT	7320

Db	7247	CCCTCGGGGAGGCTTGGCCACCTTGGTGAGGCTTCTGTGGCCCTCCCTCCCTCCCT	7306
Qy	7321	CCCTCTCTTTACTCTAGACGACGAATAAGCCCTGTGCTGTGAGTGACTACGCG	7376
Db	7307	CCCTCTCTTTACTCTAGACGACGAATAAGCCCTGTGCTGTGAGTGACTACGCG	7362

RESULT 5

US-08-223-305C-7

; Sequence 7, Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

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; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 57

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; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/223,305C

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; FILING DATE: 20-FEB-1990

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; APPLICATION NUMBER: US 07/603,751

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US89/01408

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

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; FILING DATE: 04-APR-1988

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; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7362 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

:	NAME/KEY:	CDS
:	LOCATION:	144..7163
:	FEATURE:	
:	NAME/KEY:	5'UTR
:	LOCATION:	1..143
:	FEATURE:	
:	NAME/KEY:	3'UTR
:	LOCATION:	7161..7362
:	US-08-223-305C-7	
Query Match		
Best Local Similarity 99.2%; Score 7316.4; DB 2; Length 7362;		
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;		
Qy	1	GCGCGCGGCTGCGGGGTGGGGCCGGGCAGAGTCGCTCGGTCGCGTCCGGCGGGTCCGGTG 60
Dd	1	GCGCGCGGCTGCGGGGTGGGGCCGGGCAGAGTCCG-TGCGGTCCGGCGGCTCCGGT 59
Qy	61	GCTGCTCGGCTTAGCGGCTTAGCGCGGCCCGCGGCCCTCCCTGCGGGGCGCTGGGCGG 120
Dd	60	GCTGCTCGGCTTAGCGGCTT-GGCGGCCCGCGCCCTCCCTGCGGGGCGGCTGGGCGG 118
Qy	121	GGGATGCACGGGGGCGCGGAGCATGCTCCGTTTCGGGACAGACTGGCGGCGCGCTA 180
Dd	119	GGGATGCACGGGGGCGCGGAGCATGGTCCGTTTCGGGACAGACTGGCGGCGCGCTA 178
Qy	181	TGGAGGCCCCCGCGCGGAGAGCGGGCCC CGGGGGCGCGGGCGCGGGGGGGCCCC 240
Dd	179	TGGAGGCCCCCGCGCGGAGAGCGGGCCC CGGGGGCGCGGGCGCGGGGGGGCCCC 238
Qy	241	GGGTCCGGGGGCTGCAGCCCGGCGAGCGGGTCTCTACAAGCAATCGATCGCGCAGCG 300
Dd	239	GGGTCCGGGGGCTGCAGCCCGGCGAGCGGGTCTCTACAAGCAAATCGATCGCGCAGCG 298
Qy	301	CGCGGACCATGCGGCTGTACAACCCATCCCGGTCAAGCAGAACTGCTTCAACGTCAA 360
Dd	299	CGCGGACCATGCGGCTGTACAACCCCATCCCGGTCAAGCAGAACTGCTTCAACGTCAA 358
Qy	361	CCGCTCGCTCTTCGTTTCAGCAGGACAACGCTGTCGCGAAAATACGGAAGCGCATCAC 420
Dd	359	CCGCTCGCTCTTCGTTTCAGCAGGACAACGCTGTCGCGAATAACGGAAGCGCATCAC 418
Qy	421	CGAGTGGCTCCATTGAGTATATGATCCTGGCCAACATATCGCCAACTGGATCGTGT 480
Dd	419	CGAGTGGCTCCATTGAGAATATGATCCTGGCCACCATCATCGCAACTGCATCGTGTGT 478
Qy	481	GGCCCTGGAGCAGCACTCCCTGATGGGGA AAAAACGCCCATGTCGAGCGGCTGGACGA 540
Dd	479	GGCCCTGGAGCAGCACTCCCTGATGGGGA AAAAACGCCCATGTCGAGCGGCTGGACGA 538
Qy	541	CACGAGCCCTATTTCATCGGGATCTTTTGCTTCGAGCGGGATCAAAATCATCGCTCT 600
Dd	539	CACGAGCCCTATTTCATCGGGATCTTTTGCTTCGAGCGGGATCAAAATCATCGCTCT 598
Qy	601	GGGCTTTGTCTTCCACAAGGCTCTTA CCTCGGAAACGGCTGGAAACGTCATGGACTTCGT 660
Dd	599	GGGCTTTGTCTTCCACAAGGCTCTTA CCTCGGAAACGGCTGGAAACGTCATGGACTTCGT 658
Qy	661	GGTGTCTTACAGGGATCTTGGCA CGGCTGGAACTGACTTCGACCTTCGGAACACTGAG 720
Dd	659	GGTGTCTTCAAGGGATCTTGGCA CGGCTGGAACTGACTTCGACCTTCGGAACACTGAG 718
Qy	721	GGCTGTGCTGTGTGAGGCCCTTGAAGCTGTGTCTGGGATTCCAAGTTTGCAGGTGCT 780
Dd	719	GGCTGTGCTGTGTGAGGCCCTTGAAGCTGTGTCTGGGATTCCAAGTTTGCAGGTGCT 778
Qy	781	GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCCTGCAGATTGGGCTGCTTCTCTTCT 840
Dd	779	GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCCTGCAGATTGGGCTGCTTCTCTTCT 838
Qy	841	TGCCATCTCATGTTTGGCATTCATTGGGCTGGAGTTTACATGGGCAAGTTCCACAAGGC 900
Dd	839	TGCCATCTCATGTTTGGCATTCATTGGGCTGGAGTTTACATGGGCAAGTTCCACAAGGC 898

QY	1981	GCTCTTCTTCTCTTCTGTTCAATGTTGTTCTTCGCCCTGCTGGGATGCACTGTTTGG	2040
Db	1979	GCTCTTCTTCTCTTCTGTTCAATGTTGTTCTTCGCCCTGCTGGGATGCACTGTTTGG	2038
QY	2041	GGGACAGTTCAAATTTCCAGATGAGACTCCACAACTTCGACACCTTCCCTGCCGC	2100
Db	2039	GGGACAGTTCAAATTTCCAGATGAGACTCCACAACTTCGACACCTTCCCTGCCGC	2098
QY	2101	CATCTCTCACTGTTCTTCAGATCTGACGGGAGAGACTGGAATGCACTGATGATCAAGG	2160
Db	2099	CATCTCTCACTGTTCTTCAGATCTGACGGGAGAGACTGGAATGCACTGATGATCAAGG	2158
QY	2161	GATCGAATCGCAAGCGCGCTCAGCAAAAGCATGTTCTCGTCTTTTCACTTGTCTCT	2220
Db	2159	GATCGAATCGCAAGCGCGCTCAGCAAAAGCATGTTCTCGTCTTTTCACTTGTCTCT	2218
QY	2221	GACACTGTTTCGGAAATACACTCTGCTGAATGCTTTCTGGCCATCGCTGTGGACAACT	2280
Db	2219	GACACTGTTTCGGAAATACACTCTGCTGAATGCTTTCTGGCCATCGCTGTGGACAACT	2278
QY	2281	GGCCAAAGCGCCAGAGCTGACCAAGGATGAAGAGAGATGGAAGAGCAGCCAAATCAGAA	2340
Db	2279	GGCCAAAGCGCCAGAGCTGACCAAGGATGAAGAGAGATGGAAGAGCAGCCAAATCAGAA	2338
QY	2341	GCTTGCTCTGCAAAAGCGCGCTGAAAGTGTGCTGAAAGTCAAGCCCATGTCTGCCGCAAT	2400
Db	2339	GCTTGCTCTGCAAAAGCGCGCTGAAAGTGTGCTGAAAGTCAAGCCCATGTCTGCCGCAAT	2398
QY	2401	CTTCATCGCGCCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGGAGCAGCGGCG	2460
Db	2399	CTTCATCGCGCCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGGAGCAGCGGCG	2458
QY	2461	CAGCCAGCTACGGCTGCAGAACTCGCGGCCAGCTCGAGGCGCTGTACAGCGAGATGGA	2520
Db	2459	CAGCCAGCTACGGCTGCAGAACTCGCGGCCAGCTCGAGGCGCTGTACAGCGAGATGGA	2518
QY	2521	CCCCGAGGAGCGGCTGCGCTTCCGACACTACGCGCCACCTGCGGCCCGACATGAAGACGA	2580
Db	2519	CCCCGAGGAGCGGCTGCGCTTCCGACACTACGCGCCACCTGCGGCCCGACATGAAGACGA	2578
QY	2581	CCTGGACCGGCGCTGTTGTTGAGCTGGGCGCGACCGCGCGCGCGGCGCGCTGGGAGG	2640
Db	2579	CCTGGACCGGCGCTGTTGTTGAGCTGGGCGCGACCGCGCGCGCGGCGCGCTGGGAGG	2638
QY	2641	CAAAGCCGACCTGAGGCTGCGAGGCCCCGAGGCGTTCGACCTCGCGCGCAGGACCA	2700
Db	2639	CAAAGCCGACCTGAGGCTGCGAGGCCCCGAGGCGTTCGACCTCGCGCGCAGGACCA	2698
QY	2701	CGGCGACCGGACAGGACAGACCCCGCGCGCGGCGGACCAAGNCCGAGCAGAGGCC	2760
Db	2699	CGGCGACCGGACAGGACAGACCCCGCGCGCGGCGGACCAAGNCCGAGCAGAGGCC	2758
QY	2761	GAAGCGGAGAGCGGGGAGCCCGTGCCTCGGAGAGCGCGCGCGCGCGCACCGCAGCA	2820
Db	2759	GAAGCGGAGAGCGGGGAGCCCGTGCCTCGGAGAGCGCGCGCGCGCACCGCAGCA	2818
QY	2821	CAGCAAGAGAGCGCGGCGCCCCGAGAGCGGCGAGCGCGCGCGCGCGCGCGCGCG	2880
Db	2819	CAGCAAGAGAGCGCGGCGCCCCGAGAGCGGCGAGCGCGCGCGCGCGCGCGCGCG	2878
QY	2881	CGAGGCGCGCGCGGCGCACCGCGCGGCTCCCGCGAGGAGGCGCGCGCGCGCGCG	2940
Db	2879	CGAGGCGCGCGCGGCGCACCGCGCGGCTCCCGCGAGGAGGCGCGCGCGCGCGCG	2938
QY	2941	CGAGCGCACCGCGCGCACCGCGCACCAGGATCCGAGCAAGAGTGCCTCGCGCGCGCAAGGG	3000
Db	2939	CGAGCGCACCGCGCGCACCGCGCACCAGGATCCGAGCAAGAGTGCCTCGCGCGCGCAAGGG	2998
QY	3001	CGAGCGCGCGCGCGCGCACCGCGCGGCCCCCGAGCGGCGCGCGCGCGCGCGCG	3060
Db	2999	CGAGCGCGCGCGCGCGCACCGCGCGGCCCCCGAGCGGCGCGCGCGCGCGCGCG	3058
QY	3061	GGAGGAGCGCGCGCGCGCGCACCGGCGCGCGCACCAAGCGCGCAGCTTCTCACGAGGCTGT	3120

Db	3059	GGAGGAGCGCGCGCGCGCACCGGCGCGCGCACAGCGCGAGCTGCTCACGAGGCTGT	3118
QY	3121	GGAGAGGAGACCAACGAGAGAGGAGGCAACGAGAGAGAGCTGAGATAGTGGAGCGCA	3180
Db	3119	GGAGAGGAGACCAACGAGAGAGGAGGCAACGAGAGAGAGCTGAGATAGTGGAGCGCA	3178
QY	3181	CAAGGAAAGGAGCTCCGGAACCAACAGCCCGCGGAGCCACACTGTGACCTTGGAGACCA	3240
Db	3179	CAAGGAAAGGAGCTCCGGAACCAACAGCCCGCGGAGCCACACTGTGACCTTGGAGACCA	3238
QY	3241	TGGGACTGTGACTGTGGGTCCCATGCACACACTGCCAGCAGCTGTCTTCAGAAAGGTGGA	3300
Db	3239	TGGGACTGTGACTGTGGGTCCCATGCACACACTGCCAGCAGCTGTCTTCAGAAAGGTGGA	3298
QY	3301	GGAAACGACGAGAGATGAGCAATAGCGGAACGTCACTCGCATGGGCACTCAGCCGCC	3360
Db	3299	GGAAACGACGAGAGATGAGCAATAGCGGAACGTCACTCGCATGGGCACTCAGCCGCC	3358
QY	3361	AGACCCGAAACACTTGTACATATCCAGTGTGCTGACCGGCCCTCTTCGGGAGCCAC	3420
Db	3359	AGACCCGAAACACTTGTACATATCCAGTGTGCTGACCGGCCCTCTTCGGGAGCCAC	3418
QY	3421	GGTGGTTCCTGAGTGGTAACTGGAACCTGGAAGCCTGGAAGGAGGAGGAGGAGTGA	3480
Db	3419	GGTGGTTCCTGAGTGGTAACTGGAACCTGGAAGCCTGGAAGGAGGAGGAGGAGTGA	3478
QY	3481	AGCGGATGACGCTGATGAGGAGCGGCCCGGCTTATGCTCCCATACAGCTTCATGTTCTG	3540
Db	3479	AGCGGATGACGCTGATGAGGAGCGGCCCGGCTTATGCTCCCATACAGCTTCATGTTCTG	3538
QY	3541	TTTAAAGCCCGACCAACCTGCTCCCGCTTCTGCCACTATACATGACCAATGAGGACTT	3600
Db	3539	TTTAAAGCCCGACCAACCTGCTCCCGCTTCTGCCACTATACATGACCAATGAGGACTT	3598
QY	3601	CGAGGTTGCTCACTTCTGTTGCTCATCGCTTGAAGCAGCATCGCTTGGTGTGAGGAGCC	3660
Db	3599	CGAGGTTGCTCACTTCTGTTGCTCATCGCTTGAAGCAGCATCGCTTGGTGTGAGGAGCC	3658
QY	3661	AGTGGCGACAGACTCGCCCGAGGAGCAACGCTCTGAAATACCTGGATTAATTTTCACTGG	3720
Db	3659	AGTGGCGACAGACTCGCCCGAGGAGCAACGCTCTGAAATACCTGGATTAATTTTCACTGG	3718
QY	3721	TGCTTTTACCTTTGAGATGTTGATAAAGATGATCGACTTGGGACTGCTGCTCACCCCTGG	3780
Db	3719	TGCTTTTACCTTTGAGATGTTGATAAAGATGATCGACTTGGGACTGCTGCTCACCCCTGG	3778
QY	3781	AGCTATTTTCGCGGACTTGTGGAACATTTCTGGAATTTTCTGTTGTTGTTGTTGTTGTT	3840
Db	3779	AGCTATTTTCGCGGACTTGTGGAACATTTCTGGAATTTTCTGTTGTTGTTGTTGTTGTT	3838
QY	3841	GGGTTTGTCTTCTCGAGCTTCTGAGGATCCAAAGGAGGATCCAAAGGAGGATCCAAAGG	3900
Db	3839	GGGTTTGTCTTCTC-----AGGATCCAAAGGAGGAGGATCCAAAGGAGGATCCAAAGG	3886
QY	3901	GTCTCTGAGAGTCTTCTGTTCTGCTCGGCCCTTCAAGACCATCAAAACGCGCTGCCAAGCT	3960
Db	3887	GTCTCTGAGAGTCTTCTGTTCTGCTCGGCCCTTCAAGACCATCAAAACGCGCTGCCAAGCT	3946
QY	3961	CAAGGCTGTTTGTGACTGTGTGTGAACCTTCTGGAATTTTCTGTTGTTGTTGTTGTTGTT	4020
Db	3947	CAAGGCTGTTTGTGACTGTGTGTGAACCTTCTGGAATTTTCTGTTGTTGTTGTTGTTGTT	4006
QY	4021	CTACATGCTTCTCATGTTTCTATTTTGGCGTCAATGCGGTGAGGAGTCTTCAAGGAGGTT	4080
Db	4007	CTACATGCTTCTCATGTTTCTATTTTGGCGTCAATGCGGTGAGGAGTCTTCAAGGAGGTT	4066
QY	4081	TTTCTACTGACAGATGAATCAAGAGCTGAGAGGAGCTGAGAGGAGTCTGATTTTGA	4140
Db	4067	TTTCTACTGACAGATGAATCAAGAGCTGAGAGGAGTCTGAGAGGAGTCTGATTTTGA	4126
QY	4141	TTATGAGAGGAGGAGTGGAGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	4200

Db 4127 TTATGAGAGGAGGAGTGGAGCTCAGCCAGGCGAGCTGGAAGAAATACAGACTTTTCACTA 4186
Qy
Db 4201 CGACAAATGTGCTCTGGGCTCTGCTGACGCTGTTTCAAGTGTCCACGGGAGAGGCTGGCC 4260
Db 4187 CGACAAATGTGCTCTGGGCTCTGCTGACGCTGTTTCAAGTGTCCACGGGAGAGGCTGGCC 4246
Qy 4261 CATGGTCTGAAACACTTCGGTGGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4320
Db 4247 CATGGTCTGAAACACTTCGGTGGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4306
Qy 4321 CCGCATGGAGCTGTCATCTTCACTAGTGGTCTACTTTGTGGTCTTTCCCTTCTTCTTCGT 4380
Db 4307 CCGCATGGAGCTGTCATCTTCACTAGTGGTCTACTTTGTGGTCTTTTCCCTTCTTCTTCGT 4366
Qy 4381 CAACATCTTTTGGCTTTGTATCATCATCACTTCCAGGAGCAGGGGACAAGGTGATGTC 4440
Db 4367 CAACATCTTTTGGCTTTGTATCATCATCACTTCCAGGAGCAGGGGACAAGGTGATGTC 4426
Qy 4441 TGAATGAGCCTTGGAGAAGAACGAGAGGCTTGCATTTGACTTGCCTATCAGCGCCAAACC 4500
Db 4427 TGAATGAGCCTTGGAGAAGAACGAGAGGCTTGCATTTGACTTGCCTATCAGCGCCAAACC 4486
Qy 4501 CCTGACACGGTACATGCCCCAAACCCGACGTGCTCCAGTATPAAGACGTGGACATTTGT 4560
Db 4487 CCTGACACGGTACATGCCCCAAACCCGACGTGCTCCAGTATPAAGACGTGGACATTTGT 4546
Qy 4561 GGTCTCCCGCCCTTTGAATACTTTCACTAGGCCATGATAGCCCTCAACACTGTGTGCT 4620
Db 4547 GGTCTCCCGCCCTTTGAATACTTTCACTAGGCCATGATAGCCCTCAACACTGTGTGCT 4606
Qy 4621 GATGATGAAGTTCTATGATGACCCCTATGATGACGCTGATGCTGAATGCTGGAACAT 4680
Db 4607 GATGATGAAGTTCTATGATGACCCCTATGATGACGCTGATGCTGAATGCTGGAACAT 4666
Qy 4681 CGTGTTCACATCCATGTTCTCCATGGAAATGCTGCTCAAGATCATGCCCTTTGGGGTGT 4740
Db 4667 CGTGTTCACATCCATGTTCTCCATGGAAATGCTGCTCAAGATCATGCCCTTTGGGGTGT 4726
Qy 4741 GAACTATTTTCAGAGATCCCTGGAATGCTTTGACTTTGTCACTGTGTGTTGGGAAGTATTAC 4800
Db 4727 GAACTATTTTCAGAGATCCCTGGAATGCTTTGACTTTGTCACTGTGTGTTGGGAAGTATTAC 4786
Qy 4801 TGATATTTTATGATTAACAGAGATTTGGGAAACGAAACAATTTTCAATCAA CTTCAAGCTTCTCCG 4860
Db 4787 TGATATTTTATGATTAACAGAGATTTGGGAAACGAAACAATTTTCAATCAA CTTCAAGCTTCTCCG 4846
Qy 4861 CCTCTTTTCGAGCTGCGGGCTGATCAAGCTGCTCCGCGAGGCTTACACCATCCGATCCCT 4920
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Qy 4921 GCTGTGACCTTTTGTCCAGTCTTTCAAGGCCCTGCCCTAGCTGTGTCTGCTCATTTGCCAT 4980
Db 4907 GCTGTGACCTTTTGTCCAGTCTTTCAAGGCCCTGCCCTAGCTGTGTGTCTCATTTGCCAT 4966
Qy 4981 GCTGTCTTTCATCTACGCCATCATTCGGATGCGAGTGTGTTGGGAATATTTGCCCTTGGATGA 5040
Db 4967 GCTGTCTTTCATCTACGCCATCATTCGGATGCGAGTGTGTTGGGAATATTTGCCCTTGGATGA 5026
Qy 5041 TGACACAGCATCAACCGCCACACAACTTCCGAGCGTTTTCGAGCGCTGTGATGCTGCT 5100
Db 5027 TGACACAGCATCAACCGCCACACAACTTCCGAGCGTTTTCGAGCGCTGTGATGCTGCT 5086
Qy 5101 GTTCAGGAGCGCCACGGGGAGGCTTGGCAGCATCATGCTGTCTGCTGCTGAGCAACCA 5160
Db 5087 GTTCAGGAGCGCCACGGGGAGGCTTGGCAGCATCATGCTGTCTGCTTGCCTGAGCAACCA 5146
Qy 5161 GGCCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGACTTTGCCCTACTTCTACTT 5220
Db 5147 GGCCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGACTTTGCCCTACTTCTACTT 5206
Qy 5221 CGTCTCTTTCATCTTCTGTGCTCCTTTCTGATGTTGAACTCTTTGTGCTGTGATCAT 5280
Db 5207 CGTCTCTTTCATCTTCTGTGCTCCTTTCTGATGTTGAACTCTTTGTGCTGTGATCAT 5266

Qy 5281 GGAACAATTTTGTAGTACTCAOCGGGACTTTTCCATCTTAGGTCTTCAACCACTTGGATGA 5340
Db 5267 GGAACAATTTTGTAGTACTCAOCGGGACTTTTCCATCTTAGGTCTTCAACCACTTGGATGA 5326
Qy 5341 GTTCATCCGGTCTGGCTGAAATACGACCGGCTGGTGTGGGGCATCAGTTTACATGA 5400
Db 5327 GTTCATCCGGTCTGGCTGAAATACGACCGGCTGGTGTGGGGCATCAGTTTACATGA 5386
Qy 5401 CATGTTTGTAGATCTCTGAAAACAATGTCCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC 5460
Db 5387 CATGTTTGTAGATCTCTGAAAACAATGTCCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC 5446
Qy 5461 TCGAGTTGCTTACAAGCGCTGGTTCCGATGAATGATGCCCATCTTCCAAACGAGGACATGAC 5520
Db 5447 TCGAGTTGCTTACAAGCGCTGGTTCCGATGAATGATGCCCATCTTCCAAACGAGGACATGAC 5506
Qy 5521 TGTTCATCTTCAGTCCACGCTGATGCGCTCATTCGGAAGGCACTGGAGATCAAGCTGTC 5580
Db 5507 TGTTCATCTTCAGTCCACGCTGATGCGCTCATTCGGAAGGCACTGGAGATCAAGCTGTC 5566
Qy 5581 CCAGCTGGGACAAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGAGATTTCCGTTGT 5640
Db 5567 CCAGCTGGGACAAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGAGATTTCCGTTGT 5626
Qy 5641 GTGGGCCAATCTGCCCCAGAAGAATTTTGGACTTTGTCTGGTACCAACCCCATTAAGCCTGATGA 5700
Db 5627 GTGGGCCAATCTGCCCCAGAAGAATTTTGGACTTTGTCTGGTACCAACCCCATTAAGCCTGATGA 5686
Qy 5701 GATGACAGTGGGGAAGTTTATGACGCTCTGATGATATTTGACTTTTACAAAGCAGAACAA 5760
Db 5687 GATGACAGTGGGGAAGTTTATGACGCTCTGATGATATTTGACTTTTACAAAGCAGAACAA 5746
Qy 5761 AACCAACAGAGACCATGACAGGCTCTGAGAGGCTCTCCAGATGGGTCTCTGTGTC 5820
Db 5747 AACCAACAGAGACCATGACAGGCTCTGAGAGGCTCTCCAGATGGGTCTCTGTGTC 5806
Qy 5821 CTTGTTTCCAACCTCTCAAAGGCCACCTGGAGCAGACA CAGCCGGCTGTGCTCCGAGGAGC 5880
Db 5807 CTTGTTTCCAACCTCTCAAAGGCCACCTGGAGCAGACA CAGCCGGCTGTGCTCCGAGGAGC 5866
Qy 5881 CCGGGTTTTCTTCGACAGAAAGTTTCCACCTCCCTCAGCAATGGCGGGCCATACAAAA 5940
Db 5867 CCGGGTTTTCTTCGACAGAAAGTTTCCACCTCCCTCAGCAATGGCGGGCCATACAAAA 5926
Qy 5941 CCAAGAGAGTGGCATCAAAGAGTCTGCTCTGGGCACTCAAAGGACCCAGATGACCC 6000
Db 5927 CCAAGAGAGTGGCATCAAAGAGTCTGCTCTGGGCACTCAAAGGACCCAGATGACCC 5986
Qy 6001 CCATGAGGCCAGGCCACCTCTGGAGCGTGGCCA CTTCCACAGAGATCCCTGTGGGGCGGTC 6060
Db 5987 CCATGAGGCCAGGCCACCTCTGGAGCGTGGCCA CTTCCACAGAGATCCCTGTGGGGCGGTC 6046
Qy 6061 AGGAGCAGCTGGCTGTGGAGCTTTCAGATGACAGATAA CCGGAGGGGCGCTGATGGGA 6120
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Qy 6121 GCCCAGCTGGGCTGGAGACCCAGGGTCCAGCGGCT CCAATGCCCGCTTGCGGCCGA 6180
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6421 GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGCGCGGAAACGAGAGCGCGCGAGAGCG 6480
6407 GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGCGCGGAAACGAGAGCGCGCGAGAGCG 6466
6481 GGCCCGGTCCAGAGCGAGGCGAGCCCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6540
6467 GGCCCGGTCCAGAGCGAGGCGAGCCCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6526
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6601 CCCAAGCTGCGCAACAGCTGGCCAGAGCGGGAGCCCGAAGCCCGCGAAGCCCGCTCTCTCT 6660
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RESULT 6
US-08-149-097D-7
; Sequence 7, Application US/08149097D
; Patent No. 5874236

GENERAL INFORMATION:
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; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
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; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,097D
; FILING DATE: 05-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/105,536
; FILING DATE: 11-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US92/06903
; FILING DATE: 14-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,231
; FILING DATE: 13-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/869,354
; FILING DATE: 10-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7362 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 144..7163

FEATURE:		5'UTR	
NAME/KEY:	1..143		
LOCATION:			
FEATURE:		3'UTR	
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LOCATION:			
US-08-149-097D-7			
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QY	61	GCTGCTCCGCTCTCAGAGCCCTGGGCGGCGGCGGCGGCGGCTCCCTCCGCGGGGCGGTGGGCGG	120
DB	60	GCTGCTCCGCTCTCAGAGCGCT-GGCGGCGGCGGCGGCGGCTCCCTCCGCGGGGCGGTGGGCGG	118
QY	121	GGGATGCACGCGGGGCGCGGAGGCATGGTCCGCTTCGGGGACGAGCTGGGCGGCGGTCTA	180
DB	119	GGGATGCACGCGGGGCGCGGAGGCATGGTCCGCTTCGGGGACGAGCTGGGCGGCGGTCTA	178
QY	181	TGGAGGCGCGGCGGCGGAGAGCGGGCGCGGGGGGGGGGGCGGCGGGCGGGGGGGCGCC	240
DB	179	TGGAGGCGCGCGCGGCGGAGAGCGGGCGCGGGGGGGGGGGCGGCGGGCGGGGGGGCGCC	238
QY	241	GGGTCCCGGGGGGCTGCAGCCCGGCGAGCGGGTCTCTCAAGCAATCGATCGCGCAGCG	300
DB	239	GGGTCCCGGGGGGCTGCAGCCCGGCGAGCGGGTCTCTCAAGCAATCGATCGCGCAGCG	298
QY	301	CGCGCGGACCATGGCGCTGTAAACCCCATTCGCGGTCAAGCAGAACTGCTTCAACGTCAA	360
DB	299	CGCGCGGACCATGGCGCTGTAAACCCCATTCGCGGTCAAGCAGAACTGCTTCAACGTCAA	358
QY	361	CGGCTCGCTCTTCCTTACGAGGAGCAAGTGGTCCGCAATACGCGAAGCGCATCAC	420
DB	359	CGGCTCGCTCTTCCTTACGAGGAGCAAGTGGTCCGCAATACGCGAAGCGCATCAC	418
QY	421	CGAGTGGCTCCATTCGAGTATATGATCTGGCCAGCAACCATCATCGCCAACTGCATCGT	480
DB	419	CGAGTGGCTCCATTCGAGTATATGATCTGGCCAGCAACCATCATCGCCAACTGCATCGT	478
QY	481	GGCCCTGGAGCAGCACTCCCTGATGGGGAACAAACCGCCCATGTCGAGCGGCTGGACGA	540
DB	479	GGCCCTGGAGCAGCACTCCCTGATGGGGAACAAACCGCCCATGTCGAGCGGCTGGACGA	538
QY	541	CAGGAGCCCTATTTTCATCGGATCTTTTGTTCGAGGCGAGGATCAAAATCATCGCTCT	600
DB	539	CAGGAGCCCTATTTTCATCGGATCTTTTGTTCGAGGCGAGGATCAAAATCATCGCTCT	598
QY	601	GGGCTTTGTCTTCCAAAGGCTCTTACCTGCGGAAAGGCTGGAAAGTCTATGGACTTCGT	660
DB	599	GGGCTTTGTCTTCCAAAGGCTCTTACCTGCGGAAAGGCTGGAAAGTCTATGGACTTCGT	658
QY	661	GCTGCTCTCACAGGATCTTGGCAAGGCTGGAACTGACTTCGACCTCGGAAACACTGAG	720
DB	659	GCTGCTCTCACAGGATCTTGGCAAGGCTGGAACTGACTTCGACCTCGGAAACACTGAG	718
QY	721	GGCTGTGCGGTGTGAGGCGGCTTGAAGCTGGTGTCTGGGATTCGAAAGTTTGCAGGTGGT	780
DB	719	GGCTGTGCGGTGTGAGGCGGCTTGAAGCTGGTGTCTGGGATTCGAAAGTTTGCAGGTGGT	778
QY	781	GCTCAAGTCCATCATGAGGCGATGGTTCCACTCTCGAGATTCGGGCTGCTCTCTTCTT	840
DB	779	GCTCAAGTCCATCATGAGGCGCATGGTTCCACTCTCGAGATTCGGGCTGCTCTCTTCTT	838
QY	841	TGCCATCTCATGTTTGGCATATGGCTGGAGTTCATATGGGCAAGTTTCCAAAGGC	900
DB	839	TGCCATCTCATGTTTGGCATATGGCTGGAGTTCATATGGGCAAGTTTCCAAAGGC	898
QY	901	CTGTTTCCCCCAACGACAGATGCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC	960

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Db	959	CCGAGCCCGGCTGTGCGAGGCGACACTGAGTGC CGGAGTACTTGGCCAGACCAACTT	1018
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Db	1019	TGGCATCACCAACTTTGACAATATCTGTTTGGCATCTTTCGCGGTGTTCCAGTGCATCAC	1078
Qy	1081	CATGGAGGCTGACATGACATCTCTATATAAACAAGATGCGGCGGCAACCTGGAA	1140
Db	1079	CATGGAGGCTGACATGACATCTCTATATAAACAAGATGCGGCGGCAACCTGGAA	1138
Qy	1141	CTGGCTCTACTCTCATCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTGT	1200
Db	1139	CTGGCTCTACTCTCATCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTGT	1198
Qy	1201	GGGCGTGTCTCTCGGGGAGTTTGCACAGGAGCGAGAGGGTGGAGAACCGCGCGCTT	1260
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Qy	1321	CTTCAAGGCGGAGAACTCATGTGCGCGAGGAGGACAGAAATGCGAGGAGAAAGTCCCC	1380
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Db	1679	GACCTGTATTTTTCAGAGTTTCTTTTCTGGGTCTCTTCTCACAGAGATGTCCTTGAA	1738
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Qy 901 CTGTTTCCCAACAGCAGATCGGAGCCCGTGGTGACTTCCCTGTGGCAAGAGGC 960
Db 899 CTGTTTCCCAACAGCAGATCGGAGCCCGTGGTGACTTCCCTGTGGCAAGAGGC 958
Qy 961 CCCAGCCGGTGTGCGAGGCGACACTGAGTGGCGGGAGTACTGGCCAGGACCCAACTT 1020
Db 959 CCCAGCCGGTGTGCGAGGCGACACTGAGTGGCGGGAGTACTGGCCAGGACCCAACTT 1018
Qy 1021 TGGCATCAACCAACTTTGACAAATCTGTTTGGCATCTTGACGGTGTTCAGTGCATCAC 1080
Db 1019 TGGCATCAACCAACTTTGACAAATCTGTTTGGCATCTTGACGGTGTTCAGTGCATCAC 1078
Qy 1081 CATGGAGGCTGGACTGACATCTCTATATACAAACGATCGGCGCGCAACCTGGAA 1140
Db 1079 CATGGAGGCTGGACTGACATCTCTATATACAAACGATCGGCGCGCAACCTGGAA 1138
Qy 1141 CTGGCTCTACTTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTGTCT 1200
Db 1139 CTGGCTCTACTTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTGTCT 1198
Qy 1201 GGGCGTCTCTCGGGGAGTTTGCAGGAGCGAGAGGGTGGAGAACCGCGCGCTT 1260
Db 1199 GGGCGTCTCTCGGGGAGTTTGCAGGAGCGAGAGGGTGGAGAACCGCGCGCTT 1258
Qy 1261 CTGGAAGCTGGCGCGGACGACGATCGAGCGAGCTCAAACGGGTACCTGGAGTGGAT 1320

Db 1259 CTTGAAGCTCGCGCGGACGAGCAGATCGAGCGAGAGCTCAACGGGTACTCTGGAGTGGAT 1318
Qy 1321 CTTCAAGCGCGAGGAAGTCAATGCTGGCCGAGGAGGACAGGAATGCAGAGGAGAGTCCCC 1380
Db 1319 CTTCAAGCGCGAGGAAGTCAATGCTGGCCGAGGAGGACAGGAATGCAGAGGAGAGTCCCC 1378
Qy 1381 TTTGGAGCTGCTGAAGAGAGCGGCCACCAAGAGAGCAGAAATGACTGATCAACGAGA 1440
Db 1379 TTTGGAGCTGCTGAAGAGAGCGGCCACCAAGAGAGCAGAAATGACTGATCAACGAGA 1438
Qy 1441 GGAGGAGAGAGCGGTTTGCAGATCTCTGCTGTTTGGATCCCCCTTCCCGCGGCCAG 1500
Db 1439 GGAGGAGAGAGCGGTTTGCAGATCTCTGCTGTTTGGATCCCCCTTCCCGCGGCCAG 1498
Qy 1501 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCAATACTTCCGAGGAAGAGAGATGTTCCG 1560
Db 1499 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCAATACTTCCGAGGAAGAGAGATGTTCCG 1558
Qy 1561 GTTTTTTATCCGCGCATGTGTGAAGGCTCAGAGTTCTACTGGGTGTGCTGTGCTGGT 1620
Db 1559 GTTTTTTATCCGCGCATGTGTGAAGGCTCAGAGCTTCTACTGGGTGTGCTGTGCTGGT 1618
Qy 1621 GGCCCTGAACACACTGTGTGCGCATGTGTGCAATTACAACGCGCGCGGCTTACCAC 1680
Db 1619 GGCCCTGAACACACTGTGTGCGCATGTGTGCAATTACAACGCGCGCGGCTTACCAC 1678
Qy 1681 GACCTGTATTTTCAGAGTTTGTTCCTGGGTCTCTTCTCACAGAGATGTCCTGAA 1740
Db 1679 GACCTGTATTTTCAGAGTTTGTTCCTGGGTCTCTTCTCACAGAGATGTCCTGAA 1738
Qy 1741 GATGTATGGCTGGGCGCCAGAAAGTACTTCCGGTCTCTTCAACCTGCTTGCATTTGG 1800
Db 1739 GATGTATGGCTGGGCGCCAGAAAGTACTTCCGGTCTCTTCAACCTGCTTGCATTTGG 1798
Qy 1801 GGTCACTGCTGGGAGCGTCTTTCAGTGTGCTGGGGGCCATCAAGCGGGAAGCTCCTT 1860
Db 1799 GGTCACTGCTGGGAGCGTCTTTCAGTGTGCTGGGGGCCATCAAGCGGGAAGCTCCTT 1858
Qy 1861 TGGGATCAGTGTGCTCGGGCCCTCGGCTGCTGAGGATCTTCAAACTCACGAAGTACTG 1920
Db 1859 TGGGATCAGTGTGCTCGGGCCCTCGGCTGCTGAGGATCTTCAAACTCACGAAGTACTG 1918
Qy 1921 GAGTCTCTCGGAAACCTGTGTGTGCTGCTGTGAACCTCATGAAGTCCATCAGCT 1980
Db 1919 GAGTCTCTCGGAAACCTGTGTGTGCTGCTGTGAACCTCATGAAGTCCATCAGCT 1978
Qy 1981 GCTCTTCTTCTCTTCTGTTTCAATGTTGTTCTTGGCTGCTGGGATGAGCTGTTGG 2040
Db 1979 GCTCTTCTTCTCTTCTGTTTCAATGTTGTTCTTGGCTGCTGGGATGAGCTGTTGG 2038
Qy 2041 GGGACAGTTCAAATTCAGGATGAGACTCCCAACCAACTTCGACACCTTCCCTGCGGC 2100
Db 2039 GGGACAGTTCAAATTCAGGATGAGACTCCCAACCAACTTCGACACCTTCCCTGCGGC 2098
Qy 2101 CATCTCTCATGCTTCCAGATCTCGAGGAGGAGACTGGAATGCAAGTGTATCAGG 2160
Db 2099 CATCTCTCATGCTTCCAGATCTCGAGGAGGAGACTGGAATGCAAGTGTATCAGG 2158
Qy 2161 GATCGAATCGAAGGCGGCTCAGCAAGGATGTTCTGCTCTTTCATTTTACATTTGCTCT 2220
Db 2159 GATCGAATCGAAGGCGGCTCAGCAAGGATGTTCTGCTCTTTCATTTTACATTTGCTCT 2218
Qy 2221 GACACTGTTCCGAAACTTACACTCTGCTGAATGCTTTCGCGCATCGCTGTGACAACTT 2280
Db 2219 GACACTGTTCCGAAACTTACACTCTGCTGAATGCTTTCGCGCATCGCTGTGACAACTT 2278
Qy 2281 GGCACACGCGCCAAAGCTGACCAAGATGAAGAGGAGTGGAAAGAGAGCCCAATCAGAA 2340
Db 2279 GGCACACGCGCCAAAGCTGACCAAGATGAAGAGGAGTGGAAAGAGAGCCCAATCAGAA 2338
Qy 2341 GCTTGTCTTGCRAAAGGCGCAAGAACTGCTGAAGTCAAGCCCATCTCTGCGCGGACAT 2400
Db 2339 GCTTGTCTTGCRAAAGGCGCAAGAACTGCTGAAGTCAAGCCCATCTCTGCGCGGACAT 2398

QY 2401 CTCATCGCGCCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGC 2460
DB |||||
DB 2399 CTCATCGCGCCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGC 2458
QY 2461 CAGCAGCTACGGCTCGAGAACCTCGGGCGAGCTCGGAGGCGCTGTACAGCGAGATGA 2520
DB |||||
DB 2459 CAGCCAGCTACGGCTCGAGAACCTCGGGCGAGCTCGGAGGCGCTGTACAGCGAGATGA 2518
QY 2521 CCCGAGGAGCGGCTCGCTTCGCCACTACGGCCACCTCGCGCCCGACATCAAGACCA 2580
DB |||||
DB 2519 CCCGAGGAGCGGCTCGCTTCGCCACTACGGCCACCTCGCGCCCGACATCAAGACCA 2578
QY 2581 CTGAGACCGCGCTCGTGTGTGAGCTGGGCGCGCAGCGCGCGCGGGCCCGTGGGAGG 2640
DB |||||
DB 2579 CTTGAGACCGCGCTCGTGTGTGAGCTGGGCGCGCAGCGCGCGCGGGGCGCTGGGAGG 2638
QY 2641 CAAAGCCGACCTGAGGCTCGGAGGCCCCCGAGGGCGTGCACCTTCGCGCAGGACCA 2700
DB |||||
DB 2639 CAAAGCCGACCTGAGGCTCGGAGGCCCCCGAGGGCGTGCACCTTCGCGCAGGACCA 2698
QY 2701 CCGGACCCGACCAAGCAAGACCCCGCGCGGGGACCAAGACCGAGCAGAGGCCCC 2760
DB |||||
DB 2699 CCGGACCCGACCAAGCAAGACCCCGCGCGGGGACCAAGACCGAGCAGAGGCCCC 2758
QY 2761 GAAGCGGAGAGCGGGGAGCCCGGTGCCCGGAGGAGCGCGCGCGCGCCAGGCCA 2820
DB |||||
DB 2759 GAAGCGGAGAGCGGGGAGCCCGGTGCCCGGAGGAGCGCGCGCGCGCCAGGCCA 2818
QY 2821 CAGCAAGGAGGCGCGGGGCCCCCGGAGCGCGGAGCGCGCGCGCGCCAGGCC 2880
DB |||||
DB 2819 CAGCAAGGAGGCGCGGGGCCCCCGGAGCGCGGAGCGCGCGCGCGCCAGGCC 2878
QY 2881 CGAGGCGCGCGCGGCGCACACCGCGCGGCTCCCGGAGGAGCGCGCGCGGAGGCC 2940
DB |||||
DB 2879 CGAGGCGCGCGCGGCGCACACCGCGCGGCTCCCGGAGGAGCGCGCGCGGAGGCC 2938
QY 2941 CCGAGCCACCGCGGCGCACCGGCAACAGATCCGAGCAAGGAGTCCGCGCGCGCGCAAGGG 3000
DB |||||
DB 2939 CCGAGCCACCGCGGCGCACCGGCAACAGATCCGAGCAAGGAGTCCGCGCGCGCGCAAGGG 2998
QY 3001 CGAGCGGCGCGCGGCGCACCGGCGCGGCCCCCGAGCGGGCCCCCGGAGCGGAGCGG 3060
DB |||||
DB 2999 CGAGCGGCGCGCGGCGCACCGGCGCGGCCCCCGAGCGGGCCCCCGGAGCGGAGCGG 3058
QY 3061 GGAGGAGCGGCGCGGCGCACCGGCGCGGCGCACCAAGCGCGAGCTGTCTCAAGGCTGT 3120
DB |||||
DB 3059 GGAGGAGCGGCGCGGCGCACCGGCGCGGCGCACCAAGCGCGAGCTGTCTCAAGGCTGT 3118
QY 3121 GGAGAGGAGGACCGGAGAGGAGGCCACCGAGAGGAGGCTGAGATAGTGGAGCCGA 3180
DB |||||
DB 3119 GGAGAGGAGGACCGGAGAGGAGGCCACCGAGAGGAGGCTGAGATAGTGGAGCCGA 3178
QY 3181 CAAGGAAAAGGAGCTCCGGAAACCAAGCCCGGAGGCCACACTGTGACCTGGAGACCA 3240
DB |||||
DB 3179 CAAGGAAAAGGAGCTCCGGAAACCAAGCCCGGAGGCCACACTGTGACCTGGAGACCA 3238
QY 3241 TGGGACTGTGACTGTGGTCCCATGCACACACTGCCAGCACCTGTCTCCAGAAAGTGA 3300
DB |||||
DB 3239 TGGGACTGTGACTGTGGTCCCATGCACACACTGCCAGCACCTGTCTCCAGAAAGTGA 3298
QY 3301 GGAACAGCCAGAGGATGCAGACATCAGCGGACGTCACTCGCATGGCAGTCAAGCCCC 3360
DB |||||
DB 3299 GGAACAGCCAGAGGATGCAGACATCAGCGGAAAGTCACTCGCATGGCAGTCAAGCCCC 3358
QY 3361 AGACCCGAACACTATTGTACATATCCCAAGTATCGACGGGCCCTCTTGGGGAGGCCAC 3420
DB |||||
DB 3359 AGACCCGAACACTATTGTACATATCCCAAGTATCGTACGGGCCCTCTTGGGGAGGCCAC 3418
QY 3421 GGTGGTCCAGTGTAACTGGAGCTTGGAAAGCCAAAGAGGGGAGAGGAGTGA 3480
DB |||||
DB 3419 GGTGGTCCAGTGTAACTGGAGCTTGGAAAGCCAAAGCAGAGGGGAGAGGAGTGA 3478

QY 3481 AGCGGATGCGTATGAGGAGCGGCCCGCGCTTATCGTCCCATACAGCTCATGTTCTG 3540
DB |||||
DB 3479 AGCGGATGCGTATGAGGAGCGGCCCGCGCTTATCGTCCCATACAGCTCATGTTCTG 3538
QY 3541 TTTAAGCCCAACCAACTGTCTCGCCCGCTTCTGCCACTACATCGTACCATGAGTACTT 3600
DB |||||
DB 3539 TTTAAGCCCAACCAACTGTCTCGCCCGCTTCTGCCACTACATCGTACCATGAGTACTT 3598
QY 3601 CGAGGTGTCACTTCCTGTGTCATCGGCTTGAGCAGCATCGCCCTGGCTGTGAGGACCC 3660
DB |||||
DB 3599 CGAGGTGTCACTTCCTGTGTCATCGGCTTGAGCAGCATCGCCCTGGCTGTGAGGACCC 3658
QY 3661 AGTCCGACAGACTCGGCCCAAGCAACGCTCTGAAATACCTGATTTACATTTTCACTGG 3720
DB |||||
DB 3659 AGTCCGACAGACTCGGCCCAAGCAACGCTCTGAAATACCTGATTTACATTTTCACTGG 3718
QY 3721 TGTCTTTACCTTTGAGATGTGATTAAGATGATCGACTTGGGACTGCTGTCTCAACCTGG 3780
DB |||||
DB 3719 TGTCTTTACCTTTGAGATGTGATTAAGATGATCGACTTGGGACTGCTGTCTCAACCTGG 3778
QY 3781 AGCCTATTTCCGGGACTTGTGGACATTTCTGGACTTCAATTTGTCAGTGCGCCCTGGT 3840
DB |||||
DB 3779 AGCCTATTTCCGGGACTTGTGGACATTTCTGGACTTCAATTTGTCAGTGCGCCCTGGT 3838
QY 3841 GGCCTTTGCTTTCTCGAGCTTCGTGGGAGGATCCAAAGGGAAAGACATCAATACCATCAA 3900
DB |||||
DB 3839 GGCCTTTGCTTTCTC-----AGGATCCAAAGGGAAAGACATCAATACCATCAA 3886
QY 3901 GTCTCTGAGAGTCTTCTGTCTCTGCGGCCCTCAAGACCATCAAAAGGCTGCGCCAAAGCT 3960
DB |||||
DB 3887 GTCTCTGAGAGTCTTCTGTCTCTGCGGCCCTCAAGACCATCAAAAGGCTGCGCCAAAGCT 3946
QY 3961 CAAGGCTGTCTTTGACTGTGTGTAACCTCTGAAAGATGCTCTCAACATCTTGATTTGT 4020
DB |||||
DB 3947 CAAGGCTGTCTTTGACTGTGTGTAACCTCTCTGAAAGATGCTCTCAACATCTTGATTTGT 4006
QY 4021 CTACATGCTCTTTCATGTTCAATTTCCGCTCATTTGCGGTGACGCTCTTCAAGGGAGATT 4080
DB |||||
DB 4007 CTACATGCTCTTTCATGTTTCAATTTTCCGCTCATTTGCGGTGACGCTCTTTCANAGGGAATT 4066
QY 4081 TTTCTACTGCACAGATGAATCCAAAGAGCTGGAGAGGAGCTGAGGGGCTGATTTTGA 4140
DB |||||
DB 4067 TTTCTACTGCACAGATGAATCCAAAGAGCTGGAGAGGAGCTGAGGGGCTGATTTTGA 4126
QY 4141 TTATGAGAGGAGGAGTGAAGCTCAGCCAGGCTGAGTGAAGAAATACGCTTTTCACTA 4200
DB |||||
DB 4127 TTATGAGAGGAGGAGTGAAGCTCAGCCAGGCTGAGTGAAGAAATACGCTTTCACTA 4186
QY 4201 CGAATATGCTCTGCGGCTCTGCTGACGCTGTTTCAAGTGTCCACGGGAGAGGCTGGCC 4260
DB |||||
DB 4187 CGAATATGCTCTGCGGCTCTGCTGACGCTGTTTCAAGTGTCCACGGGAGAGGCTGGCC 4246
QY 4261 CATGGTGTGAACACTCCGTGGATGCCCTATGAGGAGGAGGCTCAAGCCCTGGGA 4320
DB |||||
DB 4247 CATGGTGTGAACACTCCGTGGATGCCCTATGAGGAGGAGGCTCAAGCCCTGGGA 4306
QY 4321 CCGCATGAGGCTGTCCATCTTCTACGTGGTCTACTTTGTGGTCTTTTCCCTTCTTCTTCGT 4380
DB |||||
DB 4307 CCGCATGAGGCTGTCCATCTTCTACGTGGTCTACTTTGTGGTCTTTTCCCTTCTTCTTCGT 4366
QY 4381 CAACATCTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGGAACAAGTATGTC 4440
DB |||||
DB 4367 CAACATCTTTGTGGCTTTTGTATCATCATCACTTCCAGGAGCAGGGGGAACAAGTATGTC 4426
QY 4441 TGAATCAGGCTGGAGAGAAAGAGAGGCTTGTGACTTCCCATCAGGAGCAGGGGGAACAAGTATGTC 4500
DB |||||
DB 4427 TGAATCAGGCTGGAGAGAAAGAGAGGCTTGTGACTTCCCATCAGGAGCAGGGGGAACAAGTATGTC 4486
QY 4501 CTTGACACGGTATCATGCCCAAAACCGGCAAGTGGTTCAGTATAAGACGTGAGCACTTTGT 4560
DB |||||
DB 4487 CTTGACACGGTATCATGCCCAAAACCGGCAAGTGGTTCAGTATAAGACGTGAGCACTTTGT 4546
QY 4561 GGTCTCCCCGCTTTTGAATATCTTCAATCATGGCCATGATAGCCCTCAACACTGTGTGTCT 4620

Db	4547		GGTCTCCCGCCCTTTGAATACCTTCATCATGGCCATGATGCCCTCAACACTGFGTGCT	4606
Qy	4621		GATGATGAAGTTCTATGATGACACCTATGATGACGCTGATGCTGAAATGCCTGAAACAT	4680
Db	4607		GATGATGAAGTTCTATGATGACACCTATGATGACGCTGATGCTGAAATGCCTGAAACAT	4666
Qy	4681		CGTGTTCACATCCATGTTCTCATGGAATGGCTGCTGAAGATCATCGCTTTGGGGTGCT	4740
Db	4667		CGTGTTCACATCCATGTTCTCATGGAATGGCTGCTGAAGATCATCGCTTTGGGGTGCT	4726
Qy	4741		GAACTATTTACAGATGCTGGAATGCTTTGACTTTGCTCACTGTGTTGGGAAGTATTAC	4800
Db	4727		GAACTATTTACAGATGCTGGAATGCTTTGACTTTGCTCACTGTGTTGGGAAGTATTAC	4786
Qy	4801		TGATATTTTATGATAACAGAGATTGGGAAACGAAACAAATTTCAACAACCTCAGCTTCCTCCG	4860
Db	4787		TGATATTTTATGATAACAGAGATTGGGAAACGAAACAAATTTCAACAACCTCAGCTTCCTCCG	4846
Qy	4861		CCTCTTTGAGCTCGCGGCTGATCAAGCTGCTCCGCCAGGGCTACACCATTCGCATCCT	4920
Db	4847		CCTCTTTGAGCTCGCGGCTGATCAAGCTGCTCCGCCAGGGCTACACCATTCGCATCCT	4906
Qy	4921		GCTGTGAGCTTTGTCAAGTCCCTCAAGGCCCTGCCCTACGTGTGCTGTGCTCATTTGCCAT	4980
Db	4907		GCTGTGAGCTTTGTCAAGTCCCTCAAGGCCCTGCCCTACGTGTGCTGTGCTCATTTGCCAT	4966
Qy	4981		GCTGTCTTCATCTACGCCATCATCGGCATCGAGTGTGTTGGGAATATTGCTCTGGATGA	5040
Db	4967		GCTGTCTTCATCTACGCCATCATCGGCATCGAGTGTGTTGGGAATATTGCTCTGGATGA	5026
Qy	5041		TGACACAGCATCAACGCCCAACAACTTCCCGACGTTTTTGAAGCCCTGATGCTGCT	5100
Db	5027		TGACACAGCATCAACGCCCAACAACTTCCCGACGTTTTTGAAGCCCTGATGCTGCT	5086
Qy	5101		GTTTCAGGAGCCCAAGGGGAGGCTGGCAGAGATCATGTGTCCTGCTGAGCAACCA	5160
Db	5087		GTTTCAGGAGCCCAAGGGGAGGCTGGCAGAGATCATGTGTCCTGCTGAGCAACCA	5146
Qy	5161		GGCTGTGATGAGCAGGCGCAATGCCACGAGTGTGGAAGTACATTTGCTACTTCTACTT	5220
Db	5147		GGCTGTGATGAGCAGGCGCAATGCCACGAGTGTGGAAGTACATTTGCTACTTCTACTT	5206
Qy	5221		CGTCTCCTTCATCTTCCTGTGCTCCTTTCTGATGTTGAACCTTTTGTGGCTGTGATCAT	5280
Db	5207		CGTCTCCTTCATCTTCCTGTGCTCCTTTCTGATGTTGAACCTTTTGTGGCTGTGATCAT	5266
Qy	5281		GGACAAATTTTGAATACCTCAGCGGGACTCTTCCATCCTAGGTCTCACCACATTTGGATGA	5340
Db	5267		GGACAAATTTTGAATACCTCAGCGGGACTCTTCCATCCTAGGTCTCACCACATTTGGATGA	5326
Qy	5341		GTTTCATCCGGTCTGGGCTGAATACGACCGGCTCGGTGTGGGCGCATCAGTTACAATGA	5400
Db	5327		GTTTCATCCGGTCTGGGCTGAATACGACCGGCTCGGTGTGGGCGCATCAGTTACAATGA	5386
Qy	5401		CATGTTTGAGATGCTGAAACACATGTCCTCCGCTCTGGGGCTGGGGAAGAAATCCCTGC	5460
Db	5387		CATGTTTGAGATGCTGAAACACATGTCCTCCGCTCTGGGGCTGGGGAAGAAATCCCTGC	5446
Qy	5461		TCGAGTTGCTTACAAGGCCCTGGTTCCGATGAACATGCCCATCTCCAAACGAGGACATGAC	5520
Db	5447		TCGAGTTGCTTACAAGGCCCTGGTTCCGATGAACATGCCCATCTCCAAACGAGGACATGAC	5506
Qy	5521		TGTTTCACTTCAGCTCCAGCTGATGGCCCTCATCCGACGCGCATCTGGAGATCAAGCTGGC	5580
Db	5507		TGTTTCACTTCAGCTCCAGCTGATGGCCCTCATCCGACGCGCATCTGGAGATCAAGCTGGC	5566
Qy	5581		CCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGGAGATTTCCGTTGT	5640
Db	5567		CCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGGAGATTTCCGTTGT	5626
Qy	5641		GTGGGCCAATCTGCCCCAGAACTTTTGGACTTGTGCTAGTACCAACCCCATTAAGCCTGATGA	5700

Db	5627		GTGGGCCAATCTGCCCCAGAGACTTTTGGACTTGTGTTGCTGTTACCAACCCCATTAAGCCTGATGA	5686
Qy	5701		GATGACAGTGGGAAAGTTTATCAGCTCTGATGATATTTGACTTTTACAAGCAGAACAA	5760
Db	5687		GATGACAGTGGGAAAGTTTATCAGCTCTGATGATATTTGACTTTTACAAGCAGAACAA	5746
Qy	5761		AACCAACAGAGACAGATGACAGAGGCTCTTGAGGGCTCTCCAGATGGGTCTGTGTCT	5820
Db	5747		AACCAACAGAGACAGATGACAGAGGCTCTTGAGGGCTCTCCAGATGGGTCTGTGTCT	5806
Qy	5821		CCTGTTTCCACCTCTGAAAGGCCACCTTGAGAGCAGACACACCGGCTGTCTCCGAGGAGC	5880
Db	5807		CCTGTTTCCACCTCTGAAAGGCCACCTTGAGAGCAGACACACCGGCTGTCTCCGAGGAGC	5866
Qy	5881		CCGGTTTTTCTTCGACAGAAGAGTTCCACCTCCCTCAGCAATGGGGGCCCATACAAAA	5940
Db	5867		CCGGTTTTTCTTCGACAGAAGAGTTCCACCTCCCTCAGCAATGGGGGCCCATACAAAA	5926
Qy	5941		CCAAGAGATGGCATCAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGAGATGCACC	6000
Db	5927		CCAAGAGATGGCATCAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGAGATGCACC	5986
Qy	6001		CCATGAGGCCAGGCCACCCCTGAGAGTGGCCACTCCACAGAGATCCCTGTGGGGCGGTC	6060
Db	5987		CCATGAGGCCAGGCCACCCCTGAGAGTGGCCACTCCACAGAGATCCCTGTGGGGCGGTC	6046
Qy	6061		AGGAGCACTGGCTGTGAGACGTTTCAGATGACAGATCAACCCGAGGGGGCCCTGATGGGGA	6120
Db	6047		AGGAGCACTGGCTGTGAGACGTTTCAGATGACAGATCAACCCGAGGGGGCCCTGATGGGGA	6106
Qy	6121		GCCCGAGCTGGGCTGGAGAGCCAGGGTTCAGGGGCTCCATGCCCGGCTTGGGGCCGA	6180
Db	6107		GCCCGAGCTGGGCTGGAGAGCCAGGGTTCAGGGGCTCCATGCCCGGCTTGGGGCCGA	6166
Qy	6181		GACTCAGCCGTCACAGATGCCAGCCCATGAAGCGTCCATCTCCACGCTGGCCCGACGC	6240
Db	6167		GACTCAGCCGTCACAGATGCCAGCCCATGAAGCGTCCATCTCCACGCTGGCCCGACGC	6226
Qy	6241		GCCCGTGGGACTCATCTTTTGACAGCACACCCCGGACCGGCCACCCCTTAGCCAGGGGTC	6300
Db	6227		GCCCGTGGGACTCATCTTTTGACAGCACACCCCGGACCGGCCACCCCTTAGCCAGGGGTC	6286
Qy	6301		GTCGCACACACACACACCGCTGCCACCGCCGAGGGGACAGGAGCAGAGGTCCTTGGA	6360
Db	6287		GTCGCACACACACACACCGCTGCCACCGCCGAGGGGACAGGAGCAGAGGTCCTTGGA	6346
Qy	6361		GAAGGGCCCGAGCTGTCTCCGATATGATGGCGACCAAGCAGTCTGTGGGGCCGGG	6420
Db	6347		GAAGGGCCCGAGCTGTCTCCGATATGATGGCGACCAAGCAGTCTGTGGGGCCGGG	6406
Qy	6421		GCTGCCCCCGGAGAGGGGCTTACAGGCTGCCCGCGGAAACGAGAGCCCGCAGGAGCG	6480
Db	6407		GCTGCCCCCGGAGAGGGGCTTACAGGCTGCCCGCGGAAACGAGAGCCCGCAGGAGCG	6466
Qy	6481		GGGCGGCTCCAGAGCGGAGGAGCGCTCATCTCTCTCTCGGAGAGCAGAGCGCTTCTA	6540
Db	6467		GGGCGGCTCCAGAGCGGAGGAGCGCTCATCTCTCTCTCGGAGAGCAGAGCGCTTCTA	6526
Qy	6541		CTCTCGAGCGCTTTGGGGCCGTGAGCCCCCGAGGCCCAAGCCCTCCCTCAGCAGCCA	6600
Db	6527		CTCTCGAGCGCTTTGGGGCCGTGAGCCCCCGAGGCCCAAGCCCTCCCTCAGCAGCCA	6586
Qy	6601		CCCAAAGCTGCCCAACAGCTGGCCAGGAGCGGGACCCCAACCCACAGGGCAGTGTTCGT	6660
Db	6587		CCCAAAGCTGCCCAACAGCTGGCCAGGAGCGGGACCCCAACCCACAGGGCAGTGTTCGT	6646
Qy	6661		GAATGGAGGCCCTTGTGTCAACATCTGTGTGTAGCACCCCGCGCGCGGTGGGGGAG	6720
Db	6647		GAATGGAGGCCCTTGTGTCAACATCTGTGTGTAGCACCCCGCGCGCGGTGGGGGAG	6706
Qy	6721		GCAGCTCCCCCAGAGCCCTGACTCCCCCGCCAGCATCACCTACAAGACGCGCACTC	6780
Db	6707		GCAGCTCCCCCAGAGCCCTGACTCCCCCGCCAGCATCACCTACAAGACGCGCACTC	6766

Db 2039 GGGACAGTTCAAATTCAGGATGAGACTCCCAACCAACTTCGACACCTTCCCTGCGGC 2098
QY 2101 CATCTCACTGCTCTCCAGATCTCGACGGAGAGACTGGAATGCAGTGACGTATCAACGG 2160
Db 2099 CATCTCACTGCTCTCCAGATCTCGACGGAGAGACTGGAATGCAGTGATATCAACGG 2158
QY 2161 GATCGAATCGCAAGGCGGCTGAGCAAAAGGCATGTTCTCGTCTTTTACTTCAATGTGCT 2220
Db 2159 GATCGAATCGCAAGGCGGCTGAGCAAAAGGCATGTTCTCGTCTTTTACTTCAATGTGCT 2218
QY 2221 GACACTGTTGGAATACTACACTCTGCTGAATGCTTTTCTGGCCATCGCTGTGGCAAACT 2280
Db 2219 GACACTGTTGGAATACTACACTCTGCTGAATGCTTTTCTGGCCATCGCTGTGGCAAACT 2278
QY 2281 GCGCAAGCGCCCAAGAGCTGACCAAGATGAAGAGAGATGGAAGAAGCAGCCAAATCAGAA 2340
Db 2279 GCGCAAGCGCCCAAGAGCTGACCAAGATGAAGAGAGATGGAAGAAGCAGCCAAATCAGAA 2338
QY 2341 GCTTGCTCTGCAAAAGGCCAAAGAGTGGCTGAAGTCAAGCCCATGTCTGCCGCGAAAT 2400
Db 2339 GCTTGCTCTGCAAAAGGCCCAAGAGTGGCTGAAGTCAAGCCCATGTCTGCCGCGAAAT 2398
QY 2401 CTCCATCGCCCGCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGCG 2460
Db 2399 CTCCATCGCCCGCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGCG 2458
QY 2461 CAGCCAGCTTACGGCTGCAGAACCTCGCGGCCAGCTGCGAGGCGCTGTACAGCGAGATGGA 2520
Db 2459 CAGCCAGCTTACGGCTGCAGAACCTCGCGGCCAGCTGCGAGGCGCTGTACAGCGAGATGGA 2518
QY 2521 CCCCAGAGAGCGGCTGCGCTTCGCACTACGCGCACTCGCGGCCGACATGAAGACGCA 2580
Db 2519 CCCCAGAGAGCGGCTGCGCTTCGCACTACGCGCACTCGCGGCCGACATGAAGACGCA 2578
QY 2581 CCTGACCGGCGCTGCTGTGTGAGCTGGCCGCGACCGCGCGGGGCGCGTGGAGG 2640
Db 2579 CCTGACCGGCGCTGCTGTGTGAGCTGGCCGCGACCGCGCGGGGCGCGTGGAGG 2638
QY 2641 CAAAGCCGACTGAGGCTGCGAGGCGCCCGAGGCGCTGCACCTCGCGCGCAGGACCA 2700
Db 2639 CAAAGCCGACTGAGGCTGCGAGGCGCCCGAGGCGCTGCACCTCGCGCGCAGGACCA 2698
QY 2701 CCGCACCGCGCAAGGACAAGACCCCGCGCGGGGACAGAGACGAGCAGAGGCCCC 2760
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QY 2761 GAAAGCGGAGCGGGGAGCCGCTGCGCGGAGGAGCGCGCGCGCGCGACCGACGCA 2820
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QY 2821 CAGCAAGGAGCGCGGGGCGCCCGGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCC 2880
Db 2819 CAGCAAGGAGCGCGGGGCGCCCGGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCC 2878
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RESULT 9
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; Sequence 7, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark E.
; APPLICANT: Stauderman, Kenneth A.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
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; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, Suite 700
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/08/984,709A
; APPLICATION NUMBER: US/08/984,709A
; FILING DATE: 02-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 450-8400
; TELEFAX: (619) 587-5360
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7362 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 144..7163
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; US-08-984-709A-7

Query Match 99.2%; Score 7316.4; DB 4; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

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Db 2279 GGCACCGCCCAAGAGCTGACCAAGATGAAGAGGAGTGGAAAGAGAGTGGAAAGAGTGGAA 2338
Qy 2341 GCTTGTCTGCAAAAGCCAAAGAGTGGCTGAAGTCAAGTCCAGTCTCTCTCTCTCTCTCTCT 2400
Db 2339 GCTTGTCTGCAAAAGCCAAAGAGTGGCTGAAGTCAAGTCCAGTCTCTCTCTCTCTCTCTCT 2398
Qy 2401 CTCATCTCGCCGCGCAGGACAGAACTCGGCCAAAGGCGCTCGGTGTGGGAGCAGCGGGC 2460
Db 2399 CTCATCTCGCCGCGCAGGACAGAACTCGGCCAAAGGCGCTCGGTGTGGGAGCAGCGGGC 2458
Qy 2461 CAGCCAGCTACGCTCGGAAACCTCGGGCGCAGCTCGGAGGCGCTGTACAGCGAGATGGA 2520
Db 2459 CAGCCAGCTACGCTCGGAAACCTCGGGCGCAGCTCGGAGGCGCTGTACAGCGAGATGGA 2518
Qy 2521 CCCGAGGAGCGGCTCGGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 2580
Db 2519 CCCGAGGAGCGGCTCGGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 2578

QY	2581	CCTGAGCACGGCCGCTGGTGGTGGAGCTGGGCGCGGACCGGCGCGGGGGCCCGTGGGAGG	2640
Db	2579	CCTGGACCCGGCCGCTGGTGGTGGAGCTGGGCGCGACGCGCGCGGGGGCCCGTGGGAGG	2638
QY	2641	CAAAAGCCCGACCTGAGGCTGCGGAGGCCGCCCGCGAGGGCTGACACCTCCGCGCAGGACCA	2700
Db	2639	CAAAAGCCCGACCTGAGGCTGCGGAGGGCCCGGAGGGCTGACACCTCCGCGCAGGACCA	2698
QY	2701	CCGGCACCCCGCAAAAGGACAAGACCCCCCGCGCGGGGACAGGACCGAGCAGAGGCCCC	2760
Db	2699	CCGGCACCCCGCAAAAGGACAAGACCCCCCGCGCGGGGACAGGACCGAGCAGAGGCCCC	2758
QY	2761	GAAGCGGAGAGCGGGGAGCCCGGTCCCGGGAGAGCGGGCGCGGCGCGCACCCGACGCA	2820
Db	2759	GAAGCGGAGAGCGGGGAGCCCGGTCCCGGGAGAGCGGGCGCGGCGCGCACCCGACGCA	2818
QY	2821	CAGCAAGAGAGCCGCGGGGCCCCCGGAGGCGCGGAGCGCGGCGCGGCGCGAGGCCCGAGGCC	2880
Db	2819	CAGCAAGAGAGCCGCGGGGCCCCCGGAGGCGCGGAGCGCGGCGCGGCGCGAGGCCCGAGGCC	2878
QY	2881	CGAGGGCGCGCGCGCACACCGGCGGGCTCCCCGGAGAGAGGGCGGGCGGAGCGG	2940
Db	2879	CGAGGGCGCGCGCGCGCACACCGGCGGGCTCCCCGGAGAGAGGGCGGGCGGAGCGG	2938
QY	2941	CCGACGCCACCGCGCGCACCGGCACACAGGATCCGAGCAAGAGATGCCCGCGCGCAAGGG	3000
Db	2939	CCGACGCCACCGCGCGCACCGGCACACAGGATCCGAGCAAGAGATGCCCGCGCGCAAGGG	2998
QY	3001	CGAGGGCGCGCGCGCACACCGGGGGGCCCCCGAGCGGGGCCCGGAGCGCGGAGCGG	3060
Db	2999	CGAGGGCGCGCGCGCACACCGGGGGGCCCCCGAGCGGGGCCCGGAGCGGGAGCGGAGCGG	3058
QY	3061	GGAGGAGCGGGCGGGCGGCACCGGGCCCGGCACAAGCGCGAGCCTGCTCAACAGAGCTGT	3120
Db	3059	GGAGGAGCGGGCGGGCGGCACCGGGCCCGGCACAAGCGCGAGCCTGCTCAACAGAGCTGT	3118
QY	3121	GGAGAGGAGACCAACCGAGAAAGGAGGCCACGGAAGAGAGCTGAGATAGTGGAAAGCCGA	3180
Db	3119	GGAGAGGAGACCAACCGAGAAAGGAGGCCACGGAAGAGAGGCTCAGATAGTGGAAAGCCGA	3178
QY	3181	CAAGGMAAAGAGCTCCGGAAACACCAAGCCCGGAGCCACAGCGGAGCCACCTGTGACCTG	3240
Db	3179	CAAGGMAAAGAGCTCCGGAAACCAACAGCCCGGAGCCACCTGTGACCTGAGAGCCAG	3238
QY	3241	TGGAGCTGTGACTGTGGTCCATGCAACAATGCGGAGCCCTGTCTCCAGAGGTGGA	3300
Db	3239	TGGAGCTGTGACTGTGGTCCATGCAACAATGCGGAGCCCTGTCTCCAGAGGTGGA	3298
QY	3301	GGAACGCGAGAGATCGACACATCAGCGGAAGTCACTCGCATGGGCGAGTCAGCCCC	3360
Db	3299	GGAACGCGAGAGATCGACACATCAGCGGAAGTCACTCGCATGGGCGAGTCAGCCCC	3358
QY	3361	AGACCCGAACAATTGTGATATCCAGTGATGCTGACGCGGCCCTCTTGGGGAAGCCAC	3420
Db	3359	AGACCCGAACAATTGTGATATCCAGTGATGCTGACGCGGCCCTCTTGGGGAAGCCAC	3418
QY	3421	GGTGCTCCAGTGGTAACTGGACCTGGAAGCCCAAGCAAGAGGGGAAGAGAGTGGA	3480
Db	3419	GGTGCTCCAGTGGTAACTGGACCTGGAAGCCCAAGCAAGAGGGGAAGAGAGTGGA	3478
QY	3481	AGCGGATGACGTGATGAGGAGCGGGCCCCCGGCCCTATCGTCCCATACAGCTCCATGTTCTG	3540
Db	3479	AGCGGATGACGTGATGAGGAGCGGGCCCCCGGCCCTATCGTCCCATACAGCTCCATGTTCTG	3538
QY	3541	TTTAAAGCCCCAACCTGCTCGCGGCTTCTGCGCATACATGCTGACCATGAGGTACTT	3600
Db	3539	TTTAAAGCCCCAACCTGCTCGCGGCTTCTGCGCATACATGCTGACCATGAGGTACTT	3598
QY	3601	CGAGGTGGTCAATCTCGTGGTCACTCGCTTGAGCAGCATCGCCCTGGGCTGCTGAGACCC	3660
Db	3599	CGAGGTGGTCAATCTCGTGGTCACTCGCTTGAGCAGCATCGCCCTGGGCTGCTGAGACCC	3658
QY	3661	AGTGGCGCACAGACTCGCCCAAGGAACAAACGCTCTGAAATACCTGGGATTAATTTCACTGG	3720

[illegible]

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Qy 4801 TGATAATTTTAGTAAACAGAGATTGCGGAAACGAAACAATTTTCATCAACCTCAGCTTTCCTCCG 4860
Db 4787 TGATAATTTTAGTAAACAGAGATTGCGGAAACGAAACAATTTTCATCAACCTCAGCTTTCCTCCG 4846
Qy 4861 CCTCTTTGAGCTGCGGGCTGTATCAAGCTGTCTCGGCAGGGCTACACCATCCGATCCT 4920
Db 4847 CCTCTTTGAGCTGCGGGCTGTATCAAGCTGTCTCGGCAGGGCTACACCATCCGATCCT 4906
Qy 4921 GCTGTGACCTTTGTCCAGTCTCTTCAAGGCCCTGCCCTAGTGTGTCTGTCTATTGCCAT 4980
Db 4907 GCTGTGACCTTTGTCCAGTCTCTTCAAGGCCCTGCCCTAGTGTGTCTGTCTATTGCCAT 4966
Qy 4981 GCTGTCTTTCATCTPACGCCATCATCGGCATGCGAGTGTCTTTGGGAATATTGCCCTGGATGA 5040
Db 4967 GCTGTCTTTCATCTPACGCCATCATCGGCATGCGAGTGTCTTTGGGAATATTGCCCTGGATGA 5026
Qy 5041 TGACACAGCATTAACCCGCACAAACAATTCGCGACGTTTTTGAAGCCCTGATGTGCT 5100
Db 5027 TGACACAGCATTAACCCGCACAAACAATTCGCGACGTTTTTGAAGCCCTGATGTGCT 5086
Qy 5101 GTTCAGAGCGCCACGGGGAGGCTGSCACGAGATCATGTGTCTGCTGAGCAACCA 5160
Db 5087 GTTCAGAGCGCCACGGGGAGGCTGSCACGAGATCATGTGTCTGCTGAGCAACCA 5146
Qy 5161 GGCCTGTGATGAGCAGCGCCAAATGCCACCGAGTGTGGAAGTACTTTGCTACTTCTACTT 5220
Db 5147 GGCCTGTGATGAGCAGCGCCAAATGCCACCGAGTGTGGAAGTACTTTGCTACTTCTACTT 5206
Qy 5221 CGTCTCTCTCATCTTCTGTGCTCTCTTCTGTATGTTGAACTCTTTGTGTGGCTGTGATCAT 5280
Db 5207 CGTCTCTCTCATCTTCTGTGCTCTCTTCTGTATGTTGAACTCTTTGTGTGGCTGTGATCAT 5266
Qy 5281 GGACAATTTTGAATPACCTCAGCGGGACTCTTCCATCCTAGGTCTTCCACACTTGGATGA 5340
Db 5267 GGACAATTTTGAATPACCTCAGCGGGACTCTTCCATCCTAGGTCTTCCACACTTGGATGA 5326
Qy 5341 GTTCATCCGGTCTGGGCTGAATACGACCGGCTGCGTGTGGGGCATCAGTTTACAATGA 5400
Db 5327 GTTCATCCGGTCTGGGCTGAATACGACCGGCTGCGTGTGGGGCATCAGTTTACAATGA 5386
Qy 5401 CATGTTTGAATGTGAAACACATGTCCCGCTCTGCGGCTGGGGAGAAATGCCCTGC 5460
Db 5387 CATGTTTGAATGTGAAACACATGTCCCGCTCTGCGGCTGGGGAGAAATGCCCTGC 5446
Qy 5461 TCGAGTTGCTTACAAGCGCTGTTTCGATGAACATGCCATCTTCCAAACGAGGACATGAC 5520
Db 5447 TCGAGTTGCTTACAAGCGCTGTTTCGATGAACATGCCATCTTCCAAACGAGGACATGAC 5506
Qy 5521 TGTTCACTTTCACGTCCACGCTGATGGGCTCTCATCCGACGGCACTGGAGATCAAGCTGGC 5580
Db 5507 TGTTCACTTTCACGTCCACGCTGATGGGCTCTCATCCGACGGCACTGGAGATCAAGCTGGC 5566
Qy 5581 CCCAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGAGATTTCCGTTGT 5640
Db 5567 CCCAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGAGATTTCCGTTGT 5626
Qy 5641 GTGGGCAATCTGCCAGAGACTTTTGAAGTCTGTTGCTGTTACCCACCCCAAGCTGATGA 5700
Db 5627 GTGGGCAATCTGCCAGAGACTTTTGAAGTCTGTTGCTGTTACCCACCCCAAGCTGATGA 5686
Qy 5701 GATGACAGTGGGAAGTGTATGAGCTCTGATGATATTTGACTTCTACAAGCAGAACAA 5760
Db 5687 GATGACAGTGGGAAGTGTATGAGCTCTGATGATATTTGACTTCTACAAGCAGAACAA 5746
Qy 5761 AACCAACAGAGACAGATGACAGAGGTCTCTGGAGGCTCTTCCAGATGGGTCTGTGTC 5820
Db 5747 AACCAACAGAGACAGATGACAGAGGTCTCTGGAGGCTCTTCCAGATGGGTCTGTGTC 5806
Qy 5821 CCTGTTCCACCTCTGAAGGCCACCTGGAGCAGACACAGCCGCTGTCTCCGAGGAGC 5880
Db 5807 CCTGTTCCACCTCTGAAGGCCACCTGGAGCAGACACAGCCGCTGTCTCCGAGGAGC 5866

Qy 5881 CCGGGTTTTCTTCGACAGAAGATTCTCACTCCCTCAGCAATGGGGGCCATACAAAA 5940
Db 5867 CCGGGTTTTCTTCGACAGAAGATTCTCACTCCCTCAGCAATGGGGGCCATACAAAA 5926
Qy 5941 CCAAGAGATGGCATCAAAAGATCTGTCTCTGGGCACTCAAAAGGACCCAGGATGCACC 6000
Db 5927 CCAAGAGATGGCATCAAAAGATCTGTCTCTGGGCACTCAAAAGGACCCAGGATGCACC 5986
Qy 6001 CATATAGGCGCAGGCCCACTCCCTGAGGCTGGCCACTCCACAGAGATCCCTGTGGGGCGGTC 6060
Db 5987 CATATAGGCGCAGGCCCACTCCCTGAGGCTGGCCACTCCACAGAGATCCCTGTGGGGCGGTC 6046
Qy 6061 AGGAGCACTGGCTGTGGAACGTTTCAAGATGCAGACATAAACCCGAGGGGCTCTGATGGGGA 6120
Db 6047 AGGAGCACTGGCTGTGGAACGTTTCAAGATGCAGACATAAACCCGAGGGGCTCTGATGGGGA 6106
Qy 6121 GCGCCAGCTGGCTGGAGAGCCAGGTCGAGCGGCTCCATGCCCGCTTTCGGGCCGA 6180
Db 6107 GCGCCAGCTGGCTGGAGAGCCAGGTCGAGCGGCTCCATGCCCGCTTTCGGGCCGA 6166
Qy 6181 GACTCAGCCCGTCAAGATGCCAGCCCATGAAGCGTCTCATCTCAGCTGGCCAGCG 6240
Db 6167 GACTCAGCCCGTCAAGATGCCAGCCCATGAAGCGTCTCATCTCAGCTGGCCAGCG 6226
Qy 6241 GCGCCGTGGGACTCATCTTTTGCAGCAACACCCCGGACCCGCCACCCCTTAGCCAGGCGTC 6300
Db 6227 GCGCCGTGGGACTCATCTTTTGCAGCAACACCCCGGACCCGCCACCCCTTAGCCAGGCGTC 6286
Qy 6301 GTGCGACCAACCAACACCGCTGCCACCGCCGCGGACAGGAAGAGGTTCCTTGA 6360
Db 6287 GTGCGACCAACCAACACCGCTGCCACCGCCGCGGACAGGAAGAGGTTCCTTGA 6346
Qy 6361 GAAGGGGCCCAGGCTGTCTGCCATATGATGCGCACCAAGCAGTGTCTGTGGGGCCGG 6420
Db 6347 GAAGGGGCCCAGGCTGTCTGCCATATGATGCGCACCAAGCAGTGTCTGTGGGGCCGG 6406
Qy 6421 GCTGCCCCCGGGAGAGGGGCTTACAGGCTGCGCGGGGAAACGAGAGCGCCGCGAGGAGCG 6480
Db 6407 GCTGCCCCCGGGAGAGGGGCTTACAGGCTGCGCGGGGAAACGAGAGCGCCGCGAGGAGCG 6466
Qy 6481 GGGCGGTCCCAGAGGGGAGGCGGCTCATCTCTCTCGGAGAGCAGCGCTTCTA 6540
Db 6467 GGGCGGTCCCAGAGGGGAGGCGGCTCATCTCTCTCGGAGAGCAGCGCTTCTA 6526
Qy 6541 CTCTCGACCGCTTTGGGGGCGGTGAGCGCCCGAAGCCCAAGCCCTCCTCAGCAGCCCA 6600
Db 6527 CTCTCGACCGCTTTGGGGGCGGTGAGCGCCCGAAGCCCAAGCCCTCCTCAGCAGCCCA 6586
Qy 6601 CCCAAGCTCGCCAAACAGCTGGCCAGGAGCGGGAACCCCAACCCACAGGGCAGTGTTCCT 6660
Db 6587 CCCAAGCTCGCCAAACAGCTGGCCAGGAGCGGGAACCCCAACCCACAGGGCAGTGTTCCT 6646
Qy 6661 GAATGGAGGCCCTTGTGTCAACATCTGTGTAGTACCCCGCGCGGCTGGGGGAG 6720
Db 6647 GAATGGAGGCCCTTGTGTCAACATCTGTGTAGTACCCCGCGCGGCTGGGGGAG 6706
Qy 6721 GCAGCTCCCCCAGACGCCCTGTACTCTCCGCGCCAGCATCACCTACAAGACGCCCAATC 6780
Db 6707 GCAGCTCCCCCAGACGCCCTTGTACTCTCCGCGCCAGCATCACCTACAAGACGCCCAATC 6766
Qy 6781 CTCACCCATCACTTCCCGGGGCTCAGACCAAGCTCTCTTGCCTTCTCCCAAGCCGGCT 6840
Db 6767 CTCACCCATCACTTCCCGGGGCTCAGACCAAGCTCTCTTGCCTTCTCTCCCAAGCCGGCT 6826
Qy 6841 CAGCGTGGGCTTTCGAAACAAACCGCTCTGTGCGAGAGACCCCTCAGCCAGGCCCT 6900
Db 6827 CAGCGTGGGCTTTCGAAACAAACCGCTCTGTGCGAGAGACCCCTCAGCCAGGCCCT 6886
Qy 6901 GCGCCCTGGCTCTCGAATTTGGCTCTGACCTTACCTTGGGGAGCGTCTGACAGTGGAGC 6960
Db 6887 GCGCCCTGGCTCTCGAATTTGGCTCTGACCTTACCTTGGGGAGCGTCTGACAGTGGAGC 6946

Qy	6961	CTCTGTCTCA	CGCCCTGTGCT	GAGGACACG	CTCACTTTTCG	AGAGGCTGTG	CCACCAACTC	7020
Db	6947	CTCTGTCTCA	CGCCCTGTGCT	GAGGACACG	CTCACTTTTCG	AGAGGCTGTG	CCACCAACTC	7006
Qy	7021	GGGCGGCTCT	CTCAGAGACTT	CTCAGGTGT	CCTCCCTGAC	TCCAGTCTCAC	CCCTCTCCG	7080
Db	7007	GGGCGGCTCT	CTCAGAGACTT	CTCAGGTGT	CCTCCCTGAC	TCCAGTCTCAC	CCCTCTCCG	7066
Qy	7081	CCGCGTGC	CAACGGTTTAC	CACTGCAC	CCCTGGGACTCAG	CTCGGGTGGCCG	AGCAGCGCA	7140
Db	7067	CCGCGTGC	CAACGGTTTAC	CACTGCAC	CCCTGGGACTCAG	CTCGGGTGGCCG	AGCAGCGCA	7126
Qy	7141	CAGCTACCA	CCCACTGAC	CAAGACCACTGG	TGTAGCTGAC	CGTGACCGCTC	AGACGC	7200
Db	7127	CAGCTACCA	CCCACTGAC	CAAGACCACTGG	TGTAGCTGAC	CGTGACCGCTC	AGACGC	7186
Qy	7201	CTGCATGCAG	CAGGCGGTGT	CTCAGTGGATAG	TTTTATCAT	CCACACAGGGG	CAGTCCG	7260
Db	7187	CTGCATGCAG	CAGGCGGTGT	CTCAGTGGATAG	TTTTATCAT	CCACACAGGGG	CAGTCCG	7246
Qy	7261	CCCTCGGGG	GAGGCTTTGCC	ACCTTGGTGAGG	CTCCTGTGGCCCT	TCCCTCCCTCCCT	CT	7320
Db	7247	CCCTCGGGG	GAGGCTTTGCC	ACCTTGGTGAGG	CTCCTGTGGCCCT	TCCCTCCCTCCCT	CT	7306
Qy	7321	CCCTCTTTT	ACTCTAGAC	GACGAATAA	AGCCCTGTG	CTTGAGTGA	CGTACCGC	7376
Db	7307	CCCTCTTTT	ACTCTAGAC	GACGAATAA	AGCCCTGTG	CTTGAGTGA	CGTACCGC	7362

RESULT 10

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US-08-450-272-7
; Sequence 7, Application US/08450272
; Patent No. 6387696
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Gellespie, Alison
; APPLICANT: Feldman, Daniel
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: US
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CLASSIFICATION: 435
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; APPLICATION NUMBER: 08/404,950
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Qy	241	GGGTCCCGGGGGGTGCGAGCCCGGCCAGCGGGTCTCTACAAAGCAATCGATCGCGAGCG	300
Db	239	GGGTCCCGGGGGGTGCGAGCCCGGCCAGCGGGTCTCTACAAAGCAATCGATCGCGAGCG	298
Qy	301	CGCGGACCACTGGCGGTGTAAACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA	360
Db	299	CGCGGACCACTGGCGGTGTAAACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA	358
Qy	361	CCGCTCGCTCTTCTGTCTTACGAGGACAACGTCGTCCGCAAAATACGCGAAGCGCATCAC	420
Db	359	CCGCTCGCTCTTCTGTCTTACGAGGACAACGTCGTCCGCAAAATACGCGAAGCGCATCAC	418
Qy	421	CGAGTGGCTCCATTCGAGTATATGATCTTGGCCACCATCATCGCCAACTGCGATCGTCT	480
Db	419	CGAGTGGCTCCATTCGAGTATATGATCTTGGCCACCATCATCGCCAACTGCGATCGTCT	478
Qy	481	GGCCCTGGAGCAGCACTCCCTGATGGGGAACAAAACGCCCATGTCCGAGCGGCTGGACGA	540
Db	479	GGCCCTGGAGCAGCACTCCCTGATGGGGAACAAAACGCCCATGTCCGAGCGGCTGGACGA	538
Qy	541	CACGGAGCCATTTTCATCGGGATCTTTTGTCTCGAGGCAAGGATCAAAATCATCGCTCT	600
Db	539	CACGGAGCCATTTTCATCGGGATCTTTTGTCTCGAGGCAAGGATCAAAATCATCGCTCT	598
Qy	601	GGGCTTTGTCTTCCACAAGGCTCTTACTCGGGAAACGGCTGGAAACGTCATGGACTTCGT	660
Db	599	GGGCTTTGTCTTCCACAAGGCTCTTACTCGGGAAACGGCTGGAAACGTCATGGACTTCGT	658
Qy	661	GGTCTCTCACAGGGATCTTTCACAGGCTGGAACTGACTTCGACCTGGGAACACTGAG	720
Db	659	GGTCTCTCACAGGGATCTTTCACAGGCTGGAACTGACTTCGACCTGGGAACACTGAG	718
Qy	721	GGCTGTGCGTGTCTGAGGGCCCCGAAAGCTGGTGTCTGGGATTCGAAGTTTGCAGGTGGT	780
Db	719	GGCTGTGCGTGTCTGAGGGCCCCGAAAGCTGGTGTCTGGGATTCGAAGTTTGCAGGTGGT	778
Qy	781	GCTCAAGTCCATCATGAAGGCGCTGTTTCACTCTCGAGATTTGGGCTGCTTCTCTTCTT	840
Db	779	GCTCAAGTCCATCATGAAGGCGCTGTTTCCACTCTCGAGATTTGGGCTGCTTCTCTTCTT	838
Qy	841	TGCCATCTCATGTTTGCATCATTTGCGCTGGAGTCTACATGGGCAAGTTTCCACAAGGC	900
Db	839	TGCCATCTCATGTTTGCATCATTTGCGCTGGAGTCTACATGGGCAAGTTTCCACAAGGC	898
Qy	901	CTGTTTTCCCCAACAGCAGATGCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC	960
Db	899	CTGTTTTCCCCAACAGCAGATGCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC	958
Qy	961	CCAGCCCGGCTGTGCGAGGGCGACATGAGTGC CGGAGTACTTGGCCAGGACCCAACTT	1020
Db	959	CCAGCCCGGCTGTGCGAGGGCGACATGAGTGC CGGAGTACTTGGCCAGGACCCAACTT	1018
Qy	1021	TGGCATCAACCAACTTGCATATATCTGTTTGGCCATCTTGAAGGTTTGGGCTGATCAC	1080
Db	1019	TGGCATCAACCAACTTGCATATATCTGTTTGGCCATCTTGAAGGTTTGGGCTGATCAC	1078
Qy	1081	CATGGAGGCTGGAGTGAACCTCTATATAAACAAGATGGCGCCGGCAACACTTGGAA	1140
Db	1079	CATGGAGGCTGGAGTGNACCTCTATATATAAACAAGATGGCGCCGGCAACACTTGGAA	1138
Qy	1141	CTGGCTCTACTCATATCCCTCTCATCATCATCGGCTCTCTTCTCATGTCAAACCTGGTCT	1200
Db	1139	CTGGCTCTACTCATATCCCTCTCATCATCATCGGCTCTCTTCTCATGTCAAACCTGGTCT	1198
Qy	1201	GGGCGTCTCTCGGGGAGTTTGGCAAGGAGCGAGAGGGTGGAGAACCGCGCGGCTT	1260
Db	1199	GGGCGTCTCTCGGGGAGTTTGGCAAGGAGCGAGAGGGTGGAGAACCGCGCGGCTT	1258

Qy	1261	CCTGAAGCTCGCGGAGCAGCAGATCGAGCGAGCTCAACGGGTACTCTGAGTGGAT	1322
Db	1259	CCTGAAGCTCGCGCGCAGCAGCAGATCGAGCGAGCTCAACGGGTACTCTGAGTGGAT	1318
Qy	1321	CTTCAAGCGCGAGGAAGTCACTGTCGCCGAGGAGGACAGGAATGCAGAGGAGAAGTCCCC	1380
Db	1319	CTTCAAGCGCGAGGAAGTCACTGTCGCCGAGGAGGACAGGAATGCAGAGGAGAAGTCCCC	1378
Qy	1381	TTTGGAGCTGCTGAAGAGAGCGGCCACCACGAAGAGAGCAGAAATGACTGATCCACGCAGA	1440
Db	1379	TTTGGAGCTGCTGAAGAGAGCGGCCACCACGAAGAGAGCAGAAATGACTGATCCACGCAGA	1438
Qy	1441	GGAGGAGAGGAGCCGGTTTCAGATCTGTGTCTGTTGGATCCCCCTTGTGCCCGCGCCAG	1500
Db	1439	GGAGGAGAGGAGCCGGTTTCAGATCTGTGTCTGTTGGATCCCCCTTGTGCCCGCGCCAG	1498
Qy	1501	CCTCAAGAGCGGAGACAGCAGAGAGCTGCTCATACTTCCGAGGAAAGAGAAATGTTCCG	1560
Db	1499	CCTCAAGAGCGGAGACAGCAGAGAGCTGCTCATACTTCCGAGGAAAGAGAAATGTTCCG	1558
Qy	1561	GTTTTTTTATCCGGCGCATGGTGAAGGCTCAGAGCTTCTACTGGGTGGTGTGTGCGTGGT	1620
Db	1559	GTTTTTTTATCCGGCGCATGGTGAAGGCTCAGAGCTTCTACTGGGTGGTGTGTGCGTGGT	1618
Qy	1621	GGCCCTGAAACACTGTGTGTGGCCATGTFGTCAATTAACAACAGCCGCGCGGCTTACCAC	1680
Db	1619	GGCCCTGAAACACTGTGTGGCCATGTFGTCAATTAACAACAGCCGCGCGGCTTACCAC	1678
Qy	1681	GACCCGTATTTTGCAGAGTTTCTTTTCCCTGGGTCTCTCCCTCACAGAGATGCCCTGAA	1740
Db	1679	GACCCGTATTTTGCAGAGTTTCTTTTCCCTGGGTCTCTCCCTCACAGAGATGCCCTGAA	1738
Qy	1741	GATGTATGGCTCGGGGCCCAAGAGCTACTTCCGGTCTCTCTTCAACTGCCTTCGACTTTGG	1800
Db	1739	GATGTATGGCTCGGGGCCCAAGAGCTACTTCCGGTCTCTCTTCAACTGCCTTCGACTTTGG	1798
Qy	1801	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCCATCAAGCGGGAAGTCCCTT	1860
Db	1799	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCCATCAAGCGGGAAGTCCCTT	1858
Qy	1861	TGGGATCAGTGTCTCGGGCCCTCGCCCTGCTGAGGATCTTCAAAGTCACGAAGTACTG	1920
Db	1859	TGGGATCAGTGTCTCGGGCCCTCGCCCTGCTGAGGATCTTCAAAGTCACGAAGTACTG	1918
Qy	1921	GAGCTCCTCGGAACTCGTGTGTCTCCCTGCTGAACTCCATGAAGTCCAATCATCAGCCT	1980
Db	1919	GAGCTCCTCGGAACTCGTGTGTCTCCCTGCTGAACTCCAATGAAGTCCAATCATCAGCCT	1978
Qy	1981	GCTCTTCTTGCTCTCTCTGTTCAATGTGTCTTTCGCCCTGCTGGGATGACAGCTTTTG	2040
Db	1979	GCTCTTCTTGCTCTCTCTGTTCAATGTGTCTTTCGCCCTGCTGGGATGACAGCTTTTG	2038
Qy	2041	GGGACAGTTCAACTTCAGAGATGAGACTCCCAACAACACTTCGACACCTTCCCTGCCGC	2100
Db	2039	GGGACAGTTCAACTTCAGAGATGAGACTCCCAACAACACTTCGACACCTTCCCTGCCGC	2098
Qy	2101	CATCCTCAGTGTCTTCAGATCTCTGACGGGAGGAGCTGGAATGCAGTGAATGATCAGCG	2160
Db	2099	CATCCTCAGTGTCTTCAGATCTCTGACGGGAGGAGCTGGAATGCAGTGAATGATCAGCG	2158
Qy	2161	GATCGAATCGAAGCGGCGTCAAGAAAGCATGTCTCGTCTCTTTTACTTCAATGTCTCT	2220
Db	2159	GATCGAATCGAAGCGGCGTCAAGAAAGCATGTCTCGTCTCTTTTACTTCAATGTCTCT	2218
Qy	2221	GACACTGTTTCGAAAACATACTCTGCTGAATGTCTTTCTGGCCATCGCTGTGGACAACCT	2280
Db	2219	GACACTGTTTCGAAAACATACTCTGCTGAATGTCTTTCTGGCCATCGCTGTGGACAACCT	2278
Qy	2281	GGCCACGCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGAGAGCAGCCAAACAGAA	2340
Db	2279	GGCCACGCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGAGAGCAGCCAAACAGAA	2338
Qy	2341	GCTTGTCTTCGAAAAGGCCAAAGAGTGGCTGAAGTTCAGGCCCATGTCTGTCCGCGCAACAT	2400

[illegible]

Db	3419	GGTCGTTCCCACTGGTAACTGGGACCTGGAAAGCAACAGAGAGGGGAAGAGGAGTGGGA	3478
Qy	3481	AGCGGATGACGTGATGAGGAGCGGCCCGCCCTATCGTCCCATACACAGCTCCATGTTCTG	3540
Db	3479	AGCGGATGACGTGATGAGGAGCGGCCCGCCCTATCGTCCCATACAGCTCCATGTTCTG	3538
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RESULT 11

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; Sequence 7, Application US/08450273
; Patent No. 6653097
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Gillespie, Alison
; APPLICANT: Feldman, Daniel
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: US
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,273
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; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,950
; FILING DATE: 13-MAR-1995
; APPLICATION NUMBER: 08/336,257
; FILING DATE: 7-NOV-1994
; APPLICATION NUMBER: 08/314,083
; FILING DATE: 28-SEPT-1994
; APPLICATION NUMBER: 08/311,363
; FILING DATE: 23-SEPT-1994
; APPLICATION NUMBER: 08/290,012
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 08/223,305
; FILING DATE: 4-APR-1994
; APPLICATION NUMBER: 08/193,078
; FILING DATE: 07-FEB-1994
; APPLICATION NUMBER: 08/149,097
; FILING DATE: 5-NOV-1993
; APPLICATION NUMBER: 08/105,536
; FILING DATE: 11-AUG-1993
; APPLICATION NUMBER: 07/914,231
; FILING DATE: 13-JULY-1992
; APPLICATION NUMBER: 07/868,354
; FILING DATE: 10-APR-1992
; APPLICATION NUMBER: PCT/US92/06903
; FILING DATE: 14-AUG-1992
; APPLICATION NUMBER: 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-519812
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 238-0999
; TELEFAX: (619) 238-0062
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7362 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: 7161..7362
; US-08-450-273-7
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

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Db 2339 GCTTGTCTTGCAAAAGGCGCAAGAGTGGCTGAAGTCAAGCTTCTGCGCGGCAACAT 2398
Qy 2401 CTCCATGCGCGCAGGACGAGAACTCGGCCAAAGCGCGCTCGGTGTGGAGCAGCGGCG 2460

Db 2399 |||||CTCCATCGCCGCGCAGCAGAACTCGGCAAGGCGCGCTCGGTGTGGAGCAGCGGC 2458
Qy 2461 CAGCAGCTACGGCTGCAGAACTCTGGGGCAGCTCGGAGGCGCTCTACAGCGAGATGCA 2520
Db 2459 CAGCCAGCTACGGCTGCAGAACTCTGGGGCAGCTCGGAGGCGCTCTACAGCGAGATGCA 2518
Qy 2521 CCCGAGGAGCGCTCGCTTCGCCACTACGCGCCACTCTGCGGCCCGCAATGAAGACGCA 2580
Db 2519 CCCGAGGAGCGCTCGCTTCGCCACTACGCGCCACTCTGCGGCCCGCAATGAAGACGCA 2578
Qy 2581 CTTGGACCCGCGCTCGTGGTGGAGCTGGGCGCGCAACGCGCGCGGGGCCCGTGGAGG 2640
Db 2579 CTTGGACCCGCGCTCGTGGTGGAGCTGGGCGCGCAACGCGCGCGGGGCCCGTGGAGG 2638
Qy 2641 CAAAGCCCGACCTAGGCTCGGAGGCCCGCGAGGGCGTGCACCTTCGCGCAGGACCA 2700
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Qy 2761 GAAGCGGAGAGCGGGGCCCGCGAGCGCGGAGCGCGGCGCGGAGCGCGCGCGCGCG 2820
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Qy 2821 CAGCAAGGAGGCGCGGGGCCCGCGAGCGCGGAGCGCGGCGCGGAGCGCGCGCGCGCG 2880
Db 2819 CAGCAAGGAGGCGCGGGGCCCGCGAGCGCGGAGCGCGGCGCGGAGCGCGCGCGCGCG 2878
Qy 2881 CGAGGCGCGCGCGGCGCACACCGGCGCGGCTCCCGGAGGAGCGCGCGCGCGGAGCGCG 2940
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Qy 3061 GGAGGCGCGCGCGCGCGCACCGGCGCGGCGCGCGCACGAGGCGCGCGCGCGCGCGCGCG 3120
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Qy 3181 CAAAGGAAAGGAGCTCCGGAACCAACGCGCGCGGAGCCACATGTGACCTGGAGACCG 3240
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Qy 3421 GTCTGTTCCCATGTTACGTTGAGCTGGAAAGCCAGACAGGGGAGAGGAGTGA 3480
Db 3419 GGTCTTCCCATGTTACGTTGAGCTGGAAAGCCAGACAGGGGAGAGGAGTGA 3478
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Db 3539 TTTAAGCCCCAACCACTGCTCCGCGCTTCTGCCACTACATCTGTACCATGAGTACTT 3598
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Qy 3841 GCGGTTTGTCTTCTCGAGCTTCTGGAGGATCCAAAGGGAAAGACATCAATACCATCAA 3900
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Db 3887 GTCTCTGAGAGTCTCTCGTGTCTTGGCGCCCTCAAGACCATCAAAACGGCTGCCCAAGCT 3946
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Db 4187 CGACAAATGTCTCTGGGCTCTGCTGACGCTGTTCACAGTGTCCACGGAGAGAGGCTGGCC 4246
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Qy 4381 CAACATCTTTTGTGGCTTTGATCATCATCATCTTCCAGGAGCAGGGGACAGGGTATGTC 4440
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Db 4427 TGAATCAGCCTGGAGAGAACGAGAGGCTTTCATTTGACTTTCGCCATCAGTCGCCAAACC 4486
Qy 4501 CCTGACACGGTACATCCGCCAAAACCGGAGCTGTTCAGTATAGACGTGACATTTGT 4560
Db 4487 CCTGACACGGTACATCCGCCAAAACCGGAGCTGTTCAGTATAGACGTGACATTTGT 4546
Qy 4561 GGTCTCCCGCGCTTTGAATACTTATCATGTGCTGATAGCCCTCAACATTTGTGTGTGT 4620
Db 4547 GGTCTCCCGCGCTTTGAATACTTATCATGTGCTGATAGCCCTCAACATTTGTGTGTGT 4606

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Qy 4681 CGTGTTCACATCCATGTTCTCCATGGAAATGCTGCTGAAGATCATCGCTTTGGGGTGCT 4740
Db CGTGTTCACATCCATGTTCTCCATGGAAATGCTGCTGAAGATCATCGCTTTGGGGTGCT 4726
Qy 4741 GAACTATTTTCAGAGATGCTGGAATGCTTTTGACTTTTGCTCACTGTGTTGGGAAGTATTAC 4800
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Qy 5101 GTTCAGGAGCCCAACGGGGAGGCTGGCAGAGATCATGTGCTTCCTGCTCAGCAACCA 5160
Db GTTCAGGAGCCCAACGGGGAGGCTGGCAGAGATCATGTGCTTCCTGCTCAGCAACCA 5146
Qy 5161 GGCTGTGATGAGCAGGCCAATCACCGAGTGTGGAAGTGACTTTGCTACTTCTACTT 5220
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Qy 5341 GTTCATCCGGTCTTGGGCTGAATACGACCCGGCTGCGTGTGGCGCATCAATGA 5400
Db GTTCATCCGGTCTTGGGCTGAATACGACCCGGCTGCGTGTGGCGCATCAATGA 5386
Qy 5401 CATGTTTGAGATGCTGAAACACATGTCCCGCCCTCTGGGGCTGGGGAAGAAATCCCTGTC 5460
Db CATGTTTGAGATGCTGAAACACATGTCCCGCCCTCTGGGGCTGGGGAAGAAATCCCTGTC 5446
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Qy 5521 TGTTCACTTTCACGCTGATGGCCCTCATCCGGAACGCACTGGAGATCAAGCTGGC 5580
Db TGTTCACTTTCACGCTGATGGCCCTCATCCGGAACGCACTGGAGATCAAGCTGGC 5566
Qy 5581 CCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGAGATTTCCGTTGT 5640
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Qy 5641 GTGGGCCAATCTGCCCCAGAGACTTTTGGACTTCTGTGTAACCCCTCAAGCCCTGATGA 5700
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Qy 5821 CCTGTTCCACCCTCTGAAGGCCACCTTGGAGCAGACACGCCGCTGTGTCTCGAGGAGC 5880
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Qy 6601 CCCAAGTGTGCCAACAGCTGGCCAGGCGGAGACCCCAAGGAGAGTGGTTCCTG 6660
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Qy 6661 GAATGGGAGCCCTTGTCTCAACATCTGGTGTAGCAACCCCGCGCGGCTGGGGGAG 6720
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Qy 6721 GCAGCTCCCGCAGACGCCCTGACTCTCCCGCCCGCAGCATCACCTACAAGACGGCCTC 6780
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APPLICANT: Franco, Rodrigo
APPLICANT: Sun Chen, Ai Ru
APPLICANT: Suey, David J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/452,007
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/713,118
FILING DATE: 16-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mata, Elizabeth W.
REGISTRATION NUMBER: 38,236
REFERENCE/DOCKET NUMBER: ACC96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7266 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 92..7102
US-09-452-007-1

Query Match 97.9%; Score 7223.2; DB 3; Length 7266;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7263; Conservative 0; Mismatches 3; Indels 18; Gaps 2;
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QY 235 GGGCGGGGCTCCGGGGGCTGACGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 294
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QY 295 GCAGCGCGCGGACCATGGCGCTGTACAAACCCATCCCGCTCAAGCAGAACTCCTTCAC 354
DB 241 GCAGCGCGGGGACCATGGCGCTGTACAAACCCATCCCGCTCAAGCAGAACTCCTTCAC 300
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DB 301 CGTCAACCGCTCGCTCTTTCGCTTCAGCGAGGACAAAGTCTCGCGCAAAATACGCGAAGCG 360
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DB 361 CATCACCGAGTGGCGCTCCATTCGAGTATGATCCTGGCCACCATCATCGCCAACTGCAT 420
QY 475 CGTCTGGCCCTGGAGCAGCACCTCCCTGATGGGACAAAACGCCCATGTCCGAGCGGCT 534
DB 421 CGTCTGGCCCTGGAGCAGCACCTCCCTGATGGGACAAAACGCCCATGTCCGAGCGGCT 480
QY 535 GGAGCAGCAGGAGCGCTATTTTCATCGGATCTTTTGTCTTGAGCAGGAGTCAAAATCAT 594
DB 481 GGAGCAGCAGGAGCGCTATTTTCATCGGATCTTTTGTCTTGAGCAGGAGTCAAAATCAT 540
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Db 6823 GCCCTTGCCCTCGCTCTCGAATTTGGCTCTGAACCTTTACTGGGGCAGCGTCTGGACAG 6882
Qy 6955 TGAGGCTCTGTGTCCACGCGCTGTGAGGACACGCTCACTTTTCAGAGAGGCTGTGGCCAC 7014
Db 6883 TGAGGCTCTGTGTCCACGCGCTGTGAGGACACGCTCACTTTTCAGAGAGGCTGTGGCCAC 6942
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RESULT 14

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US-09-268-163-7
; Sequence 7, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 7177
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..6856
US-09-268-163-7
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Query Match 94.3%; Score 6958; DB 4; Length 7177;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 7177; Conservative 0; Mismatches 0; Indels 199; Gaps 2;
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Qy 1 GCGGCGCGCGCTCGGCGGTGGGGCGAGGTGCGGTGCGGTCCCGGCGCTCCGCGT 60
Db 1 GCGGCGCGCGCTCGGCGGTGGGGCGAGGTGCGGTGCGGTCCCGGCGCTCCGCGT 60
Qy 61 GCTGCTCCGCTCTGAGCGCTGCGCGCCCGCGCTCCCTCCCGGGGCGCTGGGCGG 120
Db 61 GCTGCTCCGCTCTGAGCGCTGCGCGCCCGCGCTCCCTCCCGGGGCGCTGGGCGG 120
Qy 121 GGGATGCACGCGGGGCGCGGAGCCATGGTTCGCTTTGGGGACGAGGTGGCGGCGCTA 180
Db 121 GGGATGCACGCGGGGCGCGGAGCCATGGTTCGCTTTGGGGACGAGGTGGCGGCGCTA 180
Qy 181 TGAAGGCGCGCGGCGGAGAGGGGCCCGGGCGGGGCGGGGCGGGGCGGGGCGG 240
Db 181 TGAAGGCGCGCGGCGGAGAGGGGCCCGGGCGGGGCGGGGCGGGGCGGGGCGG 240
Qy 241 GGGTCCCGGGGGGCTGCAGCCCGCCAGCGGGTCTCTTACAAGCAATCGATCCGCGAGCG 300
Db 241 GGGTCCCGGGGGGCTGCAGCCCGCCAGCGGGTCTCTTACAAGCAATCGATCCGCGAGCG 300
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QY	301	CGCGCGGACCATGGCGTGTACAAACCCCATCCCGGTCAAGCAGAACTGTTTCAACGTC	360
DB	301	CGCGCGGACCATGGCGTGTACAAACCCCATCCCGGTCAAGCAGAACTGTTTCAACGTC	360
QY	361	CGGCTCGCTCTTCTGCTCTTACGAGGAGCAACAGTGTGTCGCGAAATACGCGAAGC	420
DB	361	CGGCTCGCTCTTCTGCTCTTACGAGGAGCAACAGTGTGTCGCGAAATACGCGAAGC	420
QY	421	CGAGTGGCCCTCCATTCGAGTATATGATCTTGGCCACCATCATCGCCAACTGATG	480
DB	421	CGAGTGGCCCTCCATTCGAGTATATGATCTTGGCCACCATCATCGCCAACTGATG	480
QY	481	GGCCCTGGAGCAGACCTCCCTGATGGGGAACAAACGCCCATGTCCGACGCTGGA	540
DB	481	GGCCCTGGAGCAGACCTCCCTGATGGGGAACAAACGCCCATGTCCGACGCTGGA	540
QY	541	CACGAGCCCTATTTTCAATGGGATCTTTTGTCTTGAGGAGGATCAAAATCATGCT	600
DB	541	CACGAGCCCTATTTTCAATGGGATCTTTTGTCTTGAGGAGGATCAAAATCATGCT	600
QY	601	GGGCTTTGTCTTCCACAAAGGCTTTTACCTGGGAAACGGCTGGAAGCTCATGCT	660
DB	601	GGGCTTTGTCTTCCACAAAGGCTTTTACCTGGGAAACGGCTGGAAGCTCATGCT	660
QY	661	GGTGTCTTCAAGGATCTTGTCCACGGCTGGAACCTGACCTTGGAGGAGGATCA	720
DB	661	GGTGTCTTCAAGGATCTTGTCCACGGCTGGAACCTGACCTTGGAGGAGGATCA	720
QY	721	GGCTGTGCTGTGCTGAGGCGCTTGAAGCTGTGTCTGAGATCCAAAGTTGAGGT	780
DB	721	GGCTGTGCTGTGCTGAGGCGCTTGAAGCTGTGTCTGAGATCCAAAGTTGAGGT	780
QY	781	GCTCAAGTCCATCATGAAGGCCATGTTTCCACTCTGCGAGATTGGGCTCTCTCT	840
DB	781	GCTCAAGTCCATCATGAAGGCCATGTTTCCACTCTGCGAGATTGGGCTCTCTCT	840
QY	841	TGCGATCTCATGTTTGGCCATCATTTGGCTGGAGTTCTACATGGGCAAGTTCC	900
DB	841	TGCGATCTCATGTTTGGCCATCATTTGGCTGGAGTTCTACATGGGCAAGTTCC	900
QY	901	CTGTTTCCCAACAGACAGATGCGAGCGCCGCTGGTGTGATCTTCCCTGTGG	960
DB	901	CTGTTTCCCAACAGACAGATGCGAGCGCCGCTGGTGTGATCTTCCCTGTGG	960
QY	961	CCAGCGCGGCTGTGCGAGGGCGACACTGAGTGCAGGAGTACTGGCCAGGACCA	1020
DB	961	CCAGCGCGGCTGTGCGAGGGCGACACTGAGTGCAGGAGTACTGGCCAGGACCA	1020
QY	1021	TGGCATCAACCACTTTGACAAATATCTGTTTGGCCATCTTGAAGGTTTCCAGT	1080
DB	1021	TGGCATCAACCACTTTGACAAATATCTGTTTGGCCATCTTGAAGGTTTCCAGT	1080
QY	1081	CATGAGGCTGGATGATCTCTATAATAACAAACGATGGCGCGGCAACCTGGA	1140
DB	1081	CATGAGGCTGGATGATCTCTATAATAACAAACGATGGCGCGGCAACCTGGA	1140
QY	1141	CTGGCTCTACTTCTTCACTCTCATCATCTGGCTCTCTTCTCATCTCACTT	1200
DB	1141	CTGGCTCTACTTCTTCACTCTCATCATCTGGCTCTCTTCTCATCTCACTT	1200
QY	1201	GGGCGTGTCTCGGGGAGTTTGGCAAGGAGGAGAGGGTGGAGAACCGCGGCT	1260
DB	1201	GGGCGTGTCTCGGGGAGTTTGGCAAGGAGGAGAGGGTGGAGAACCGCGGCT	1260
QY	1261	CCTGAAGCTGCGCGGAGCAGCAGATCGAGCGAGAGCTCAACGGGTACCTGGAGT	1320
DB	1261	CCTGAAGCTGCGCGGAGCAGCAGATCGAGCGAGAGCTCAACGGGTACCTGGAGT	1320
QY	1321	CTTCAAGCGGAGGAGTCTGCTGGCCGAGGAGAGAGGATCGAGGAGAGTCCCC	1380
DB	1321	CTTCAAGCGGAGGAGTCTGCTGGCCGAGGAGAGAGGATCGAGGAGAGTCCCC	1380

QY	1381	TTTGGAGTGTCTGAAGAGAGCGGCCACCAAGAGAGCAGAAATGACCTGTATCCAGC	1440
DB	1381	TTTGGAGTGTCTGAAGAGAGCGGCCACCAAGAGAGCAGAAATGACCTGTATCCAGC	1440
QY	1441	GGAGGAGAGGACCGGTTTTCAGATCTCTGTGTCTGTTGGATCCCCCTTTCGCGCGG	1500
DB	1441	GGAGGAGAGGACCGGTTTTCAGATCTCTGTGTCTGTTGGATCCCCCTTTCGCGCGG	1500
QY	1501	CCTCAAGAGCGGGAAGACAGAGAGCTCGTATATCTTCCGAGGAGGAGAGATGTTCC	1560
DB	1501	CCTCAAGAGCGGGAAGACAGAGAGCTCGTATATCTTCCGAGGAGGAGAGATGTTCC	1560
QY	1561	GTCTTTTATCCGCGCATGTGTAAGGCTCAGAGCTTCTACTTGGGTGTGCTGCGTGT	1620
DB	1561	GTCTTTTATCCGCGCATGTGTAAGGCTCAGAGCTTCTACTTGGGTGTGCTGCGTGT	1620
QY	1621	GGCCCTGAAACACACTGTGTGTGSCCATGTGTGCAATTAACAACAGCGCGGCTTAC	1680
DB	1621	GGCCCTGAAACACACTGTGTGTGSCCATGTGTGCAATTAACAACAGCGCGGCTTAC	1680
QY	1681	GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTCTTCTCCTCAGAGATGCTCCGAA	1740
DB	1681	GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTCTTCTCCTCAGAGATGCTCCGAA	1740
QY	1741	GATGTATGGCTTGGGCGCCAGAAAGTACTTCCGCTCCTCCTTCAACTGTCTTGG	1800
DB	1741	GATGTATGGCTTGGGCGCCAGAAAGTACTTCCGCTCCTCCTTCAACTGTCTTGG	1800
QY	1801	GCTCATCGTGGGAGCGTCTTTTGAAGTGTCTTGGGCGCCATCAAGCGCGGAGCTCT	1860
DB	1801	GCTCATCGTGGGAGCGTCTTTTGAAGTGTCTTGGGCGCCATCAAGCGCGGAGCTCT	1860
QY	1861	TGGATCAGTGTCTCGGCGCCCTCGGCTGTGAGATCTTCAAGTCAAGTCAAGTACTG	1920
DB	1861	TGGATCAGTGTCTCGGCGCCCTCGGCTGTGAGATCTTCAAGTCAAGTCAAGTACTG	1920
QY	1921	GAGCTCCTCGGAAACCTGGTGTGTCTTCTGAACTCCATGAAGTCCATCATCAGCCT	1980
DB	1921	GAGCTCCTCGGAAACCTGGTGTGTCTTCTGAACTCCATGAAGTCCATCATCAGCCT	1980
QY	1981	GCTCTTCTGCTCTTCTGTTTCAATGTGTCTTTCGCTGTCTGGGATGCTGTGTGG	2040
DB	1981	GCTCTTCTGCTCTTCTGTTTCAATGTGTCTTTCGCTGTCTGGGATGCTGTGTGG	2040
QY	2041	GGGACAGTTCACCTTCCAGGATGAGATCCCAACCACTTCCAGACCTTCCCTGCGC	2100
DB	2041	GGGACAGTTCACCTTCCAGGATGAGATCCCAACCACTTCCAGACCTTCCCTGCGC	2100
QY	2101	CATCTCCTCATGCTTCCAGATCCTGACGGGAGGAGTGGAAATGCAATGATCAGCG	2160
DB	2101	CATCTCCTCATGCTTCCAGATCCTGACGGGAGGAGTGGAAATGCAATGATCAGCG	2160
QY	2161	GATCGAATCGCAAGGCGGCTCAGAAAGGATGTTCTCGTCTCTTTTACTTATGTTCT	2220
DB	2161	GATCGAATCGCAAGGCGGCTCAGAAAGGATGTTCTCGTCTCTTTTACTTATGTTCT	2220
QY	2221	GACACTGTTTCGAAACTACACTCTGTGTAATGTCTTCTGGCCATCGCTGTGAGAAC	2280
DB	2221	GACACTGTTTCGAAACTACACTCTGTGTAATGTCTTCTGGCCATCGCTGTGAGAAC	2280
QY	2281	GGCCAAACCGCCAGAGCTGACCAAGGATGGAAGGAGTGGAAAGAGCAGCAATCAGAA	2340
DB	2281	GGCCAAACCGCCAGAGCTGACCAAGGATGGAAGGAGTGGAAAGAGCAGCAATCAGAA	2340
QY	2341	GCTTGTCTGCAAAAGGCGCAAGAGTGTGAGTCAAGCCCATGTCTGCGGAGAT	2400
DB	2341	GCTTGTCTGCAAAAGGCGCAAGAGTGTGAGTCAAGCCCATGTCTGCGGAGAT	2400
QY	2401	CTCCATCGCGCGCAGCAGCAAACTCGGCCAAGCGCGCTCGGTGTGGGAGCAGCGGC	2460
DB	2401	CTCCATCGCGCGCAGCAGCAAACTCGGCCAAGCGCGCTCGGTGTGGGAGCAGCGGC	2460
QY	2461	CAGCCAGCTACGGCTGCAAGAACCTTGGGCGCAGCTGCGAGGCGCTGTGTAAGCAGAGATGGA	2520

Db	2461		CAGCCAGCTACGGGTGCAGAACTCTGCGGGCCAGCTGGGAGCGCTGTATACGCGAGATGGA	2520	
Qy	2521		CCCCGAGGAGCGGCTGGCTTCGGCCACTACGCGGCCACTGCGGCGCCGACATGAAGACGCA	2580	
Db	2521		CCCCGAGGAGCGGCTGGCTTCGGCCACTACGCGGCCACTGCGGCGCCGACATGAAGACGCA	2580	
Qy	2581		CCTGGACCGGCGCTGTGTGTGTGGAGCTGGGCGCGACGGCGCGCGGGGGCCCGTGGGAGG	2640	
Db	2581		CCTGGACCGGCGCTGTGTGTGTGGAGCTGGGCGCGACGGCGCGCGGGGGCCCGTGGGAGG	2640	
Qy	2641		CAAAAGCCCGACCTGAGGCTGGGAGGCCCCCGGAGGGGCTGACCCCTTCGCGCAGGCAACCA	2700	
Db	2641		CAAAAGCCCGACCTGAGGCTGGGAGGCCCCCGGAGGGGCTGACCCCTTCGCGCAGGCAACCA	2700	
Qy	2701		CCGCGCACCGCGACAAGACAAAGACCCCGCGGGCGGGGGAACAGAGACCGAGCAGAGGCCCC	2760	
Db	2701		CCGCGCACCGCGACAAGACAAAGACCCCGCGGGCGGGGGAACAGAGACCGAGCAGAGGCCCC	2760	
Qy	2761		GAAGGCGGAGACGGGGAGCCGCTGTGCCGCGGAGAGCGCGCGCGGCCGCAACCGCAGCCCA	2820	
Db	2761		GAAGGCGGAGACGGGGAGCCGCTGTGCCGCGGAGAGCGCGCGCGGCCGCAACCGCAGCCCA	2820	
Qy	2821		CAGCAAGGAGGCCCGCGGGGCCCGCGGAGGCGCGAGCGCGCGCGCGCCGAGGCCCAAGCCCC	2880	
Db	2821		CAGCAAGGAGGCCCGCGGGGCCCGCGGAGGCGCGAGCGCGCGCGCGCGCCGAGGCCCAAGCCCC	2880	
Qy	2881		CGAGGGCGGGCGGGCGGACCAACCGCGCGCTCCCGGAGGAGCGCGCGCGCGAGCGGGAGCC	2940	
Db	2881		CGAGGGCGGGCGGGCGGACCAACCGCGCGCTCCCGGAGGAGCGCGCGCGCGAGCGGGAGCC	2940	
Qy	2941		CCGACGCCACCGCGCGCACCGGACACCGGATCCCGAGCAAGAGTGCCTCGCGCGCAAGGG	3000	
Db	2941		CCGACGCCACCGCGCGCACCGGACACCGGATCCCGAGCAAGAGTGCCTCGCGCGCAAGGG	3000	
Qy	3001		CGAGCGGCGCGCGCGGCAACCGCGCGGGCCCCCGAGCGGGGGCCCCCGGAGCGCGAGAGCGG	3060	
Db	3001		CGAGCGGCGCGCGCGGCAACCGCGCGGGCCCCCGAGCGGGGGCCCCCGGAGCGCGAGAGCGG	3060	
Qy	3061		GGAGGAGCCGCGGGCGGCAACCGCGCGGGCCCCCGAGCGGGGGCCCCCGAGGGCTGT	3120	
Db	3061		GGAGGAGCCGCGGGCGGCAACCGCGCGGGCCCCCGAGCGGGGGCCCCCGAGGGCTGT	3120	
Qy	3121		GGAGAAGGAGACCAACCGAGAGGAGGCGCAACCGAGAGGAGGCTGAGATAGTGAAGCCGA	3180	
Db	3121		GGAGAAGGAGACCAACCGAGAGGAGGCGCAACCGAGAGGAGGCTGAGATAGTGAAGCCGA	3180	
Qy	3181		CAAGGAAAAAGAGCTCCGGAAACCAACGAGCCCCGGGAGCCACTGTGACCTGGAGACCAAG	3240	
Db	3181		CAAGGAAAAAGAGCTCCGGAAACCAACGAGCCCCGGGAGCCACTGTGACCTGGAGACCAAG	3240	
Qy	3241		TGGGACTGTGACTGTGGGTCCCATGCAACACTGCCAGCACACTGTCTCCAGAGGTGGA	3300	
Db	3241		TGGGACTGTGACTGTGGGTCCCATGCAACACTGCCAGCACACTGTCTCCAGAGGTGGA	3300	
Qy	3301		GGAAACGACGAGGATGACAGACAATCAGCGGAAAGCTCACTCGCATGGGCGAGTCAAGCCCC	3360	
Db	3301		GGAAACGACGAGGATGACAGACAATCAGCGGAAAGCTCACTCGCATGGGCGAGTCAAGCCCC	3360	
Qy	3361		AGACCCGGAACATAATTGTACATATCCAGTGATGCTGACGGGCCCTCTTGGGGAAGCCAC	3420	
Db	3361		AGACCCGGAACATAATTGTACATATCCAGTGATGCTGACGGGCCCTCTTGGGGAAGCCAC	3420	
Qy	3421		GGTCTGTTCCAGTGGTAACTGGACCTTGGAAAGCCAGAGGGGGAAGAGGGGTGGA	3480	
Db	3421		GGTCTGTTCCAGTGGTAACTGGACCTTGGAAAGCCAGAGGGGGAAGAGGGGTGGA	3480	
Qy	3481		AGCGGATGACGTGTATGAGGAGCGGCCCGCGGCTTATCGTCCCATACAGCTTCCATGTTCTG	3540	
Db	3481		AGCGGATGACGTGTATGAGGAGCGGCCCGCGGCTTATCGTCCCATACAGCTTCCATGTTCTG	3540	
Qy	3541		TTTAAAGCCCCCAACCAACCTGCTCCCGCGCTTCTGCGCACTACATCGTGACCAATGAGGTACTT	3600	

3541	Db	TTTAAAGCCCCAACAACTGTCTCGCGCGCTTCTGCGCATACATCGTAGACCAATGAGGTACTTT	3600
3601	Qy	CGAGGTGGTCAATTCTCTGTGTCTATCGCTTTCAGCAGCATCGCCCTGGCTGCTGAGGACCC	3660
3601	Db	CGAGGTGGTCAATTCTCTGTGTCTATCGCTTTCAGCAGCATCGCCCTGGCTGCTGAGGACCC	3660
3661	Qy	AGTGGGCACAGACTCGCCCAAGAAACAACGCTCTGAAATACCTGATTTACATTTTCACTGG	3720
3661	Db	AGTGGGCACAGACTCGCCCAAGAAACAACGCTCTGAAATACCTGATTTACATTTTCACTGG	3720
3721	Qy	TGCTTTTACCTTTTCAGATGCTGATTAAGATGATCGACTTGGGACTGCTGCTTCAACCCCTGG	3780
3721	Db	TGCTTTTACCTTTTCAGATGCTGATTAAGATGATCGACTTGGGACTGCTGCTTCAACCCCTGG	3780
3781	Qy	AGCCTATTTCCGGGACTTTGTGGAACTTCTCGACTTCAATTGTGTGTCAGTGGCGCCCTGGT	3840
3781	Db	AGCCTATTTCCGGGACTTTGTGGAACTTCTCGACTTCAATTGTGTGTCAGTGGCGCCCTGGT	3840
3841	Qy	GGCGTTTCTTCTCGAGCTTCGTGGGAGATCCAAAGGGAAGACATCAATACCATCAA	3900
3841	Db	GGCGTTTCTTCTCGAGCTTCGTGGGAGATCCAAAGGGAAGACATCAATACCATCAA	3888
3901	Qy	GTCTCTGAGAGTCTTCTGCTGCTCGCGGCCCTCAAGACCATCAAAACGGCTGCCCAAGCT	3960
3889	Db	GTCTCTGAGAGTCTTCTGCTGCTCGCGGCCCTCAAGACCATCAAAACGGCTGCCCAAGCT	3948
3961	Qy	CAAGGCTGTGTTTGAATGCTGTGTGTAATCCCTCGAAGAAATGCTCTCAACATCTTGATTGT	4020
3949	Db	CAAGGCTGTGTTTGAATGCTGTGTGTAATCCCTCGAAGAAATGCTCTCAACATCTTGATTGT	4008
4021	Qy	CTACATGCTCTTTCATGTTTCATAATTTGCCGTCAATTTGCGTGAGCTCTTCAAAGGGAAGTT	4080
4009	Db	CTACATGCTCTTTCATGTTTCATAATTTGCCGTCAATTTGCGTGAGCTCTTCAAAGGGAAGTT	4068
4081	Qy	TTTCTACTGCACAGATGAATCCAAAGGAGCTGAGAGGGAATGTCAGGGGTCAAGTATTTTGA	4140
4069	Db	TTTCTACTGCACAGATGAATCCAAAGGAGCTGAGAGGGAATGTCAGGGGTCAAGTATTTTGA	4128
4141	Qy	TTATGAGAAGGAGGAGCTGGAAGCTCAGCCAGGAGCTGGAAGAAATACGACTTTTCACTA	4200
4129	Db	TTATGAGAAGGAGGAGTGGAGGCTCAGCCAGGAGCTGGAAGAAATACGACTTTTCACTA	4188
4201	Qy	CGACAAATGTGCTCTGGGCTCTGCTGACGCTGTTTCAAGTGTCCAAGGAGAGGCTGGCC	4260
4189	Db	CGACAAATGTGCTCTGGGCTCTGCTGACGCTGTTTCAAGTGTCCAAGGAGAGGCTGGCC	4248
4261	Qy	CATGGTGCTGAACACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAGCCCTGGGTA	4320
4249	Db	CATGGTGCTGAACACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAGCCCTGGGTA	4308
4321	Qy	CCGCATGAGCTGTCCATCTTTACGTGGTCTACTTTGTGGTCTTTCCCTCTCTCTTCCTGT	4380
4309	Db	CCGCATGAGCTGTCCATCTTTACGTGGTCTACTTTGTGGTCTTTCCCTCTCTCTTCCTGT	4368
4381	Qy	CAACATCTTTTGGCTTTTGATCATCATCACCTCTCCAGGAGCAGGGGACAAGGTGATGTC	4440
4369	Db	CAACATCTTTTGGCTTTTGATCATCATCACCTCTCCAGGAGCAGGGGACAAGGTGATGTC	4428
4441	Qy	TGAATGAGCCTGGAGAAGAAACGAGAGGGCTTGCAATTGACTTGCCCATCAGCGCCAAAC	4500
4429	Db	TGAATGAGCCTGGAGAAGAAACGAGAGGGCTTGCAATTGACTTGCCCATCAGCGCCAAAC	4488
4501	Qy	CCTGACACGCTACATGCCCCAAACCGGAGTGGTTCACGATATAAGACGTGGACATTTGT	4560
4489	Db	CCTGACACGCTACATGCCCCAAACCGGAGTGGTTCACGATATAAGACGTGGACATTTGT	4548
4561	Qy	GGTCTCCCGCCCTTTTGAATACTTTCATCATGGCCATGATAGCCCTCAACACTGTGGTCT	4620
4549	Db	GGTCTCCCGCCCTTTTGAATACTTTCATCATGGCCATGATAGCCCTCAACACTGTGGTCT	4608
4621	Qy	GATGATGAAGTTCTATGATGCAACCTTATGATGATCGAGCTGATGCTGAAATGCCGTGAACAT	4680
4609	Db	GATGATGAAGTTCTATGATGCAACCTTATGATGATCGAGCTGATGCTGAAATGCCGTGAACAT	4668

QY	4681	CGTGTTCACATCCATGTTCTTCATGGAATGCGTGTGAAGATCATCGCCTTTGGGGTCT	4740
Db	4669	CGTGTTCACATCCATGTTCTTCATGGAATGCGTGTGAAGATCATCGCCTTTGGGGTCT	4728
QY	4741	GAACTATTTAGATGATGCTCGGAATGCTTTGACTTTGTCTACTGTGTTGGGAAGATTATC	4800
Db	4729	GAACTATTTAGATGATGCTCGGAATGCTTTGACTTTGTCTACTGTGTTGGGAAGATTATC	4788
QY	4801	TGATATTTAGTAACAGAGATTGCGGAACGAACTTTTCATCAACCTCAGCTTCTCGG	4860
Db	4789	TGATATTTAGTAACAGAGATTGCGGAACGAACTTTTCATCAACCTCAGCTTCTCGG	4848
QY	4861	CCTCTTTGAGCTGCGCGCTGATCAAGCTGCTCGCGAGGCTACACCATCGCATCCT	4920
Db	4849	CCTCTTTGAGCTGCGCGCTGATCAAGCTGCTCGCGAGGCTACACCATCGCATCCT	4908
QY	4921	GCTGTGAGCTTTGTGCTCAGTCTTCAAGCCCTGCGCTTCAAGTGTCTGCTCAATGSCAT	4980
Db	4909	GCTGTGAGCTTTGTGCTCAGTCTTCAAGCCCTGCGCTTCAAGTGTCTGCTCAATGSCAT	4968
QY	4981	GCTGTCTTTCATCTAGCCCATCATCGGCATGAGGTGTTGGGAATATTTGCCCTGGATGA	5040
Db	4969	GCTGTCTTTCATCTAGCCCATCATCGGCATGAGGTGTTGGGAATATTTGCCCTGGATGA	5028
QY	5041	TGACACAGCATCAACCGGCCACAACTTTCCGGAGCTTTTTCGAAGCCCTGATGCTGCT	5100
Db	5029	TGACACAGCATCAACCGGCCACAACTTTCCGGAGCTTTTTCGAAGCCCTGATGCTGCT	5088
QY	5101	GTTTACAGAGCGCAGCGGGAGGCTTGCGACAGATCATGCTGCTCCTGCTGAGCAACA	5160
Db	5089	GTTTACAGAGCGCAGCGGGAGGCTTGCGACAGATCATGCTGCTCCTGCTGAGCAACA	5148
QY	5161	GGCCTGTGATGAGCAGGCCAATGCCACAGGTGCGAGTGAGCTTTGCTACTTCTACTT	5220
Db	5149	GGCCTGTGATGAGCAGGCCAATGCCACAGGTGCGAGTGAGCTTTGCTACTTCTACTT	5208
QY	5221	CGTCTCTTTCATCTTCTGCTGCTCTTCTGATGTTGAACTTCTTGTGGCTGTGATCAT	5280
Db	5209	CGTCTCTTTCATCTTCTGCTGCTCTTCTGATGTTGAACTTCTTGTGGCTGTGATCAT	5268
QY	5281	GGACAAATTTGATGATCTCACCGGGACTCTTCCATCTTAGTCTCTCAACCTTGGATGA	5340
Db	5269	GGACAAATTTGATGATCTCACCGGGACTCTTCCATCTTAGTCTCTCAACCTTGGATGA	5328
QY	5341	GTTTCATCCGGGTCTCGGCTGATATACACCGGCTGCGTGTGGCGCATCAGTTCAATGA	5400
Db	5329	GTTTCATCCGGGTCTCGGCTGATATACACCGGCTGCGTGTGGCGCATCAGTTCAATGA	5388
QY	5401	CATGTTTGAGATGCTGAAACACATGTCCTCGGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5460
Db	5389	CATGTTTGAGATGCTGAAACACATGTCCTCGGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5448
QY	5461	TGAGTTGCTTACAGCGCTGTTGCGATGAACATGCCCATCTTCCATCTTCAACAGAGCATGAC	5520
Db	5449	TGAGTTGCTTACAGCGCTGTTGCGATGAACATGCCCATCTTCCATCTTCAACAGAGCATGAC	5508
QY	5521	TGTTCACTTTCAGTCCAGCTGATGSCCTCATCCGGACGGCTTGGAGATCAAGCTGGC	5580
Db	5509	TGTTCACTTTCAGTCCAGCTGATGSCCTCATCCGGACGGCTTGGAGATCAAGCTGGC	5568
QY	5581	CCAGCTGGGACAAAGCAGCATCAGTGTGACGCGAGTTGAGGAAGGAGATTTCGGTTGT	5640
Db	5569	CCAGCTGGGACAAAGCAGCATCAGTGTGACGCGAGTTGAGGAAGGAGATTTCGGTTGT	5628
QY	5641	GTGGGCCAATCTGCCCCAGAGACTTTTGGACTTGTGTATACCAACCCCATTAAGCCTGATGA	5700
Db	5629	GTGGGCCAATCTGCCCCAGAGACTTTTGGACTTGTGTATACCAACCCCATTAAGCCTGATGA	5688
QY	5701	GATGACGTGGGGAAGTTTATGAGCTCTGATGATATTTGACTTCTTACAGAGAGAAACA	5760
Db	5689	GATGACGTGGGGAAGTTTATGAGCTCTGATGATATTTGACTTCTTACAGAGAGAAACA	5748

QY	5761	AACACACAGAGACACAGATGACAGAGGCTCCTGGAGGCTCTCCAGATGGGTCTCTGTCT	5820
Db	5749	AACACACAGAGACACAGATGACAGAGGCTCCTGGAGGCTCTCCAGATGGGTCTCTGTCT	5808
QY	5821	CCTGTTCCACCCTCTGAAGGCCACCTCGGAGCAGACAGCCGCTGTGCTCCGAGGAGC	5880
Db	5809	CCTGTTCCACCCTCTGAAGGCCACCTCGGAGCAGACAGCCGCTGTGCTCCGAGGAGC	5868
QY	5881	CCGGGTTTTCTTCGACAGAAAGATTCCACTCCTCAGCAATGGCGGGCCATACAAAA	5940
Db	5869	CCGGGTTTTCTTCGACAGAAAGATTCCACTCCTCAGCAATGGCGGGCCATACAAAA	5928
QY	5941	CCAAGAGATGGCATCAAGAGTCTGCTCTGGGGCACTCAAAGGACCCAGGATGCACC	6000
Db	5929	CCAAGAGATGGCATCAAGAGTCTGCTCTGGGGCACTCAAAGGACCCAGGATGCACC	5988
QY	6001	CCATGAGGCGAGGCCACCCCTCGAGCGTGGCCACTCCACAGAGATCCTGTGGGCGGTC	6060
Db	5989	CCATGAGGCGAGGCCACCCCTCGAGCGTGGCCACTCCACAGAGATCCTGTGGGCGGTC	6048
QY	6061	AGGAGCACTGGCTGTGACGTTCAAGATGACAGATTAACCCGGAGGGGCTCTGATGGGGA	6120
Db	6049	AGGAGCACTGGCTGTGACGTTCAAGATGACAGATTAACCCGGAGGGGCTCTGATGGGGA	6108
QY	6121	GCCCGAGCTGGGCTGAGAGCCAGGCTCGAGCGGCTCCATGCCCGCTTGGCGCGGA	6180
Db	6109	GCCCGAGCTGGGCTGAGAGCCAGGCTCGAGCGGCTCCATGCCCGCTTGGCGCGGA	6168
QY	6181	GACTACGCGCTCAAGATGCCAGCCCATGAAGCGCTCCATCTTCAACGCTGCGCCACGC	6240
Db	6169	GACTACGCGCTCAAGATGCCAGCCCATGAAGCGCTCCATCTTCAACGCTGCGCCACGC	6228
QY	6241	GCCCGTGGGACTCATCTTTGACAGCACCCCGGACCGCCCAACCCCTTA3CCAGGGGCTC	6300
Db	6229	GCCCGTGGGACTCATCTTTGACAGCACCCCGGACCGCCCAACCCCTTA3CCAGGGGCTC	6288
QY	6301	GTGCAACACACACACCGCTGCCACCGCCGAGGACAGGAAGCAGAG3GTCCCTTGA	6360
Db	6289	GTGCAACACACACACCGCTGCCACCGCCGAGGACAGGAAGCAGAG3GTCCCTTGA	6348
QY	6361	GAAAGGGGCCAGGCTGTCTGCGATATGATGCGGCAACCAAGCAGTGTCTGTGGGCGGG	6420
Db	6349	GAAAGGGGCCAGGCTGTCTGCGATATGATGCGGCAACCAAGCAGTGTCTGTGGGCGGG	6408
QY	6421	GCTGCCCGCGGAGAGGGGCTACAGGCTGCGCGGCGGACAGAGGCGCGAGGAGCG	6480
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QY	6481	GGGCGGCTCCAGAGCGGAGCGGCTCATCTCTCTCGGAGAAAGCAGCGCTTCTA	6540
Db	6469	GGGCGGCTCCAGAGCGGAGCGGCTCATCTCTCTCGGAGAAAGCAGCGCTTCTA	6528
QY	6541	CTCTGTGGAACCGCTTTTGGGGCCGTGAGCCCCCGAAGCCCAAGCCCTCTCTCAAGCACA	6600
Db	6529	CTCTGTGGAACCGCTTTTGGGGCCGTGAGCCCCCGAAGCCCAAGCCCTCTCTCAAGCACA	6588
QY	6601	CCCAAGTGTGCCAAAGCTGGCCAGAGCGGAGCCCAACCCCAAGGGGCA3TGGTTCCT	6660
Db	6589	CCCAAGTGTGCCAAAGCTGGCCAGAGCGGAGCCCAACCCCAAGGGGCA3TGGTTCCT	6631
QY	6661	GAATGGGAGCCCCCTTGTGTCAACATCTGTGTAGCAACCCCGCGCGGCG3TGGGCGGAG	6720
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QY	6781	CTCAACCATCACTCTCGCGGGGCTCAGACAGCTCCCTCGCTTCTTCCCLAGGCCGGCT	6840
Db	6632	CTCAACCATCACTCTCGCGGGGCTCAGACAGCTCCCTCGCTTCTTCCCLAGGCCGGCT	6641
QY	6841	CAGCCCTGGGCTTTTCGAAACAAACGCCCTGTGTGACAGAGAGACCCCTCTCAGCAGCCCCCT	6900

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RESULT 15

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; Sequence 8, Application US/08455543A
; Patent No. 5792846

GENERAL INFORMATION:

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; APPLICANT: Ellis, Steven
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; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; MEDIUM OF INVENTION: METHODS

NUMBER OF SEQUENCES: 57

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COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995

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; PRIOR APPLICATION DATA: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
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; REFERENCE/DOCKET NUMBER: 6362-52517
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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 144..6857
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..143
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 6855..7175
; US-08-455-543A-8

Query Match 94.0%; Score 6932.4; DB 1; Length 7175;

Best Local Similarity 97.3%; Pred. No. 0;
Matches 7174; Conservative 0; Mismatches 1; Indels 201; Gaps 4;

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Db	4787	TGATATTTTGTAGTAAAGAGATTGCGAAACGAAATTTTCATCAACCTCAGCTTCTCTCG				
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Db	4847	CCTCTTTTCGAGCTCGCGGCTGATCAAGCTGCTCCGCGAGGCTACACCATCGCATCTT	Db	5927	CCAAGAGAGTGGCATCAAGAGTCTGTCTCTCTGGGGCACTCAAAAGGACCCAGGATGCAC	5986
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QY	4981	GCTGTCTTCATCTACGCCATCATCGGCATGCAAGTGTGGGAATATTTGCCCTGATGA	QY	6061	AGGAGCACTGGCTGTGGACGTTTCAGATGTCAGAGCATAAACCCGAGGGGCTCTGTATGGGA	6120
Db	4967	GCTGTCTTCATCTACGCCATCATCGGCATGCAAGTGTGGGAATATTTGCCCTGATGA	Db	6047	AGGAGCACTGGCTGTGGACGTTTCAGATGTCAGAGCATAAACCCGAGGGGCTCTGTATGGGA	6106
QY	5041	TGACACGAGCATCAACCGGCACAACTTCGCGACGTTTTCGAGGCGCTCATGTCGTCT	QY	6121	GCCCTCAGCTGGCTGAGAGCCAGGGTGCAGCGGCTTCATGCTCCGCTTTCGGGCGGA	6180
Db	5027	TGACACGAGCATCAACCGGCACAACTTCGCGACGTTTTCGAGGCGCTCATGTCGTCT	Db	6107	GCCCTCAGCTGGCTGAGAGCCAGGGTGCAGCGGCTTCATGCTCCGCTTTCGGGCGGA	6166
QY	5101	GTTTCAGAGCGCCACGGGGAGCGCTGGCACGAGATCATGCTGTCTGCTGAGCAACCA	QY	6181	GACTCAGCCCGTCAAGATGCCAGCCCATGAGCGCTCCATCTCCACGCTGGGCCACGC	6240
Db	5087	GTTTCAGAGCGCCACGGGGAGCGCTGGCACGAGATCATGCTGTCTGCTGAGCAACCA	Db	6167	GACTCAGCCCGTCAAGATGCCAGCCCATGAGCGCTCCATCTCCACGCTGGGCCACGC	6226
QY	5161	GGCTGTGATGACAGCGCAATGCCACCGAGTGTGGAAGTACTTTGCCCTACTTACTTT	QY	6241	GCCCTGTGGGACTCATCTTTGCAGCACCAACCCCGGACCGCCACCCCTTAGCCAGGCGTC	6300
Db	5147	GGCTGTGATGACAGCGCAATGCCACCGAGTGTGGAAGTACTTTGCCCTACTTACTTT	Db	6227	GCCCTGTGGGACTCATCTTTGCAGCACCAACCCCGGACCGCCACCCCTTAGCCAGGCGTC	6286
QY	5221	CGTCTCCTTTCATCTCTGTGCTCTTTCTGTATGTTGAACCTCTTTGTGGCTGTGATCAT	QY	6301	GTGCGACCAACCAACCAACCGCTGCCACCCGCGAGGGAAGAGAGAGAGAGAGAGAG	6360
Db	5207	CGTCTCCTTTCATCTCTGTGCTCTTTCTGTATGTTGAACCTCTTTGTGGCTGTGATCAT	Db	6287	GTGCGACCAACCAACCAACCGCTGCCACCCGCGAGGGAAGAGAGAGAGAGAGAG	6346
QY	5281	GGACAAATTTGAGTACTCAACCGGGAATCTTCCATCTAGTCTCCACCTTGGATGA	QY	6361	GAAGGGCCCGAGCTGTCTCCGATATGGATGGCGGCAACCAAGCAETGCTGTGGGGCGGG	6420
Db	5267	GGACAAATTTGAGTACTCAACCGGGAATCTTCCATCTAGTCTCCACCTTGGATGA	Db	6347	GAAGGGCCCGAGCTGTCTCCGATATGGATGGCGGCAACCAAGCAETGCTGTGGGGCGGG	6406
QY	5341	GTTTCATCCGGCTCTGGGCTGAATACGACCCGCGTGTGGTGGCGCATCTGATCAATGA	QY	6421	GCTGCCCCCGGAGAGAGGGGCTTACAGGCTGCCCGCGGGAACGAGAGCGCGGAGAGCG	6480
Db	5327	GTTTCATCCGGCTCTGGGCTGAATACGACCCGCGTGTGGTGGCGCATCTGATCAATGA	Db	6407	GCTGCCCCCGGAGAGAGGGGCTTACAGGCTGCCCGCGGGAACGAGAGCGCGGAGAGCG	6466
QY	5401	CATGTTTGTAGATGCTGAACACATGTCCTCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	QY	6481	GGGCGGCTCCAGAGCGGAGGAGCGCTCATCTCTCTCTCGGAGAGAGAGAGAGAGAG	6540
Db	5387	CATGTTTGTAGATGCTGAACACATGTCCTCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	Db	6467	GGGCGGCTCCAGAGCGGAGGAGCGCTCATCTCTCTCTCGGAGAGAGAGAGAGAGAG	6526
QY	5461	TCGAGTTGCTTACAGCGCTGGTTCGATGAACATGCCATCTCCACAGAGGACATGAC	QY	6541	CTCTGCGACCGCTTTTGGGGCGGTGAGCCCCGGAAGCCCAAGCCCTCTCCCTCAGCAGCCA	6600
Db	5447	TCGAGTTGCTTACAGCGCTGGTTCGATGAACATGCCATCTCCACAGAGGACATGAC	Db	6527	CTCTGCGACCGCTTTTGGGGCGGTGAGCCCCGGAAGCCCAAGCCCTCTCCCTCAGCAGCCA	6586
QY	5521	TGTTCACTTTCAGCTCCACGCTGATGGCCCTCATCCGAGCGGACCTGGAGATCAAGCTGGC	QY	6601	CCCAAGCTCGCCAAACAGCTGGCCAGGAGCGGGAGCCCCACCCACAGGGGCAATGGTCCGT	6660
Db	5507	TGTTCACTTTCAGCTCCACGCTGATGGCCCTCATCCGAGCGGACCTGGAGATCAAGCTGGC	Db	6587	CCCAAGCTCGCCAAACAGCTGGCCAGGAGCGGGAGCCCCACCCACCA-----	6629
QY	5581	CCAGCTGGGACAAAGAGCATCACTGTGACGCGAGTTGAGGAAGGAGATTTCCGTTGT	QY	6661	GAATGGGAGCCCCCTTGTCTCTCAACATCTGTGTAGCACCCCGCGCGCGTGGGCGGAG	6720
Db	5567	CCAGCTGGGACAAAGAGCATCACTGTGACGCGAGTTGAGGAAGGAGATTTCCGTTGT	Db	6630	-----	6629
QY	5641	GTGGSCAATCTGCCCCAGAGACTTTCGATTTGGTGTGTAACCCCAATAGCCCTGATGA	QY	6721	GCAGTCCCCCAGACGCCCTCTGATCTCCCGCCCCAGCATCACCTACAAAGAGGCGCAATC	6780
Db	5627	GTGGSCAATCTGCCCCAGAGACTTTCGATTTGGTGTGTAACCCCAATAGCCCTGATGA	Db	6630	-----	6629
QY	5701	GATGACGTGGGGAAGGTTTATGACGCTCTGATGATATTTTGACTTCTACAGAGCAACAA	QY	6781	CTCACCCATCCACTTTCGCGGGGCTCAGACAGCTCCCTGCTCTCTCCCTCAGGCGGCT	6840
Db	5687	GATGACGTGGGGAAGGTTTATGACGCTCTGATGATATTTTGACTTCTACAGAGCAACAA	Db	6630	-----	6639
QY	5761	AACCAACAGACAGATGACAGGCTCTCGAGGCTCTCCAGATGGGTCTCTGTGTC	QY	6841	CAGCCGTGGGCTTTCCGAACAAAGCCCTGTCTGAGAGAGAGAGAGAGAGAGAGAGAG	6900
Db	5747	AACCAACAGACAGATGACAGGCTCTCGAGGCTCTCCAGATGGGTCTCTGTGTC	Db	6640	CAGCCGTGGGCTTTCCGAACAAAGCCCTGTCTGAGAGAGAGAGAGAGAGAGAGAGAG	6699
QY	5821	CCTGTTTCAACCTCTGAAGGCCACCTGAGAGACAGCGGCTGTGCTCGAGGAGC	QY	6901	GGCCCTTGGCTCTCGAATTTGGCTTGAACCTTTACTCTGGGGAGAGCTCTGGAAGTGAAGC	6960
Db	5807	CCTGTTTCAACCTCTGAAGGCCACCTGAGAGACAGCGGCTGTGCTCGAGGAGC	Db	6700	GGCCCTTGGCTCTCGAATTTGGCTTGAACCTTTACTCTGGGGAGAGCTCTGGAAGTGAAGC	6759
QY	5881	CGGGTTTTCTTTCGACAGAGAGTTCACCTCTCTCCTCAGCAATGGCGGGGCCATACAAAA	QY	6961	CTCTGTCCACGCGCTCTGAGGACAGCTCTTTCGAGGAGGCTGTGGCCACCAACTC	7020

Db	6760	CTGTGTCACGCCCTGCTGAGGACACGCTCACTTTGAGGAGGCTGTGGCCAACTC	6819
Qy	7021	GGGCCGCTCTCCAGGACTTCTACGTGTCTCCCTGACCTCCGAGTCTCACCCCTCTCCG	7080
Db	6820	GGGCCGCTCTCTCCAGGACTTCTACGTGTCTCCCTGACCTCCGAGTCTCACCCCTCTCCG	6879
Qy	7081	CCGCGTGCCCAACGGTTACCACTGCACCTGCGGACTCAGCTCGGGTGGCCGAGCACGGCA	7140
Db	6880	CCGCGTGCCCAACGGTTACCACTGCACCTGCGGACTCAGCTCGGGTGGCCGAGCACGGCA	6939
Qy	7141	CAGCTACCAACACCCCTGACCAAGACCACTGTGTCTAGTGCACCGTGACCGCTCAGACGC	7200
Db	6940	CAGCTACCAACACCCCTGACCAAGACCACTGTGTCTAGTGCACCGTGACCGCTCAGACGC	6999
Qy	7201	CTGCATGACGACGCGCTGTGTTCAGTGGATGAGTTTTATCATCCACACGCGGCGAGTCGG	7260
Db	7000	CTGCATGACGACGCGCTGTGTTCAGTGGATGAGTTTTATCATCCACACGCGGCGAGTCGG	7059
Qy	7261	CCCTCGGGGAGGCGCTTGCCACCTTGGTGAGGCTCCTGTGGCCCTCCCTCCCCCTCCT	7320
Db	7060	CCCTCGGGGAGGCGCTTGCCACCTTGGTGAGGCTCCTGTGGCCCTCCCTCCCCCTCCT	7119
Qy	7321	CCCTCTTTTACTCTAGACGACGAATAAGCCCTGTGTGCTTGAGTGACGTACCGC	7376
Db	7120	CCCTCTTTTACTCTAGACGACGAATAAGCCCTGTGTGCTTGAGTGACGTACCGC	7175

Search completed: September 27, 2004, 01:31:25
Job time : 372 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2004, 22:19:23 ; Search time 2104 Seconds
(without alignments)
17756.210 Million cell updates/sec

Title: US-10-033-026-3

Perfect score: 7376

Sequence: 1 gcggcggtggtgcggcggt.....tgcttgagtgtacgtaccgc 7376

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3337386 seqs, 2532474682 residues

Total number of hits satisfying chosen parameters: 6674772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/FCT_NEW_PUB.seq.*
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- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7376	100.0	7376	14	US-10-033-026-3
2	7342	99.5	7364	9	US-09-954-456-1179
3	7342	99.5	7364	14	US-10-033-026-5
4	7316.4	99.2	7362	16	US-10-375-253-11
5	6958	94.3	7177	14	US-10-033-026-7
6	6932.4	94.0	7175	16	US-10-375-253-13
7	6535	88.6	6792	17	US-10-627-370-1
8	5289.8	71.7	7011	14	US-10-033-026-9
9	5200.4	70.5	7023	17	US-10-627-370-3
10	2582.6	35.0	6639	9	US-09-917-800A-1586
11	2507.2	34.0	7808	16	US-10-375-253-33
12	2502.2	33.9	7791	16	US-10-375-253-35
13	2488.2	33.7	7827	15	US-10-101-510-422
14	2408.4	32.7	7291	17	US-10-322-696-83

15	2402.4	32.6	7032	16	US-10-375-253-37	Sequence 37, Appl
16	2362.2	32.0	7348	17	US-10-322-696-175	Sequence 175, App
17	2362.2	32.0	7477	17	US-10-322-696-177	Sequence 177, App
18	2356.2	31.9	7089	16	US-10-375-253-39	Sequence 39, Appl
19	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
20	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
21	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
22	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
23	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
24	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
25	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
26	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
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33	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
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36	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
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38	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
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41	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
42	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
43	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
44	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
45	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App

ALIGNMENTS

RESULT 1
US-10-033-026-3
; Sequence 3, Application US/10033026
; Publication No. US20020147309A1
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/10/033,026
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7376
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..7174
US-10-033-026-3

Query Match	100.0%;	Score 7376;	DB 14;	Length 7376;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 7376;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
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Db	1	GC	GC	GC
Qy	61	GC	GC	GC
Db	61	GC	GC	GC

QY	121	GGATGACCGGGGCGCGGAGCCATGCTCGCTTCGGGACGAGCTGGCGGCGCTA	180
Db	121	GGATGACCGCGGGCCCGGAGCCATGCTCGCTTCGGGAGCAGCTGGCGGCGCTA	180
QY	181	TGAGAGCCCGCGGGGCGGAGAGCGGGCGCGGGGCGCGGGGCGGGGGCC	240
Db	181	TGAGAGCCCGCGGGGCGGAGAGCGGGCGCGGGGCGCGGGGCGGGGGCC	240
QY	241	GGGTCCCGGGGGCTCAGACCCGGCCAGCGGGCTCTTACAAGCAATCATCGCGAGCG	300
Db	241	GGGTCCCGGGGGCTCAGACCCGGCCAGCGGGCTCTTACAAGCAATCATCGCGAGCG	300
QY	301	CGCGCGACCATGGCGCTGTACAACCCCATCCGGTCAAAGCAAACTGCTTCAACGTCAA	360
Db	301	CGCGCGACCATGGCGCTGTACAACCCCATCCGGTCAAAGCAAACTGCTTCAACGTCNA	360
QY	361	CGGCTCGCTCTTGGTCTTCAAGAGAGCAAAAGTGTGTCGCAAAATACGCGAAGCATCAC	420
Db	361	CGGCTCGCTCTTGGTCTTCAAGAGAGCAAAAGTGTGTCGCAAAATACGCGAAGCATCAC	420
QY	421	CGAGTGGCTCCATTGGAGTATATGATCCTGGCCACCATCATCGCCAACTGATCGTGT	480
Db	421	CGAGTGGCTCCATTGGAGTATATGATCCTGGCCACCATCATCGCCAACTGATCGTGT	480
QY	481	GGCCCTGGAGAGCACTCCCTGATGGGCAAAAAGCGCCATGTCCGAGCGGCTGGACGA	540
Db	481	GGCCCTGGAGAGCACTCCCTGATGGGCAAAAAGCGCCATGTCCGAGCGGCTGGACGA	540
QY	541	CAGGAGCCCTATTTTCATCGGATCTTTTGGCTTCAGGAGGGATCAAAATCATCGCTCT	600
Db	541	CAGGAGCCCTATTTTCATCGGATCTTTTGGCTTCAGGAGGGATCAAAATCATCGCTCT	600
QY	601	GGGCTTTGTCTTCCAAAGGGCTCTTACCTGGGAAAGCGCTGGAACGCTCATGAGCTCGT	660
Db	601	GGGCTTTGTCTTCCAAAGGGCTCTTACCTGGGAAAGCGCTGGAACGCTCATGAGCTCGT	660
QY	661	GTCGTCTCTCAAGGGATCTCTTGGCAAGGCTGGAACTGACTTGGACCTCGGAACACTGAG	720
Db	661	GTCGTCTCTCAAGGGATCTCTTGGCAAGGCTGGAACTGACTTGGACCTCGGAACACTGAG	720
QY	721	GGCTGTGGGTGCTGAGGCGCCCTGAAGCTGTGTCTGGGATTCGAAGTTTCGAGTGGT	780
Db	721	GGCTGTGGGTGCTGAGGCGCCCTGAAGCTGTGTCTGGGATTCGAAGTTTCGAGTGGT	780
QY	781	GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCTCTGCAGATGGGCTGCTTCTTCTT	840
Db	781	GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCTCTGCAGATGGGCTGCTTCTTCTT	840
QY	841	TGCCATCTCATGTTTGGCATCATTTGGCGTGGAGTTCTACATGGGCAAGTTCCAAAGGC	900
Db	841	TGCCATCTCATGTTTGGCATCATTTGGCGTGGAGTTCTACATGGGCAAGTTCCAAAGGC	900
QY	901	CTGTTTCCCAACACACAGATCGGAGCCCGTGGGTGACTTCCCTGTGGCAGAGGAGGC	960
Db	901	CTGTTTCCCAACACACAGATCGGAGCCCGTGGGTGACTTCCCTGTGGCAGAGGAGGC	960
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Db	961	CCAGCCCGGTGTGCGAGGGCGACA CTGAGTGGCGGAGTACTGGCCAGGACCCAACTT	1020
QY	1021	TGGCATCAACCACTTTGACAATATCCTGTTTGGCAATCTTGAAGGTTCAGTGCATCAC	1080
Db	1021	TGGCATCAACCACTTTGACAATATCCTGTTTGGCAATCTTGAAGGTTCAGTGCATCAC	1080
QY	1081	CATGAGGGCTGGACTGACATCTCTATAATAACAAACGATCGGCGCCGCAACCTGGA	1140
Db	1081	CATGAGGGCTGGACTGACATCTCTATAATAACAAACGATCGGCGCCGCAACCTGGA	1140
QY	1141	CTGGCTTACTTCACTCTCATCATCATCGGCTCTCTTCAATGCTCAACCTGGTGT	1200
Db	1141	CTGGCTTACTTCACTCTCATCATCATCGGCTCTCTTCAATGCTCAACCTGGTGT	1200

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Db	1201	GGGCTGTCTCTCGGGGAGTTTGCACAGGACGAGAGGGTGGAGAACCCCGCGGCTT	1260
QY	1261	CCTGAAGCTGCGCGCGGACGACGAGATCGACGAGAGCTCAACGGGTACCTTGGAGTGGAT	1320
Db	1261	CCTGAAGCTGCGCGCGGACGACGAGATCGACGAGAGCTCAACGGGTACCTTGGAGTGGAT	1320
QY	1321	CTTCAAGCGGAGGAAGTCACTGTGCGGAGGAGGACAGGAATGCAGAGGAAGTCCCC	1380
Db	1321	CTTCAAGCGGAGGAAGTCACTGTGCGGAGGAGGACAGGAATGCAGAGGAAGTCCCC	1380
QY	1381	TTTGGACGTGTGAAGAGAGCGGCCACCAAGAGAGCAGAAATGACCTGTACACGAGAGA	1440
Db	1381	TTTGGACGTGTGAAGAGAGCGGCCACCAAGAGAGCAGAAATGACCTGTACACGAGAGA	1440
QY	1441	GGAGGAGAGGACCGGTTTGCAGATCTCTGTGCTTGGATCCGCCCTTCCGCGCGCAG	1500
Db	1441	GGAGGAGAGGACCGGTTTGCAGATCTCTGTGCTTGGATCCGCCCTTCCGCGCGCAG	1500
QY	1501	CCTCAAGCGGGAAGACAGAGAGCTCGTCACTACTTCCGAGGAGGAGAGATGTTCCG	1560
Db	1501	CCTCAAGCGGGAAGACAGAGAGCTCGTCACTACTTCCGAGGAGGAGAGATGTTCCG	1560
QY	1561	GTTTTTTTATCCGGCGCATGGTGAAGGCTCAGAGCTTCTACTGGGTGTGCTGTGCTGGT	1620
Db	1561	GTTTTTTTATCCGGCGCATGGTGAAGGCTCAGAGCTTCTACTGGGTGTGCTGTGCTGGT	1620
QY	1621	GGCCCTGAAACACTGTGTGTCGCAATGATGTCATTAACACGACGCGCGGCTTACCA	1680
Db	1621	GGCCCTGAAACACTGTGTGTCGCAATGATGTCATTAACACGACGCGCGGCTTACCA	1680
QY	1681	GACCTGTATTTTGCAGAGTTTCTTCTGGGTCTCTTCTCACAGAGATGTCCTGAA	1740
Db	1681	GACCTGTATTTTGCAGAGTTTCTTCTGGGTCTCTTCTCACAGAGATGTCCTGAA	1740
QY	1741	GATGTATGGCTGGGGCCAGAAAGTACTTCCGGTCTCTCTTCAACTGCTTTCGACTTTGG	1800
Db	1741	GATGTATGGCTGGGGCCAGAAAGTACTTCCGGTCTCTCTTCAACTGCTTTCGACTTTGG	1800
QY	1801	GGTCATCTGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCATCAAGCGGGAAGCTCCTT	1860
Db	1801	GGTCATCTGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCATCAAGCGGGAAGCTCCTT	1860
QY	1861	TGGATCAGTGTCTCGGGCCCTCGGCTGTGAGGATCTTCAAGTCAAGGACTG	1920
Db	1861	TGGATCAGTGTCTCGGGCCCTCGGCTGTGAGGATCTTCAAGTCAAGGACTG	1920
QY	1921	GAGTCTCTCGGAACTCGTGTGTCTCTGCTGAACTCCATGAAGTCCAATCAGCCT	1980
Db	1921	GAGTCTCTCGGAACTCGTGTGTCTCTGCTGAACTCCATGAAGTCCAATCAGCCT	1980
QY	1981	GCTCTTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2040
Db	1981	GCTCTTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2040
QY	2041	GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCAACTTCCGACACCTTCCCTCCCG	2100
Db	2041	GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCAACTTCCGACACCTTCCCTCCCG	2100
QY	2101	CATCT	2160
Db	2101	CATCT	2160
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QY	2221	GACACTGTTTGGGAACTACACTCTGCTGAATCTCTTCTTGGCCATCGCTGTGAGCAACCT	2280
Db	2221	GACACTGTTTGGGAACTACACTCTGCTGAATCTCTTCTTGGCCATCGCTGTGAGCAACCT	2280
QY	2281	GGCCACGCCCAAGAGCTGACCAAGATGAAGAGGATGGGAAGAGCAGCNAATCAGAA	2340

Db	2281	GGCCAAAGCGCCCAAGAGCTGACCAAGGATGAAGAGAGATGGAAGACGACCAATCAGAA	2340
Qy	2341	GCTTGGCTCTGCAAAAGGCCAAAGAGTGGCTGAAGTCAAGCCCCATGCTGCGCGCAACAT	2400
Db	2341	GCTTGGCTCTGCAAAAGGCCAAAGAGTGGCTGAAGTCAAGCCCCATGCTGCGCGCAACAT	2400
Qy	2401	CTCCATCGCCGCCAGGACGACGAGAACTCGCGCAAGCGCGCTGCTGCTGGAGACAGCGGGC	2460
Db	2401	CTCCATCGCCGCCAGGACGACGAGAACTCGCGCAAGCGCGCTGCTGCTGGAGACAGCGGGC	2460
Qy	2461	CAGCAGCTAGCGGTGAGAACCTGCGGCCAGCTGCGAGCGCTGTACAGCGAGATGGA	2520
Db	2461	CAGCAGCTAGCGGTGAGAACCTGCGGCCAGCTGCGAGCGCTGTACAGCGAGATGGA	2520
Qy	2521	CCCCGAGAGCGGCTGGCGCTTCGCGCACTACCGCGCACCTGCGGCCCGACATGAAGACGCA	2580
Db	2521	CCCCGAGAGCGGCTGGCGCTTCGCGCACTACCGCGCACCTGCGGCCCGACATGAAGACGCA	2580
Qy	2581	CTTGGACCGGCCGCTGCTGCTGGAGCTGGGCGCGACCGCGCGCGGGCGCCGCTGGGAGG	2640
Db	2581	CTTGGACCGGCCGCTGCTGCTGGAGCTGGGCGCGACCGCGCGCGGGCGCCGCTGGGAGG	2640
Qy	2641	CAAAAGCCGACCTGAGGCTGCGAGGCGCCCGAGGGCGTCAACCTCGCGCAGGACCA	2700
Db	2641	CAAAAGCCGACCTGAGGCTGCGAGGCGCCCGAGGGCGTCAACCTCGCGCAGGACCA	2700
Qy	2701	CCGGCACCGGACCAAGGACCAAGACCCCGCGCGCGGGGACCAAGACCGAGCAGAGGCCCC	2760
Db	2701	CCGGCACCGGACCAAGGACCAAGACCCCGCGCGCGGGGACCAAGACCGAGCAGAGGCCCC	2760
Qy	2761	GAAGCGGAGAGCGGGAGCGCCGCTGCTCGGAGGAGCGCGCGCGCGCCGCAACCGACGCA	2820
Db	2761	GAAGCGGAGAGCGGGAGCGCCGCTGCTCGGAGGAGCGCGCGCGCGCCGCAACCGACGCA	2820
Qy	2821	CAGCAAGAGGCGCGGGGCCCCCGGAGGCGCGAGCGCGCGCGCGCGCGAGGCCCAGGCC	2880
Db	2821	CAGCAAGAGGCGCGGGGCCCCCGGAGGCGCGAGCGCGCGCGCGCGCGAGGCCCAGGCC	2880
Qy	2881	CGAGGCGCGCGCGGACCAACCGCGCGGCTCCCGGAGGAGCGCGCGAGCGGGAGGCC	2940
Db	2881	CGAGGCGCGCGCGGACCAACCGCGCGGCTCCCGGAGGAGCGCGCGAGCGGGAGGCC	2940
Qy	2941	CCGACGCCACCGCGCGCACCGGACCAAGGATCCGAGCAAGAGGTGCGCGCGCGCCAAAGGG	3000
Db	2941	CCGACGCCACCGCGCGCACCGGACCAAGGATCCGAGCAAGAGGTGCGCGCGCGCCAAAGGG	3000
Qy	3001	CGACGCGCGCGCGGACACCGCGCGCGCCCCCGAGCGGGGCCCCCGGAGCGCGAGCGGG	3060
Db	3001	CGACGCGCGCGCGGACACCGCGCGCGCCCCCGAGCGGGGCCCCCGGAGCGCGAGCGGG	3060
Qy	3061	GGAGGAGCGCGCGGGGACACCGGCGCGGACCAAGCGCAGCGCTGCTCACGAGGCTGT	3120
Db	3061	GGAGGAGCGCGCGGGGACACCGGCGCGGACCAAGCGCAGCGCTGCTCACGAGGCTGT	3120
Qy	3121	GGAGGAGGAGACCAAGGAGGAGGCGCACCGAGAGGAGGCTGAGATAGTGGAGGCGGA	3180
Db	3121	GGAGGAGGAGACCAAGGAGGAGGCGCACCGAGAGGAGGCTGAGATAGTGGAGGCGGA	3180
Qy	3181	CAAGGAAAAGAGCTCCGGAAACCAACGAGCCCCCGGAGCGCACCTGTGACCTTGGAGCCAG	3240
Db	3181	CAAGGAAAAGAGCTCCGGAAACCAACGAGCCCCCGGAGCGCACCTGTGACCTTGGAGCCAG	3240
Qy	3241	TGGGACTGTGACTGTGGGTCCATGCAACACTCCGAGCACCTGCTCCAGAGAGGTGA	3300
Db	3241	TGGGACTGTGACTGTGGGTCCATGCAACACTCCGAGCACCTGCTCCAGAGAGGTGA	3300
Qy	3301	GGAAAGCAGCAGAGGATGAGCAAACTCAGCGGAAAGCTCACTCGCATGGCGAGTCAAGCCCC	3360
Db	3301	GGAAAGCAGCAGAGGATGAGCAAACTCAGCGGAAAGCTCACTCGCATGGCGAGTCAAGCCCC	3360
Qy	3361	AGACCCGAAACATATTGTATATATCCAGTGATGCTGACGGGCGCTCTTGGGGAGGCCAC	3420
Db	3361	AGACCCGAAACATATTGTATATATATCCAGTGATGCTGACGGGCGCTCTTGGGGAGGCCAC	3420

Db	3361	AGACCCGAAACATATTGTATATATATCCAGTGATGCTGACGGGCGCTCTTGGGGAGGCCAC	3420
Qy	3421	GGTCGTTCCAGTGGTAAACGTGGACCTGGAAAGCAACAGCAGAGGGGGAAGAGGAGTGA	3480
Db	3421	GGTCGTTCCAGTGGTAAACGTGGACCTGGAAAGCAACAGCAGAGGGGGAAGAGGAGTGA	3480
Qy	3481	AGCGATGACGTGATGAGGAGCGGCCCCCGGCTATCGTCCCATACAGCTCCATGTTCTG	3540
Db	3481	AGCGATGACGTGATGAGGAGCGGCCCCCGGCTATCGTCCCATACAGCTCCATGTTCTG	3540
Qy	3541	TTTAAAGCCCCACCAACCTGCTCCGCGCTCTGCACTACATCGTGACCATGAGGTACTT	3600
Db	3541	TTTAAAGCCCCACCAACCTGCTCCGCGCTCTGCACTACATCGTGACCATGAGGTACTT	3600
Qy	3601	CGAGGTGGTCAATCTCGTGGTCAATCGCTTGGAGCAGCATCGCCCTGCTGCTGAGGACCC	3660
Db	3601	CGAGGTGGTCAATCTCGTGGTCAATCGCTTGGAGCAGCATCGCCCTGCTGCTGAGGACCC	3660
Qy	3661	AGTGGGCAAGACCTCGGCCAGGAAACACGCTCTGAATACCTGGATTACATTTTCACTGG	3720
Db	3661	AGTGGGCAAGACCTCGGCCAGGAAACACGCTCTGAATACCTGGATTACATTTTCACTGG	3720
Qy	3721	TGCTTTTACCTTTGAGATGCTGATGAAGATGATCGACTTGGGACTGCTGCTCACCCCTGG	3780
Db	3721	TGCTTTTACCTTTGAGATGCTGATGAAGATGATCGACTTGGGACTGCTGCTCACCCCTGG	3780
Qy	3781	AGCCTATTTCCGGGACTTTGTGGAAACATTTCTGGACTTCAATTTGTGTCAAGTGGCGCCCTGGT	3840
Db	3781	AGCCTATTTCCGGGACTTTGTGGAAACATTTCTGGACTTCAATTTGTGTCAAGTGGCGCCCTGGT	3840
Qy	3841	GGCGTTTCTTCTCGAGCTTCTGAGAGGATCCAAAGGGAAAGACATCAATACCATCAA	3900
Db	3841	GGCGTTTCTTCTCGAGCTTCTGAGAGGATCCAAAGGGAAAGACATCAATACCATCAA	3900
Qy	3901	GTCTCTGAGAGTCTTCTGCTGCTCGCGGCCCTCAAGACCATCAAAAGGGTGGCCAAAGCT	3960
Db	3901	GTCTCTGAGAGTCTTCTGCTGCTCGCGGCCCTCAAGACCATCAAAAGGGTGGCCAAAGCT	3960
Qy	3961	CAAGGCTGTCTTTGACTGTGTGTGAATCTCCCTGAAGAAATGCTCTCAACATCTTGATTTGT	4020
Db	3961	CAAGGCTGTCTTTGACTGTGTGTGAATCTCCCTGAAGAAATGCTCTCAACATCTTGATTTGT	4020
Qy	4021	CTACATGCTCTTCAATGTTTCAATTTGCGGTCAATTTGCGGTGAGCTCTTCAAGAGGAAAGTT	4080
Db	4021	CTACATGCTCTTCAATGTTTCAATTTGCGGTCAATTTGCGGTGAGCTCTTCAAGAGGAAAGTT	4080
Qy	4081	TTTCTACTGCACAGATGAATCCAGGAGCTGGAGAGGAGCTGCAAGGCGTCAAGTATTTTGA	4140
Db	4081	TTTCTACTGCACAGATGAATCCAGGAGCTGGAGAGGAGCTGCAAGGCGTCAAGTATTTTGA	4140
Qy	4141	TTATGAGAGGAGGAAAGTGAAGCTCAGCCAGGAGTGAAGAAATACGACTTTTCACTA	4200
Db	4141	TTATGAGAGGAGGAAAGTGAAGCTCAGCCAGGAGTGAAGAAATACGACTTTTCACTA	4200
Qy	4201	CGACAAATGCTCTGGGCTCTGTGAGCTGTGTTTCAAGTGTCCAAGGCTGGCC	4260
Db	4201	CGACAAATGCTCTGGGCTCTGTGAGCTGTGTTTCAAGTGTCCAAGGCTGGCC	4260
Qy	4261	CATGGTCTGAAACATCTCGTGGATGCCCTATGAGGAGCGGCTCAAGCCCTGGGTA	4320
Db	4261	CATGGTCTGAAACATCTCGTGGATGCCCTATGAGGAGCGGCTCAAGCCCTGGGTA	4320
Qy	4321	CCGATGAGGCTGTGCATCTTACGCTGGTCTACTTTTGTGGTCTTTTCCCTTCTTCTTCGT	4380
Db	4321	CCGATGAGGCTGTGCATCTTCTACGCTGGTCTACTTTTGTGGTCTTTTCCCTTCTTCTTCGT	4380
Qy	4381	CAACATCTTTTGGCTTTGATCATCATCATCATCTCCAGGAGCAGGGGCAAGGTGATGC	4440
Db	4381	CAACATCTTTTGGCTTTGATCATCATCATCATCTCCAGGAGCAGGGGCAAGGTGATGC	4440
Qy	4441	TGAATCAGGCTCGAGAGAGACGAGAGGGCTTGCATTTGACTTCCCATCAGCGCCAAACC	4500
Db	4441	TGAATCAGGCTCGAGAGAGACGAGAGGGCTTGCATTTGACTTCCCATCAGCGCCAAACC	4500

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QY 4621 GATGATGAAGTTCTATGATGCACCCCTATGAGTACGAGCTGATGCTGAATGCTCTGAACAT 4680
DB GATGATGAAGTTCTATGATGCACCCCTATGAGTACGAGCTGATGCTGAATGCTCTGAACAT 4680
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RESULT 2
US-09-954-456-1179
; Sequence 1179, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1179
; LENGTH: 7364
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1179

Query Match 99.5%; Score 7342; DB 9; Length 7364;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7364; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

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1741 GATGTATGGCTTGGGCGCCAGAGCTACTTCGGTCTCTTCTCAAGAGATGTCCTTGA 1800
1741 GATGTATGGCTTGGGCGCCAGAGCTACTTCGGTCTCTTCTCAAGAGATGTCCTTGA 1800
1801 GGTCACTGTGGAGCGTCTTTTGAAGTGTCTGGCGGCGCATCAAGCGGGAAGCTCTT 1860
1801 GGTCACTGTGGAGCGTCTTTTGAAGTGTCTGGCGGCGCATCAAGCGGGAAGCTCTT 1860
1861 TGGATCAGTGTGTGCGGCGCTCCGCTCTGAGGATCTTCAAAGTCAAGAGTACTG 1920
1861 TGGATCAGTGTGTGCGGCGCTCCGCTCTGAGGATCTTCAAAGTCAAGAGTACTG 1920

1921 GAGCTCCTGCGGAACCTGTGGTGTCCCTGCTGAACTCCATGAAGTCCATCATCAGCCT 1980
1921 GAGCTCCTGCGGAACCTGTGGTGTCCCTGCTGAACTCCATGAAGTCCATCATCAGCCT 1980
1981 GCTCTTCTGCTCTTCTCTGTTTCAATTTGGTCTTGCCTCTGCTGGGATGAGCTGTTGG 2040
1981 GCTCTTCTGCTCTTCTCTGTTTCAATTTGGTCTTGCCTCTGCTGGGATGAGCTGTTGG 2040
2041 GGGACAGTTCAACTTCCAGGATGAGCTCCCAACAACCTTCCACACCTTCCCTGCGGC 2100
2041 GGGACAGTTCAACTTCCAGGATGAGCTCCCAACAACCTTCCACACCTTCCCTGCGGC 2100
2101 CATCTCCTCTCTCTTCCAGATCCCTGAGAGGAGTGGAAATGCAATGATGATCAGG 2160
2101 CATCTCCTCTCTTCCAGATCCCTGAGAGGAGTGGAAATGCAATGATGATCAGG 2160
2161 GATCGAATCGCAAGCGCGCTGACAAAGGATGTTCTCGTCTCTTTTACTTCAATGTCT 2220
2161 GATCGAATCGCAAGCGCGCTGACAAAGGATGTTCTCGTCTCTTTTACTTCAATGTCT 2220
2221 GACACTGTTGGAAGTCTACTCTGCTGAAATGTTCTTCTGCGCATCGCTGTGACACCT 2280
2221 GACACTGTTGGAAGTCTACTCTGCTGAAATGTTCTTCTGCGCATCGCTGTGACACCT 2280
2281 GGCACACCGCCAAAGAGCTGACAAAGGATGAGAGGAGTGAAGAGCAGCAGCAATCAGAA 2340
2281 GGCACACCGCCAAAGAGCTGACAAAGGATGAGAGGAGTGAAGAGCAGCAGCAATCAGAA 2340
2341 GCTTGTCTCTGAAAGGCGCCAAAGAGTGGCTGAAGTCAAGCCCATGTCTGCCCGCAACAT 2400
2341 GCTTGTCTCTGAAAGGCGCCAAAGAGTGGCTGAAGTCAAGCCCATGTCTGCCCGCAACAT 2400
2401 CTCATCGCGCGCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGGC 2460
2401 CTCATCGCGCGCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGGC 2460
2461 CAGCAGCTACGCTGCGAAGCTTGGGGCCAGCTGCGAGCGCTGTACA3CGAGATGGA 2520
2461 CAGCAGCTACGCTGCGAAGCTTGGGGCCAGCTGCGAGCGCTGTACA3CGAGATGGA 2520
2521 CCCGAGAGCGGCTGGCTTCCCACTAGCGCCACCTCGCGCCGCGACATGAAGACGCA 2580
2521 CCCGAGAGCGGCTGGCTTCCCACTAGCGCCACCTCGCGCCGCGACATGAAGACGCA 2580
2581 CTTGGAACCGCCCTGCTGTGTGAGTGGGCGCGAGCGCGCGGGGGCTCGTGGAGG 2640
2581 CTTGGAACCGCCCTGCTGTGTGAGTGGGCGCGAGCGCGCGGGGGCTCGTGGAGG 2640
2641 CAAAGCCCGACCTGAGGCTGCGGAGGCCCCCGAGGCGCTCGACCTCCGCG3CAGGACCA 2700
2641 CAAAGCCCGACCTGAGGCTGCGGAGGCCCCCGAGGCGCTCGACCTCCGCG3CAGGACCA 2700
2701 CCGGCAACCGGCAACAGCAAGACCCCGCGCGGGGACCCAGGAACGAGAGCGCCC 2760
2701 CCGGCAACCGGCAACAGCAAGACCCCGCGCGGGGACCCAGGAACGAGAGCGCCC 2760
2761 GAAGGCGGAGAGCGGGAGCCCGGTGCTCCCGAGGAGCGCGCGCGCGCGCGAGC 2820
2761 GAAGGCGGAGAGCGGGAGCGCGGTGCTCCCGAGGAGCGCGCGCGCGCGCGAGC 2820
2821 CAGCAAGGAGGCGCGGGGCCCCCGGAGCGCGGAGCGCGCGCGCGCGCGAGC 2880
2821 CAGCAAGGAGGCGCGGGGCCCCCGGAGCGCGGAGCGCGCGCGCGCGCGAGC 2880
2881 CAGAGGCGCGCGCGCGCAACACCGGGCGGCTCCCGAGGAGCGCGCGCGCGCGAGC 2940
2881 CAGAGGCGCGCGCGCGCGCAACACCGGGCGGCTCCCGAGGAGCGCGCGCGCGAGC 2940
2941 CCGACGCCACCGCGCGCACCGGACCCAGGATCCGAGCAAGAGTGGCGCG3CGCAAGG 3000
2941 CCGACGCCACCGCGCGCACCGGACCCAGGATCCGAGCAAGAGTGGCGCGCG3CGCAAGG 3000
3001 CGAGCGCGCGCGCGCGCACCGCGCGGGCCCCCGAGCGGGGGCCCCCGGAGCG3CGAGAGCGG 3060

Db 3001 CGACGGCGCGCGGACACCGCGGCGCCCCCGAGCGGGCCCCCGGGAGCGGAGCGG 3060
Qy |||||
Db 3061 GGAGGAGCGCGCGCGGCGCACCGGGCGCGGACCAAGCGCGAGCCTGCTCACAGGCTGT 3120
Qy |||||
Db 3061 GGAGGAGCGCGCGCGGCGCACCGGGCGCGGACCAAGCGCGAGCCTGCTCACAGGCTGT 3120
Qy |||||
Db 3121 GGAGAGGAGAGCACCGAGAGAGGAGGCCACGAGAGAGGAGGCTGAGATAGTGGAAAGCCGA 3180
Qy |||||
Db 3121 GGAGAGGAGAGCACCGAGAGAGGAGGCCACGAGAGAGGAGGCTGAGATAGTGGAAAGCCGA 3180
Qy |||||
Db 3181 CAAGGAAAGAGAGCTCCGGAAACACCGAGCCCGGGAGGCCACACTGTGACCTGGAGAGCCAG 3240
Qy |||||
Db 3181 CAAGGAAAGAGAGCTCCGGAAACACCGAGCCCGGGAGGCCACACTGTGACCTGGAGAGCCAG 3240
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Db 3241 TGGGACTGTGACTGTGGGTCCCATGACACACACTCCCGAGCACCTGTCTCCAGAAAGTGGGA 3300
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Db 3301 GGAAACAGCCAGAGGATGACAGCAATACAGCGGAACGTCACTGCGATGGGCGAGTCAGCCCCC 3360
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Db 3301 GGAAACAGCCAGAGGATGACAGCAATACAGCGGAACGTCACTGCGATGGGCGAGTCAGCCCCC 3360
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Db 3361 AGACCCGNAACATTTGTACATATCCCACTGATGCTGACGGGCCCTCTTGGGAGAGCCAC 3420
Qy |||||
Db 3361 AGACCCGNAACATTTGTACATATCCCACTGATGCTGACGGGCCCTCTTGGGAGAGCCAC 3420
Qy |||||
Db 3421 GGTGGTCCCAAGTGGTAACTGGGACCTGGAAAGCCAAAGAGAGGAGGAGTGGGA 3480
Qy |||||
Db 3421 GGTGGTCCCAAGTGGTAACTGGGACCTGGAAAGCCAAAGAGAGGAGGAGTGGGA 3480
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Db 3481 AGCGGATGAGTGATGAGGAGCGGCCCGGCCCTATCGTCCCATACAGCTCCATGTTCTG 3540
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Db 3541 TTTTAAGCCCAACCACTGCTCCGCGCTTCTGCGCACTACATCTGACCATGAGGTACTT 3600
Qy |||||
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Db 3601 CGAGGTGGTCAATTCGTGGTGCATCGGCTTGAGCAGCATCGCCCTGGTGTCTGAGGACCC 3660
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Qy |||||
Db 3661 AGTGGCACAGACTCGGCCAGGAAACACGCTCTGAATACCTGGAATACATTTTCACTGG 3720
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Db 3721 TGTCTTTTACCTTTGAGATGGTGAATAAGATGATCGACTTGGGACTGCTTCAACCTGG 3780
Qy |||||
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Db 3781 AGCCTATTTCCGGACTTGTGGAACATTTGAGCTTCAATTTGCTGAGTGGCGCCCTGGT 3840
Qy |||||
Db 3781 AGCCTATTTCCGGACTTGTGGAACATTTGAGCTTCAATTTGCTGAGTGGCGCCCTGGT 3840
Qy |||||
Db 3841 GGCCTTTGCTTTCTC-----AGGATCCAAAGGAAAGACATCAATACCATCAA 3888
Qy |||||
Db 3841 GGCCTTTGCTTTCTC-----AGGATCCAAAGGAAAGACATCAATACCATCAA 3888
Qy |||||
Db 3901 GTCTCTGAGAGTCCCTGCTGCTGCGGCCCTCAGACCCATCAACGGCTGCCCAAGCT 3960
Qy |||||
Db 3889 GTCTCTGAGAGTCCCTGCTGCTGCGGCCCTCAGACCCATCAACGGCTGCCCAAGCT 3948
Qy |||||
Db 3961 CAAGGCTGTGTTTCACTGTGTGGTGAATCCCTCAAGAAATGCTCCTCAACATCTTGTATTGT 4020
Qy |||||
Db 3949 CAAGGCTGTGTTTCACTGTGTGGTGAATCCCTCAAGAAATGCTCCTCAACATCTTGTATTGT 4008
Qy |||||
Db 4021 CTACATGCTCTTCAATGTTCAATTTGCGGTCAATTCGGTGCAGCTTTCAAAGGAAAGTT 4080
Qy |||||
Db 4009 CTACATGCTCTTCAATGTTCAATTTGCGGTCAATTCGGTGCAGCTTTCAAAGGAAAGTT 4068
Qy |||||
Db 4081 TTTTCTACTGCACAGATGAATCCAAAGGAGCTGGAGAGGAGCTGACAGGGGTCAATTTTGGGA 4140
Qy |||||

4069 TTTTCTACTGCACAGATGAATCCAAAGAGCTGGAGAGGAGCTGCAGGGGTCAATTTTGGGA 4128
Qy |||||
4141 TTATGAGAGAGGAGAGTGGAAAGCTCAGCCAGCGCAGTGGAAAGAAATACGACTTTTCACTA 4200
Qy |||||
4129 TTATGAGAGAGGAGAGTGGAAAGCTCAGCCAGCGCAGTGGAAAGAAATACGACTTTTCACTA 4188
Qy |||||
4201 CGACAATGTGCTCTGGGCTCTGCTGAGCGCTGTTTCAAGTGTCTCACGGGAGAAAGCTGGCC 4260
Qy |||||
4189 CGACAATGTGCTCTGGGCTCTGCTGAGCGCTGTTTCAAGTGTCTCACGGGAGAAAGCTGGCC 4248
Qy |||||
4261 CATGGTGTCAAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4320
Qy |||||
4249 CATGGTGTCAAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4308
Qy |||||
4321 CCGCATGGAGCTGTCCATCTTCTACGTGGTCTACTTTTGTGGTCTTTTCCCTTCTTCTTCGT 4380
Qy |||||
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Qy |||||
4381 CAACATCTTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGACAAGGTGATGTC 4440
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4489 CCTGCACACGTTACATGTCACCCCAAAACCGGCACTGTTCCAGTATAAGACGTGGACATTTGT 4548
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4561 GGTCTCCCGCCCTTTGATATCTTTCATCATGCGCATGATAGCCCTCAACACTGTGTGCT 4620
Qy |||||
4549 GGTCTCCCGCCCTTTGAATACCTTTCATCATGCGCATGATAGCCCTCAACACTGTGTGCT 4608
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Qy |||||
4609 GATGATGAAGTCTTATGATGACACCTATGATGACGAGCTGATGCTGAAATGCCTGGAACAT 4668
Qy |||||
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Qy |||||
4669 CGTGTTCACATCCATGTTTCCATGGAAATGCGTGTGCTGGAAGATCATCGCCCTTTGGGGTGT 4728
Qy |||||
4741 GAACTATTTTCAAGATGCTCGGAAATGCTTTGACTTTTGTCACTGTGTGGGAGATATTAC 4800
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4729 GAACTATTTTCAAGATGCTCGGAAATGCTTTGACTTTTGTCACTGTGTGGGAGATATTAC 4788
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Qy |||||
4849 CCTCTTTTCAAGCTGCGCGCTGATCAAGCTGCTCCGCGAGGGCTACACCATCCGATCCT 4908
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4921 GCTGTGGAACCTTTGTCCAGTCTTCAAGGCCCTGCCCCCTACGTGTGTCTCATTTGCGCAT 4980
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4909 GCTGTGGAACCTTTGTCCAGTCTTCAAGGCCCTGCCCCCTACGTGTGTCTCATTTGCGCAT 4968
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4969 GCTGTGTTTTCATCTACGCCATCATCGGCATGAGGTGTTTGGGAATATTGCGCTGGATGA 5028
Qy |||||
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Qy |||||
5029 TGACACAGCATCAACCGCCACAACTTTCCGGAGCTTTTTCAGAGCCCTGATGTGCT 5088
Qy |||||
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Qy |||||
5089 GTTCAGAGCGCCACCGGGGAGGCTTGGACAGATCATGCTGCTGCTGCTGAGCAACCA 5148
Qy |||||
5161 GGCTGTGATGAGCAGGCCAAATGCCACCGAGTGTGGAAGTACTTTGCTTACTTCTTACTT 5220
Qy |||||
5149 GGCTGTGATGAGCAGGCCAAATGCCACCGAGTGTGGAAGTACTTTGCTTACTTCTTACTT 5208
Qy |||||

QY	5221	CGTCTCCTTCAATCTTCTGTGCTCCTTTCTGATGTTGAACCTCTTTGTGGCTGTGATCAT	5280
Db	5209	CGTCTCCTTCAATCTTCTGTGCTCCTTTCTGATGTTGAACCTCTTTGTGGCTGTGATCAT	5268
QY	5281	GGACAATTTTGAAGTACCTCAAGCGGGAATCTTCCATCTTAGTFCCTCACCACCTTGGATGA	5340
Db	5269	GGACAATTTTGAAGTACCTCAAGCGGGAATCTTCCATCTTAGTFCCTCACCACCTTGGATGA	5328
QY	5341	GTTCAATCCGGGTCTGGGCTGAATACACCGGCTGCTGTGGCGCATCAGTTACAATGA	5400
Db	5329	GTTCAATCCGGGTCTGGGCTGAATACACCGGCTGCTGTGGCGCATCAGTTACAATGA	5388
QY	5401	CATGTTTGAATGCTGAAACACATGTCCTCGGCTCTGGGCTGGGGAAGAAATGCCCTGC	5460
Db	5389	CATGTTTGAATGCTGAAACACATGTCCTCGGCTCTGGGCTGGGGAAGAAATGCCCTGC	5448
QY	5461	TCAGTGTGTTTACAAGGCTGTTGCGATGAACATGCTCCATCTCAACAGGACATGAC	5520
Db	5449	TCAGTGTGTTTACAAGGCTGTTGCGATGAACATGCTCCATCTCAACAGGACATGAC	5508
QY	5521	TGTTTCACTTCACTGCTCAAGCTGATGCTGCTCAATCGGACGCACTGGAGATCAAGCTGGC	5580
Db	5509	TGTTTCACTTCACTGCTCAAGCTGATGCTGCTCAATCGGACGCACTGGAGATCAAGCTGGC	5568
QY	5581	CCAGCTGGGACAAAGCAGCATCAGTGTGAACCGGAGTTGAGGAAGGATTTCCGTTGT	5640
Db	5569	CCAGCTGGGACAAAGCAGCATCAGTGTGAACCGGAGTTGAGGAAGGATTTCCGTTGT	5628
QY	5641	GTGGGCAATCTGCCCCAGAACACTTGGACTGCTGCTGCTACACCCATAGACCTGATGA	5700
Db	5629	GTGGGCAATCTGCCCCAGAACACTTGGACTGCTGCTGCTACACCCATAGACCTGATGA	5688
QY	5701	GATGACAGTGGGGAAGTTTATGCACTCTGATGATATTGACTTCTCAAGACGAAACAA	5760
Db	5689	GATGACAGTGGGGAAGTTTATGCACTCTGATGATATTGACTTCTCAAGACGAAACAA	5748
QY	5761	AACCAACAGACACAGATGCAAGGCTCCTGGAGGCTCTCCAGATGGGTCTGTGTGC	5820
Db	5749	AACCAACAGACACAGATGCAAGGCTCCTGGAGGCTCTCCAGATGGGTCTGTGTGC	5808
QY	5821	CCTGTTTCACTCTGAGGCGCACCTGGAGCAGACACAGCGGCTGTGCTCCGAGGAGC	5880
Db	5809	CCTGTTTCACTCTGAGGCGCACCTGGAGCAGACACAGCGGCTGTGCTCCGAGGAGC	5868
QY	5881	CCGGTFTTCTTCGACAGAAGAGTTCCACCTCCCTCAGCAATGGCGGGGCATACAAAA	5940
Db	5869	CCGGTFTTCTTCGACAGAAGAGTTCCACCTCCCTCAGCAATGGCGGGGCATACAAAA	5928
QY	5941	CCAAGAGATGGCATCAAGAGTCTGTCTCTGGGGCACTCAAGGACCCAGGATGCACC	6000
Db	5929	CCAAGAGATGGCATCAAGAGTCTGTCTCTGGGGCACTCAAGGACCCAGGATGCACC	5988
QY	6001	CCATGAGGCAGGCGCACCCCTGGAGCGTGGCCACTCCACAGAGATCCTGTGGGCGGTC	6060
Db	5989	CCATGAGGCAGGCGCACCCCTGGAGCGTGGCCACTCCACAGAGATCCTGTGGGCGGTC	6048
QY	6061	AGGAGCATCTGGCTGTGGACGTTTCAATGCAGAGCATACCCGGAGGGGCGCTGTGGGGA	6120
Db	6049	AGGAGCATCTGGCTGTGGACGTTTCAATGCAGAGCATACCCGGAGGGGCGCTGTGGGGA	6108
QY	6121	GCCCCAGCTGGCTGGAGAGCCAGGCTCGAGCGGCTCCATGCGCGCTTGGCGCGGA	6180
Db	6109	GCCCCAGCTGGCTGGAGAGCCAGGCTCGAGCGGCTCCATGCGCGCTTGGCGCGGA	6168
QY	6181	GACTCAGCCCGTCAAGATGCCAGCCCCCATGAAGCGTTCATCTCCACGCTGGGCCAGCG	6240
Db	6169	GACTCAGCCCGTCAAGATGCCAGCCCCCATGAAGCGTTCATCTCCACGCTGGGCCAGCG	6228
QY	6241	GCCCCGTGGGACTCATCTTTTGCAGACCAACCCCGGACCGGCCCTAGCAGGCGTC	6300
Db	6229	GCCCCGTGGGACTCATCTTTTGCAGACCAACCCCGGACCGGCCCTAGCAGGCGTC	6288

QY	6301	GTGCGACCAACCAACCAACCGCTGCCACCGCGCAGGGAAGAGAGAGTCCCTTGA	6360
Db	6289	GTGCGACCAACCAACCAACCGCTGCCACCGCGCAGGGAAGAGAGAGTCCCTTGA	6348
QY	6361	GAAGGGGCCAGACCTGTCTGCCGATATGGATGGCGCACCAAGCAGTGTCTGTGGGCGCGG	6420
Db	6349	GAAGGGGCCAGACCTGTCTGCCGATATGGATGGCGCACCAAGCAGTGTCTGTGGGCGCGG	6408
QY	6421	GCTGCCCGCGGAGAGGGGCTTACAGGCTGCGCGGGAAGCAGAGAGCGCGGAGGAGCG	6480
Db	6409	GCTGCCCGCGGAGAGGGGCTTACAGGCTGCGCGGGAAGCAGAGAGCGCGGAGGAGCG	6468
QY	6481	GGGCGGCTTCCAGGAGCGGAGGAGCCTCATCTCTCTCTCGGAGAGCAGCGCTTCTA	6540
Db	6469	GGGCGGCTTCCAGGAGCGGAGGAGCCTCATCTCTCTCTCGGAGAGCAGCGCTTCTA	6528
QY	6541	CTCTGCGACCGCTTTTGGGGCGCTGAGCCCCCGGAAGCCCAAGCCCTCTCAGCAGCCCA	6600
Db	6529	CTCTGCGACCGCTTTTGGGGCGCTGAGCCCCCGGAAGCCCAAGCCCTCTCAGCAGCCCA	6588
QY	6601	CCCAACCTTCCGCAACAGCTGCGCAGGAGCGGAGACCCCAACCAAGGCAATGCTCCGT	6660
Db	6589	CCCAACCTTCCGCAACAGCTGCGCAGGAGCGGAGACCCCAACCAAGGCAATGCTCCGT	6648
QY	6661	GAATGGAGAGCCCTTGTCTCAACATCTGTGTGTAGCACCCCGCGCGCTGGGGGAG	6720
Db	6649	GAATGGAGAGCCCTTGTCTCAACATCTGTGTGTAGCACCCCGCGCGCTGGGGGAG	6708
QY	6721	GCAGTCCCCCAGACGCGCCCTGACTCCCGCCCGCAGATCACTACAAGAAGGCCAATC	6780
Db	6709	GCAGTCCCCCAGACGCGCCCTGACTCCCGCCCGCAGATCACTACAAGAAGGCCAATC	6768
QY	6781	CTCACCCATCACTCTGCGCGGGCTCAGACCGCTCCCTGCGCTTCTCCGAGCGGCT	6840
Db	6769	CTCACCCATCACTCTGCGCGGGCTCAGACCGCTCCCTGCGCTTCTCCGAGCGGCT	6828
QY	6841	CAGCGTGGGCTTTTCCGAAACACACGCGCTGTGTCAGAGAGACCCCTCAAGCAGCCCT	6900
Db	6829	CAGCGTGGGCTTTTCCGAAACACACGCGCTGTGTCAGAGAGACCCCTCAAGCAGCCCT	6888
QY	6901	GGCGCTGGCTCTCGAATTTGGCTCTGACCTTACCTTGGGGAGCGTCTGGAAGTGAAGC	6960
Db	6889	GGCGCTGGCTCTCGAATTTGGCTCTGACCTTACCTTGGGGAGCGTCTGGAAGTGAAGC	6948
QY	6961	CTCTGTCCAGCGCTCTGAGGACACGCTCACTTTCGAGGAGGCTGTGSCACCAACTC	7020
Db	6949	CTCTGTCCAGCGCTCTGAGGACACGCTCACTTTCGAGGAGGCTGTGSCACCAACTC	7008
QY	7021	GGCGCGCTCTCCAGGACTTCTTAAGTCTCTCTCTCTGACCTCCAGTCTCAACCTCTCG	7080
Db	7009	GGCGCGCTCTCCAGGACTTCTTAAGTCTCTCTCTCTGACCTCCAGTCTCAACCTCTCG	7068
QY	7081	CCGCGTGGCCAGGGTTACCACTGACACCTGGGACTCAGCTGGGTGGCGAGCAGGCA	7140
Db	7069	CCGCGTGGCCAGGGTTACCACTGACACCTGGGACTCAGCTGGGTGGCGAGCAGGCA	7128
QY	7141	CAGTACCAACCCCTGACCAAGACCACTGTGTGTAGCTGACCGTCAAGCAGC	7200
Db	7129	CAGTACCAACCCCTGACCAAGACCACTGTGTGTAGCTGACCGTCAAGCAGC	7188
QY	7201	CTGCATGACAGCGGCTGTGTTCCAGTGGATGAGTTTATCATCCACAGCGGCGAGTCCG	7260
Db	7189	CTGCATGACAGCGGCTGTGTTCCAGTGGATGAGTTTATCATCCACAGCGGCGAGTCCG	7248
QY	7261	CCCTGGGGGAGGCTTGGCCACCTTGGTGGGCTCTGTGGCCCTCCCTCCCTCTCT	7320
Db	7249	CCCTGGGGGAGGCTTGGCCACCTTGGTGGGCTCTGTGGCCCTCCCTCCCTCTCT	7308
QY	7321	CCCTCTTTTACTCTAGACGACGAATAAAGCCCTGTGCTGTGAGTGTAGTACCGC	7376
Db	7309	CCCTCTTTTACTCTAGACGACGAATAAAGCCCTGTGCTGTGAGTGTAGTACCGC	7364

RESULT 3

US-10-033-026-5
; Sequence 5, Application US/10033026
; Publication No. US20020147309A1
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/10/033,026
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 7364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..7162

US-10-033-026-5

Query Match 99.5%; Score 7342; DB 14; Length 7364;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 7364; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

Qy	1	CGCGCGGGGCTGGCGGCTGGGCGGGCGAGTCCGCTGCGGTCCCGGGCGTCCGCTG 60	
Db	1	CGCGCGGGGCTGGCGGCTGGGCGGGCGAGTCCGCTGCGGTCCCGGGCGTCCGCTG 60	
Qy	61	GCTGCTCGCTCTGAGCGCTGGGCGCGCCCGCGCTCCCTGCGGGCGGCTGGGCGG 120	
Db	61	GCTGCTCGCTCTGAGCGCTGGGCGCGCCCGCGCTCCCTGCGGGCGGCTGGGCGG 120	
Qy	121	GGGATGACCGGGGCGCGGAGCATGGTCCGCTTCGGGAGCAGCTGGGCGCGCTA 180	
Db	121	GGGATGACCGGGGCGCGGAGCATGGTCCGCTTCGGGAGCAGCTGGGCGCGCTA 180	
Qy	181	TGGAGGCGCGCGCGGAGCGGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGG 240	
Db	181	TGGAGGCGCGCGCGGAGCGGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGG 240	
Qy	241	GGTCCCGGGGGCTGACGCCCGCGCGAGCGGTCTCTACAAGCAATCGATCGCGAGCG 300	
Db	241	GGTCCCGGGGGCTGACGCCCGCGCGAGCGGTCTCTACAAGCAATCGATCGCGAGCG 300	
Qy	301	CGCGCGACCATGCGCTGTACACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA 360	
Db	301	CGCGCGACCATGCGCTGTACACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA 360	
Qy	361	CGGTCGCTCTTCTTACGAGGACCAAGTCCGCGTCCGCAATACGCGAAGCGCATCAC 420	
Db	361	CGGTCGCTCTTCTTACGAGGACCAAGTCCGCGTCCGCAATACGCGAAGCGCATCAC 420	
Qy	421	CGAGTGGCTCCATTCGAGTATATGATCTGGCCACCATCATGCCAACTGCATCGTCT 480	
Db	421	CGAGTGGCTCCATTCGAGTATATGATCTGGCCACCATCATGCCAACTGCATCGTCT 480	
Qy	481	GGCCCTGGAGCAGCATCTCCCTGATGGGACAAAACGCCATGTCGAGCGGCTGGACGA 540	
Db	481	GGCCCTGGAGCAGCATCTCCCTGATGGGACAAAACGCCATGTCGAGCGGCTGGACGA 540	
Qy	541	CACGAGCCCTATTTCATTCGGGATCTTTGCTTCGAGCGGGATCAAAATCATCGCTCT 600	
Db	541	CACGAGCCCTATTTCATTCGGGATCTTTGCTTCGAGCGGGATCAAAATCATCGCTCT 600	
Qy	601	GGGCTTTGCTTCCACAGGGCTTACCTCGGAAAGGCTGGAAAGCTCATGGACTTCGT 660	
Db	601	GGGCTTTGCTTCCACAGGGCTTACCTCGGAAAGGCTGGAAAGCTCATGGACTTCGT 660	

Qy	661	GGTGGTCTCTCACAGGGATCTTGGCAGGGCTGGAACTGACTTGCACCTGCGAACTGAG 720	
Db	661	GGTGGTCTCTCACAGGGATCTTGGCAGGGCTGGAACTGACTTGCACCTGCGAACTGAG 720	
Qy	721	GGCTGTGCGTGTCTGAGGCCCTGAAAGCTGCTGGGATTCGAAGTTTGGAGTTGGT 780	
Db	721	GGCTGTGCGTGTCTGAGGCCCTGAAAGCTGCTGGGATTCGAAGTTTGGAGTTGGT 780	
Qy	781	GCTCAAGTCCATCATGAAGGCCATGGTTCCACCTCTGAGATTGGGCTGCTTCTTCTT 840	
Db	781	GCTCAAGTCCATCATGAAGGCCATGGTTCCACCTCTGAGATTGGGCTGCTTCTTCTT 840	
Qy	841	TGCCATCTCATGTTTGGCCATCATTTGSCCTTGGAGTTCTAATGGGCAAGTTCCAAAGGC 900	
Db	841	TGCCATCTCATGTTTGGCCATCATTTGSCCTTGGAGTTCTAATGGGCAAGTTCCAAAGGC 900	
Qy	901	CTGTTTCCCAACAGACAGATCGGAGCCCTGGGTGACTTCCCTGTGCGAAGGAGGC 960	
Db	901	CTGTTTCCCAACAGACAGATCGGAGCCCTGGGTGACTTCCCTGTGCGAAGGAGGC 960	
Qy	961	CCGAGCCCGCTGTGGAGGCGGACACTGAGTGCCTGGGAGTCTTGAAGGTTTCAAGTGCATCAC 1020	
Db	961	CCGAGCCCGCTGTGGAGGCGGACACTGAGTGCCTGGGAGTCTTGAAGGTTTCAAGTGCATCAC 1020	
Qy	1021	TGGCATCACCACTTTGACAAATCTCTTATACAAAGATCGGCGGCGGCAACCTTGGAA 1140	
Db	1021	TGGCATCACCACTTTGACAAATCTCTTATACAAAGATCGGCGGCGGCAACCTTGGAA 1140	
Qy	1141	CTGGCTTACTTCTCATCTCATCATCGGCTCTCTTCTTCAATGCTCAACCTGGTGTCT 1200	
Db	1141	CTGGCTTACTTCTCATCTCATCATCGGCTCTCTTCTTCAATGCTCAACCTGGTGTCT 1200	
Qy	1201	GGGCGTGTCTCTGGGGAGTTTCCAAAGGAGCAGAGAGGTTGGAGAACCGCGCGCTT 1260	
Db	1201	GGGCGTGTCTCTGGGGAGTTTCCAAAGGAGCAGAGAGGTTGGAGAACCGCGCGCTT 1260	
Qy	1261	CCTGAGTCTGCGCGCGCAGCAGATCGAGCAGAGCTCAAGGGTACCTGGAGTGGAT 1320	
Db	1261	CCTGAGTCTGCGCGCGCAGCAGATCGAGCAGAGCTCAAGGGTACCTGGAGTGGAT 1320	
Qy	1321	CTTCAAGCGCGAGGAGTCAATGCTGGCGGAGGAGCAGGAAATGACAGAGAGTCCCC 1380	
Db	1321	CTTCAAGCGCGAGGAGTCAATGCTGGCGGAGGAGCAGGAAATGACAGAGAGTCCCC 1380	
Qy	1381	TTTGGAGCTGCTGAAAGAGCGGCGCACCAAGAGAGAGAGAAATGACTGATCCACGAGA 1440	
Db	1381	TTTGGAGCTGCTGAAAGAGCGGCGCACCAAGAGAGAGAGAAATGACTGATCCACGAGA 1440	
Qy	1441	GGAGGAGAGGACCGGTTTGCAGATCTCTGCTGTGGATCCCTTCCCGCGCGCAG 1500	
Db	1441	GGAGGAGAGGACCGGTTTGCAGATCTCTGCTGTGGATCCCTTCCCGCGCGCAG 1500	
Qy	1501	CCTCAAGAGCGGAGAGCAGAGAGCTCGTATATCTTCCGAGGAGAGAGAGATGTTCCG 1560	
Db	1501	CCTCAAGAGCGGAGAGCAGAGAGCTCGTATATCTTCCGAGGAGAGAGAGATGTTCCG 1560	
Qy	1561	GTGTTTATCTCGGCGCATGGTGAAGGCTCAGAGCTTCTACTGGGTGGTGTGCTGGTGGT 1620	
Db	1561	GTGTTTATCTCGGCGCATGGTGAAGGCTCAGAGCTTCTACTGGGTGGTGTGCTGGTGGT 1620	
Qy	1621	GGCCCTGAAACACTGTGTGGCCATGTGCTATTAACACAGCCGCGCGGCTTACCAC 1680	
Db	1621	GGCCCTGAAACACTGTGTGGCCATGTGCTATTAACACAGCCGCGCGGCTTACCAC 1680	
Qy	1681	GACCTGTATTTTGGCAGAGTTTCTTTTCTTGGGTCTCTTCTCACAGAGATGCTCCCTGAA 1740	
Db	1681	GACCTGTATTTTGGCAGAGTTTCTTTTCTTGGGTCTCTTCTCACAGAGATGCTCCCTGAA 1740	

QY 1741 GATGTATGGCTTGGGCGCCAGAAAGTACTTTCCGGTCTCTTCAACTGCTTCGACTTTGG 1800
Db 1741 GATGTATGGCTTGGGCGCCAGAAAGTACTTTCCGGTCTCTTCAACTGCTTCGACTTTGG 1800
QY 1801 GGTCACTGTGGGAGAGCTCTTTGAAGTGTCTGGGGCGGCATCAAGCCGGGAAGCTCTTT 1860
Db 1801 GGTCACTGTGGGAGAGCTCTTTGAAGTGTCTGGGGCGGCATCAAGCCGGGAAGCTCTTT 1860
QY 1861 TGGGATCAGTGTCTTGGGCGCCCTCCGGCTCTGTGAGGATCTTTCAAAGTCACGAAGTACTG 1920
Db 1861 TGGGATCAGTGTCTTGGGCGCCCTCCGGCTCTGTGAGGATCTTTCAAAGTCACGAAGTACTG 1920
QY 1921 GAGCTCCCTCGGAACTCTGGTGTCTCTGTGTAATCTCATGAAGTCAATCAGGCT 1980
Db 1921 GAGCTCCCTCGGAACTCTGGTGTCTCTGTGTAATCTCATGAAGTCAATCAGGCT 1980
QY 1981 GCTCTTTCTTGTCTTCTCTGTTCAATTTGTGTCTTCCGCTGTCTGGGATGCAGCTTTTGG 2040
Db 1981 GCTCTTTCTTGTCTTCTCTGTTCAATTTGTGTCTTCCGCTGTCTGGGATGCAGCTTTTGG 2040
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Db 2041 GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCAACTTCGACACCTTCCCTGCCGC 2100
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Db 2101 CATCTCACTGTCTTCAGATCCTGACGGGAGAGACTGGAATGCAGTGTATCA CGG 2160
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Db 2401 CTTCATTCGCGCGCAAGAGAGAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGC 2460
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Db 3061 GGAGGAGCGCGCGCGGCGGACCGGGCCCGGCAACGCGCGAGCTCTC ACAGAGCTGT 3120
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Db 3121 GGAGAGGAGAGACCAACCGAGAGAGGAGGCGGAGAGAGGCTGAGATAGTGGAAAGCCGA 3180
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RESULT 4
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; TITLE OF INVENTION: METHODS
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; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 7362
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144)...(7163)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(143)
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7161)...(7362)
US-10-375-253-11

Query Match 99.2%; Score 7316.4; DB 16; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

QY 1 GCGGCGCGGCTGCGGCGGTGGGCGCGGAGGTCCGCTCGGCTCCCGGCGGCTCCG 60
Db 1 GCGGCGCGGCTGCGGCGGTGGGCGCGGAGGTCCG-TGCGGTCCCGGCGGCTCCG 59
QY 61 GCTGCTCCGCTCTGAGCGGCTGGCGGCGCGGCGGCTCCCTGCGGGGCGGCTGG 120
Db 60 GCTGCTCCGCTCTGAGCGGCT-GCGGCGCGGCGGCTCCCTGCGGGGCGGCTGG 118

Qy	121	GGGATGACGCGGGGCGGGAGGCCATTGGTTCGGCTTCGGGGACGAGCTGGGCGGCGCGCTA	180
Db	119	GGGATGACGCGGGGCGGGAGGCATGGTTCGGCTTCGGGGACGAGCTGGGCGGCGCGCTA	178
Qy	181	TGAGAGGCCCGGGCGGGAGAGCGGGCGCGGGGCGGGCGGGGCGGGGCGGGGCGCC	240
Db	179	TGAGAGGCCCGGGCGGGAGAGCGGGCGCGGGGCGGGGCGGGGCGGGGCGGGGCGCC	238
Qy	241	GGGTCCCGGGGGGTGACGCCCGGCAGCGGGTCCCTCTACAAGCAATCGATCGCGACGC	300
Db	239	GGGTCCCGGGGGGTGACGCCCGGCAGCGGGTCCCTCTACAAGCAATCGATCGCGACGC	298
Qy	301	CGCGCGAACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA	360
Db	299	CGCGCGAACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTCAACGTCAA	358
Qy	361	CCGCTCGCTCTTCGCTTCACGAGGAGCAACGTCGTCGCAATAACGCGAAGGCGCATCAC	420
Db	359	CCGCTCGCTCTTCGCTTCACGAGGAGCAACGTCGTCGCAATAACGCGAAGGCGCATCAC	418
Qy	421	CGAGTGGCCTCCATTTCGAGTATATGATCTTGGCCACCACCATCATCGCCAACTGCATCGTGC	480
Db	419	CGAGTGGCCTCCATTTCGAGTATATGATCTTGGCCACCACCATCATCGCCAACTGCATCGTGC	478
Qy	481	GGCCCTGGAGAGCAGCACTCCCTCGATGGGGACAAAGCGCCCATGTCGAGCGGCTGGACGA	540
Db	479	GGCCCTGGAGAGCAGCACTCCCTCGATGGGGACAAAGCGCCCATGTCGAGCGGCTGGACGA	538
Qy	541	CACGGAGCCCTATTTCATCGGGATCTTTGCTTCGAGCGAGGATCAAAATCATCGCTCT	600
Db	539	CACGGAGCCCTATTTCATCGGGATCTTTGCTTCGAGCGAGGATCAAAATCATCGCTCT	598
Qy	601	GGGCTTTGCTTCCACAAGGCTCTTACCTGCGGAACGGCTGGAACTCATGGAATTCGT	660
Db	599	GGGCTTTGCTTCCACAAGGCTCTTACCTGCGGAACGGCTGGAACTCATGGAATTCGT	658
Qy	661	GGTGGCTCTCACAGGGATCTTGGCAGCGCTGGAACTGACTTCGACCTGGCAACACTGAG	720
Db	659	GGTGGCTCTCACAGGGATCTTGGCAGCGCTGGAACTGACTTCGACCTGGCAACACTGAG	718
Qy	721	GGCTGGGTGCTGTAGGCCCCCTGAGCTGGTCTGCGGATTCGAAGTTTGCAAGTGGT	780
Db	719	GGCTGGGTGCTGTAGGCCCCCTGAGCTGGTCTGCGGATTCGAAGTTTGCAAGTGGT	778
Qy	781	GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCCTGCAGATTTGGGCTGCTTCTTCTT	840
Db	779	GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCCTGCAGATTTGGGCTGCTTCTTCTT	838
Qy	841	TGCCATCCTCATGTTTGCCATCATATGCTGGAGTTCTACATGGGCAAGTTTCCAAAGGC	900
Db	839	TGCCATCCTCATGTTTGCCATCATATGCTGGAGTTCTACATGGGCAAGTTTCCAAAGGC	898
Qy	901	CTGTTTTCCCAACAGCAGATGCGGAGCCCCGTGGTGACTTCCCCTGTGGCAAGGAGGC	960
Db	899	CTGTTTTCCCAACAGCAGATGCGGAGCCCCGTGGTGACTTCCCCTGTGGCAAGGAGGC	958
Qy	961	CCAGCGCGGTGTGCGAGGCGCACACTGAGTGGCGGAGTACTGGCGCAGGACCCAACTT	1020
Db	959	CCAGCGCGGTGTGCGAGGCGCACACTGAGTGGCGGAGTACTGGCGCAGGACCCAACTT	1018
Qy	1021	TGGCATCACCAACTTTGACAATATCTGTTTGGCATCTTGAACGTTTCCAGTGGCATCAC	1080
Db	1019	TGGCATCACCAACTTTGACAATATCTGTTTGGCATCTTGAACGTTTCCAGTGGCATCAC	1078
Qy	1081	CATGGAGGCTGGACTGACATCTCTATATACAAACGATGCGGCGCGGCAACACTTGGAA	1140
Db	1079	CATGGAGGCTGGACTGACATCTCTATATACAAACGATGCGGCGCGGCAACACTTGGAA	1138
Qy	1141	CTGGCTCTACTTTCATCCCTCTCATCATCATCGGCTCTTCTTTCATGCTCAACCTGGTCT	1200
Db	1139	CTGGCTCTACTTTCATCCCTCTCATCATCATCGGCTCTTCTTTCATGCTCAACCTGGTCT	1198
Qy	1201	GGGCGTGTCTTCGGGGGAGTTTGGCAAGGAGCGAGAGGGGTGGAGAACCGCGCGGCTT	1260

Db	1199	GGCGTGTCTCTCGGGGAGTTTCCCAAGGAGCCAGAGAGGGTGGAGAACCGCCGCGCCTT	1358
Qy	1261	CCTGAAGCTCGCGCGGCAGCAGCAGATCGAGCGAGAGCTCAACGGGTACTCTGGAGTGGAT	1320
Db	1259	CCTGAAGCTCGCGCGGCAGCAGCAGATCGAGCGAGAGCTCAACGGGTACTCTGGAGTGGAT	1318
Qy	1321	CTTCAAGCGCGGAGGAATCATATGCTGCGCGAGAGAGACAGGAATCGAGAGAGAAATCCCC	1380
Db	1319	CTTCAAGCGCGGAGGAATCATATGCTGCGCGAGAGAGACAGGAATCGAGAGAGAAATCCCC	1378
Qy	1381	TTTGGAGCTCTCAAGAGAGCGGCCCAAGAGAGACAGAAATACCTGATCCACGCAGA	1440
Db	1379	TTTGGAGCTCTCAAGAGAGCGGCCCAAGAGAGACAGAAATACCTGATCCACGCAGA	1438
Qy	1441	GGAGGAGAGGACCGGTTTCAGATCTCTGTGCTGTTGGATCCCCCTTCGCCCGCGCCAG	1500
Db	1439	GGAGGAGAGGACCGGTTTCAGATCTCTGTGCTGTTGGATCCCCCTTCGCCCGCGCCAG	1498
Qy	1501	CCTCAAGAGCGGGAAGACAGAGAGCTGTCATATCTCCCGGAGGAAGAGATGTTCCG	1560
Db	1499	CCTCAAGAGCGGGAAGACAGAGAGCTGTCATATCTCCCGGAGGAAGAGATGTTCCG	1558
Qy	1561	GTTTTTTATCCGGGCAATGCTGAAGCTCAGAGCTTCTACTGCGTGGTGTCTGTGCGTGT	1620
Db	1559	GTTTTTTATCCGGGCAATGCTGAAGCTCAGAGCTTCTACTGCGTGGTGTCTGTGCGTGT	1618
Qy	1621	GGCCCTGAAACACTGTGTGGCCATGGTGCATTACAACAGCGCGCGGGCTTACCAC	1680
Db	1619	GGCCCTGAAACACTGTGTGGCCATGGTGCATTACAACAGCGCGCGGGCTTACCAC	1678
Qy	1681	GACCCGTATTTTGCAGAGTTTGTGTTTCTCGGTCTCTCCTCACAGAGATGCTCCGTAA	1740
Db	1679	GACCCGTATTTTGCAGAGTTTGTGTTTCTCGGTCTCTCCTCACAGAGATGCTCCGTAA	1738
Qy	1741	GATGATAGCCCTGGGCCCAAGACTATCTCCGTCTCTCCTTCAACTGCTTCGACTTTGG	1800
Db	1739	GATGATAGCCCTGGGCCCAAGACTATCTCCGTCTCTCCTTCAACTGCTTCGACTTTGG	1798
Qy	1801	GGTCATCGTGGGAGCGTCTTTCAAGTGGTCTGGCGCGCCATCAAGCGCGGAAGCTCCTT	1860
Db	1799	GGTCATCGTGGGAGCGTCTTTCAAGTGGTCTGGCGCGCCATCAAGCGCGGAAGCTCCTT	1858
Qy	1861	TGGGATCAGTGTCTCGGGCCCTCCGCTGCTGAGGATCTTCAAAGTCAAGAGTACTG	1920
Db	1859	TGGGATCAGTGTCTCGGGCCCTCCGCTGCTGAGGATCTTCAAAGTCAAGAGTACTG	1918
Qy	1921	GAGCTCCCTCGGAAACCTGCTGCTGCTGCTGAACTCATGAATGTCATCATCAGCCT	1980
Db	1919	GAGCTCCCTCGGAAACCTGCTGCTGCTGCTGAACTCATGAATGTCATCATCAGCCT	1978
Qy	1981	GCCTCTTCTGCTCTTCTGTTTCAATGTGTGCTTTCGCCCTGCTGGGATGAGCTGTTTG	2040
Db	1979	GCCTCTTCTGCTCTTCTGTTTCAATGTGTGCTTTCGCCCTGCTGGGATGAGCTGTTTG	2038
Qy	2041	GGGACAGTTCAAATTCAGGATGAGATCCCAACAACTTCGACACCTTCCTGCGCGC	2100
Db	2039	GGGACAGTTCAAATTCAGGATGAGATCCCAACAACTTCGACACCTTCCTGCGCGC	2098
Qy	2101	CATCTCTCATGCTTTCAGATCTCGAGGAGGACTGGAATGCGAGTGAATGATCAGG	2160
Db	2099	CATCTCTCATGCTTTCAGATCTCGAGGAGGACTGGAATGCGAGTGAATGATCAGG	2158
Qy	2161	GATCGAATCGCAAGCGGCGTCAGCAAGGATGTTCTCGTCTCTTTTACTTCAATGTCCCT	2220
Db	2159	GATCGAATCGCAAGCGGCGTCAGCAAGGATGTTCTCGTCTCTTTTACTTCAATGTCCCT	2218
Qy	2221	GACACTGTTCCGAAAATTACACTCTGCTGAATGCTTTTCTGSCCATCGCTGTGACAACT	2280
Db	2219	GACACTGTTCCGAAAATTACACTCTGCTGAATGCTTTTCTGSCCATCGCTGTGACAACT	2278
Qy	2281	GGCCAAAGCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAAGACGCCAATCAGAA	2340

Db 2279 GGCCTAACGCCAAGAGCTGACCAAGATGAAGAGGAGATGGAAGAACAGCCAAATCAGAA 2338
QY 2341 GCTTGCTCTGCAAAAGGCGCAAGAGTGGCTGAGCTCAGCCCATGCTGCGCGCAACAT 2400
Db 2339 GCTTGCTCTGCAAAAGGCGCAAGAGTGGCTGAGCTCAGCCCATGCTGCGCGCAACAT 2398
QY 2401 CTCATCGCGCGCAGCAGCAGAACTCGGCCAAGGCGCGCTCGGTGTGGAGCAGCGGGC 2460
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QY 2581 CTTGACCGCGCGCTGCTGGTGTGAGCTGGGCGCGCAGCGCGCGCGGGCGCCCGTGGGAGG 2640
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QY 2641 CAAAGCCGACCTGAGGCTGCGGAGGCGCCCGAGGCGCTGACCCCTGCGCGAGGACCA 2700
Db 2639 CAAAGCCGACCTGAGGCTGCGGAGGCGCCCGAGGCGCTGACCCCTGCGCGAGGACCA 2698
QY 2701 CCGGCACCGCAGCAAGGACAAAGACCCCGCGCGCGGGACACAGACCGAGCAGAGGCGCC 2760
Db 2699 CCGGCACCGCAGCAAGGACAAAGACCCCGCGCGCGGGACACAGACCGAGCAGAGGCGCC 2758
QY 2761 GAAGCGGAGAGCGGGGAGCCCGGTGCCGGGAGAGCGCGCGCGCGCCACCGCAGCCA 2820
Db 2759 GAAGCGGAGAGCGGGGAGCCCGGTGCCGGGAGAGCGCGCGCGCGCCACCGCAGCCA 2818
QY 2821 CAGCAAGGAGCGCGGGCGCCCGGAGCGCGGAGCGCGCGCGCGCCAGGCGCCAGGCGCC 2880
Db 2819 CAGCAAGGAGCGCGGGGAGCCCGGAGCGCGGAGCGCGCGCGCGCCAGGCGCCAGGCGCC 2878
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QY 3061 GGAGAGCGCGCGCGCGCACCGGGCGCGCACAAAGCGCGAGCTTGCTACGAGGCTGT 3120
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QY 3121 GGAGAGGAGACCGGAGAGGAGGCGCACCGGAGGAGGCTGAGATGTGGAAGCGGA 3180
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QY 3181 CAAGGAAAAGAGCTCCGGAAACCAAGCCCGCGGAGCCACACTGTGACCTGGAGACCG 3240
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QY 3661 AGTCGCACAGACTCGGCCAGGAAACACGCTCTGAAATACCTGGATTACATTTTCACTGG 3720
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DB 5867 CCGGGTTTTCTTCGACAGAAAGTTTCCACTCTCTCAGCAATGGCGGGGCCATACAAAA 5926
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RESULT 5
US-10-033-026-7
; Sequence 7, Application US/10033026
; Publication No. US20020147309A1
; GENERAL INFORMATION:
; APPLICANT: Liposome, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/10/033,026
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 7177
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146...6856
US-10-033-026-7

Query Match 94.3%; Score 6958; DB 14; Length 7177;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 7177; Conservative 0; Mismatches 0; Indels 199; Gaps 2;
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Db 6229 GCCCCGTGGGACTCATCTTTGACAGCACACCCCGGACCGGCCCTTACCCAGGCGTC 6288
Qy 6301 GTGCAACCAACCAACCACTGCGCACCGCCGCGGAGGAGCAGAGGTCCTTGA 6360
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Qy 6361 GAAGGGCCAGCTGTCTGCGGATATGAGTGGCGCACCAAGCAGTGTCTGTGGGGCCGG 6420
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; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10/375,253
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354


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/ PRIOR FILING DATE: 1992-07-13
/ PRIOR APPLICATION NUMBER: 08/314,083
/ PRIOR FILING DATE: 1994-09-28
/ PRIOR APPLICATION NUMBER: 07/914,231
/ PRIOR FILING DATE: 1992-07-13
/ PRIOR APPLICATION NUMBER: 07/603,751
/ PRIOR FILING DATE: 1990-11-09
/ PRIOR APPLICATION NUMBER: 08/290,012
/ PRIOR FILING DATE: 1994-08-11
/ PRIOR APPLICATION NUMBER: 08/149,097
/ PRIOR FILING DATE: 1993-11-05
/ PRIOR APPLICATION NUMBER: 08/105,536
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/ FEATURE:
/ NAME/KEY: 3'UTR
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QY 121 GGGATGCA CGCGGGGCGCGGAGCCATGCTCGCTTCGCGGAGCGAGCTGGGCGCGCTA 180
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QY 181 TGGAGGCGCGCGCGGAGAGCGGCGCGCGGCGCGGCGCGCGGCGCGGCGCGCGCG 240
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DB 1319 CTTTCAAGCGGAGGAAGTATGCTGCTGCGGAGGAGCAGGAATTCAGAGGAGAGTCCCC 1378

QY 1381 TTTTGAAGCTGCTGAAGAGAGCGGCCCAAGAGAGCAGAAATGACCTGATCCACGACGA 1440
DB 1379 TTTTGAAGCTGCTGAAGAGAGCGGCCCAAGAGAGCAGAAATGACCTGATCCACGACGA 1438

QY 1441 GGAAGGAGAGGAGCGGTTTTCAGATCTCTGTGCTGTGGATCCCCCTTCCGCGCGCCAG 1500
DB 1439 GGAAGGAGAGGAGCGGTTTTCAGATCTCTGTGCTGTGGATCCCCCTTCCGCGCGCCAG 1498

QY 1501 CTTCAAGAGCGGAGAGCAGAGAGCTGCTCATCTTCCGAGGAAGAGAGATGTTCCG 1560
DB 1499 CTTCAAGAGCGGAGAGCAGAGAGCTGCTCATCTTCCGAGGAAGAGAGATGTTCCG 1558

QY 1561 GTTTTTTATCCGCGCATGCTGAAGGCTCAGAGCTTCTACTGGTGGTCTGCTGGTGGT 1620
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Qy	1621	GGCCCTGAAACACA	CTGTGTGTGGCCATGTGTGCATTACAAACAGCGCGGGGGCTTACAC	1680
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Qy	1681	GACCCCTGATTTTGCAGAGTTTGTTCCTGGGTCCTCTCTCACAGAGTGTCCCTGAA	1740	
Db	1679	GACCCCTGATTTTGCAGAGTTTGTTCCTGGGTCCTCTCTCACAGAGTGTCCCTGAA	1738	
Qy	1741	GATGTATGGCTGGGGCCCAAGAGCTACTTCCTGGTCTCTCTTCAACTGCTTTCGACTTTGG	1800	
Db	1739	GATGTATGGCTGGGGCCCAAGAGCTACTTCCTGGTCTCTCTTCAACTGCTTTCGACTTTGG	1798	
Qy	1801	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCCATCAAGCCGGGAAGCTCCTT	1860	
Db	1799	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCCATCAAGCCGGGAAGCTCCTT	1858	
Qy	1861	TGGGATCAGTGTGTGGGGCCCTCCGCTGCTGAGGATCTTCAAGTCAAGTACTG	1920	
Db	1859	TGGGATCAGTGTGTGGGGCCCTCCGCTGCTGAGGATCTTCAAGTCAAGTACTG	1918	
Qy	1921	GAGCTCCTCGGAACTGTGTGTCTCCCTGCTGAACTCCATGAAGTCCATCATCAGCCT	1980	
Db	1919	GAGCTCCTCGGAACTGTGTGTCTCCCTGCTGAACTCCATGAAGTCCATCATCAGCCT	1978	
Qy	1981	GCTCTTCTGCTCTTCTGTTTCATTGTGTCTTCCGCTGCTGGGATGCAGCTGTTGG	2040	
Db	1979	GCTCTTCTGCTCTTCTGTTTCATTGTGTCTTCCGCTGCTGGGATGCAGCTGTTGG	2038	
Qy	2041	GGGACAGTTCAACTTCCAGGATGAGACTCCCAACAACTTCGACACCTTCCCTGCGC	2100	
Db	2039	GGGACAGTTCAACTTCCAGGATGAGACTCCCAACAACTTCGACACCTTCCCTGCGC	2098	
Qy	2101	CATCCTCACTGTCTTCCAGATCTCTGAGGGAGAGACTGGAATGCACTGATATCAGG	2160	
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Qy	2161	GATCGAATCGCAAGCGCGTACGAAAGGCATGTTCTCGTCTCTTTTACTTTCATTGTCCT	2220	
Db	2159	GATCGAATCGCAAGCGCGTACGAAAGGCATGTTCTCGTCTCTTTTACTTTCATTGTCCT	2218	
Qy	2221	GACACTGTTGGAACTACACTCTGCTGATGTCTTTCTGGCCATCGCTGTGGACACCT	2280	
Db	2219	GACACTGTTGGAACTACACTCTGCTGATGTCTTTCTGGCCATCGCTGTGGACACCT	2278	
Qy	2281	GGCCAAAGCCCAAGAGCTGACCAAGGATGAAGAGAGATGAAGAGAGATGGAAGAGATGGA	2340	
Db	2279	GGCCAAAGCCCAAGAGCTGACCAAGGATGAAGAGAGATGGAAGAGATGGAAGAGATGGA	2338	
Qy	2341	GCTTGTCTCTGAAAGGCCAAGAGTGGCTGAAAGTCAGCCCACTGTCTGCGCGAATCAT	2400	
Db	2339	GCTTGTCTCTGAAAGGCCAAGAGTGGCTGAAAGTCAGCCCACTGTCTGCGCGAATCAT	2398	
Qy	2401	CTCCATCGCCCGCAGGAGAGAACTCTGGCCCAAGCGCGCTCGTGTGGAGCAGCGGC	2460	
Db	2399	CTCCATCGCCCGCAGGAGAGAACTCTGGCCCAAGCGCGCTCGTGTGGAGCAGCGGC	2458	
Qy	2461	CAGCCAGCTACGGCTGCAGAACCTCGCGCCAGCTGCGAGCGCTGTACAGCGAGATGGA	2520	
Db	2459	CAGCCAGCTACGGCTGCAGAACCTCGCGCCAGCTGCGAGCGCTGTACAGCGAGATGGA	2518	
Qy	2521	CCCCGAGGAGCGGTGGGCTTCGCCACTACGCGCACCTGCGGCCCGACATGAGAGCGCA	2580	
Db	2519	CCCCGAGGAGCGGTGGGCTTCGCCACTACGCGCACCTGCGGCCCGACATGAGAGCGCA	2578	
Qy	2581	CTTGACCGGCGCTGTGTGTGGAGTGTGGGCGCGAGCGCGCGGGGGCGCTGGGAGG	2640	
Db	2579	CTTGACCGGCGCTGTGTGTGGAGTGTGGGCGCGAGCGCGCGGGGGCGCTGGGAGG	2638	
Qy	2641	CAAAAGCCGACCTCAGGCTGGAGGGCCCGCGAGGGCGTGACCCCTCCGCGCAGGACCA	2700	
Db	2639	CAAAAGCCGACCTCAGGCTGGAGGGCCCGCGAGGGCGTGACCCCTCCGCGCAGGACCA	2698	

Qy	2701	CCGGCACCGCGACAAGGACAGACCCCGCGCGCGGGGACCAAGACCGAGCAGAGGCCCC	2760
Db	2699	CCGGCACCGCGACAAGGACAGACCCCGCGCGCGGGGACCAAGACCGAGCAGAGGCCCC	2758
Qy	2761	GAAGGCGGAGAGCGGAGCGCCCGTGTCCCGGAGGAGCGCGCCGCGCCGACACGACGCCA	2820
Db	2759	GAAGGCGGAGAGCGGAGCGCCCGTGTCCCGGAGGAGCGCGCCGCGCCGACACGACGCCA	2818
Qy	2821	CAGCAAGGAGCGCGCGGGCCCGGAGGCGCGAGCGCGCGCGCGGACCGCCAGGCC	2880
Db	2819	CAGCAAGGAGCGCGCGGGCCCGGAGGCGCGAGCGAGCGCGCGCGGACCGCCAGGCC	2878
Qy	2881	CGAGGCGCGCGCGCGGACCAACCGCGCGCGCTCCCGGAGGAGCGCGCGCGAGGCC	2940
Db	2879	CGAGGCGCGCGCGCGGACCAACCGCGCGCGCTCCCGGAGGAGCGCGCGCGAGGCC	2938
Qy	2941	CCGACGCCACCGCGCGCACCGCGCACAGGATCCGAGCAAGAGTGTGCGCGCGCCCAAGGG	3000
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Qy	3001	CGAGCGCGCGCGCGGACCAACCGCGCGCGCCCGGAGGCGCGCCCGGAGCGCGAGCGG	3060
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Qy	3061	GGAGGAGCGCGCGCGGCGCACCGCGCGCGCCCGGAGGCGCGCCCGGAGCGCGAGCGG	3120
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Qy	3121	GGAGAGGAGACCAACCGAGAGGAGGAGCGCGAGAGGAGGCTGAGATGTGGAAGCCGA	3180
Db	3119	GGAGAGGAGACCAACCGAGAGGAGGAGCGCGAGAGGAGGCTGAGATGTGGAAGCCGA	3178
Qy	3181	CAAGGAAAAGAGAGCTCCGGAAACCAACAGCCCGCGGAGCCACACTGTGACCTTGAGAGCCAG	3240
Db	3179	CAAGGAAAAGAGAGCTCCGGAAACCAACAGCCCGCGGAGCCACACTGTGACCTTGAGAGCCAG	3238
Qy	3241	TGGGACTGTGTGTGGTCCATGACACACTGCGCCAGCACCTGTCTCCAGAGAGTGGA	3300
Db	3239	TGGGACTGTGTGTGGTCCATGACACACTGCGCCAGCACCTGTCTCCAGAGAGTGGA	3298
Qy	3301	GGAGCAGCAGAGGATGACAGCAATCAGCGGAACGTCACCTCGCATGCGGAGTCAGGCCCC	3360
Db	3299	GGAGCAGCAGAGGATGACAGCAATCAGCGGAACGTCACCTCGCATGCGGAGTCAGGCCCC	3358
Qy	3361	AGACCCGGAACACTATTTGTATCATATCCAGTGCTGACGGGCCCTCTTGGGGAAGCCAC	3420
Db	3359	AGACCCGGAACACTATTTGTATCATATCCAGTGCTGACGGGCCCTCTTGGGGAAGCCAC	3418
Qy	3421	GGTCTGTCAGTGTGTAAACGTGGAACCTGGAAAGCCAGAGAGGGAAGAGAGTGGA	3480
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Qy	3541	TTTAAAGCCCAACCAACCTGCTCCGCGCTTCTGCCACTACATCGTGAACCATGAGTACTT	3600
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Qy	3661	AGTGCCGACAGACTCGCCGAGGAACCGCTCTGAAATACCTGGAATACATTTTCACTGG	3720
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Qy	3721	TGTCTTTTACCTTTGAGATGGTGATAAGATGATCGACTTGGGACTGCTGCTTCCACCTGG	3780
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Qy	6121	GCCCCAGCCTGGGCTGAGAGCCAGGGCTCGAGCGGCCCTCCATGCCCGCCCTTGGCGCCGA	6180
Db	6107	GCCCCAGCCTGGGCTGAGAGCCAGGGCTCGAGCGGCCCTCCATGCCCGCCCTTGGCGCCGA	6166
Qy	6181	GACTCAGCCCGTCAAGATGCAAGCCCATGAAGCGTTCATATCCACGTGTGGCCACGCG	6240
Db	6167	GACTCAGCCCGTCAAGATGCAAGCCCATGAAGCGTTCATATCCACGTGTGGCCACGCG	6226
Qy	6241	GCCCGTGGGACATCTTTTGCAGCACACCCCGGACGGCCCAACCCCTAGCCAGCGGTC	6300
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Qy	6301	GTCCACACACCAACCAACACCGCTGCCACCGCCGAGGACAGGAGTCCCTTGA	6360
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Qy	6361	GAAGGGCCCAAGCTGTCTGCCGATATGGATGGCGCACCAAGCAGTCTGTGGGGCCGGG	6420
Db	6347	GAAGGGCCCAAGCTGTCTGCCGATATGGATGGCGCACCAAGCAGTCTGTGGGGCCGGG	6406
Qy	6421	GCTGCCCGCGGAGAGGGGCTACAGGCTGCCGCGGGAGAGAGCGCGGACAGAGCG	6480
Db	6407	GCTGCCCGCGGAGAGGGGCTACAGGCTGCCGCGGGAGAGAGCGCGGACAGAGCG	6466
Qy	6481	GGGCGGCTCCAGAGCGGAGGAGCGCTCATCTCTCTCTCGAGAGAGCAGCGCTTCTA	6540
Db	6467	GGGCGGCTCCAGAGCGGAGGAGCGCTCATCTCTCTCTCGAGAGAGCAGCGCTTCTA	6526
Qy	6541	CTCTCGAGCGCTTTGGGGCCGTGAGCCCCCGAAGCCCAAGCCCTCTCTCAGCAGCCA	6600
Db	6527	CTCTCGAGCGCTTTGGGGCCGTGAGCCCCCGAAGCCCAAGCCCTCTCTCAGCAGCCA	6586
Qy	6601	CCCAAGCTGCCACACGTGGCAGGAGCGGGACCCCAACCCACAGGGCAGTGTTCGT	6660
Db	6587	CCCAAGCTGCCACACGTGGCAGGAGCGGGACCCCAACCCCAAGCCCTCTCTCAGCAGCCA	6629
Qy	6661	GAATGGAGGCCCTTGTGTCAACATCTGTGTCTAGCACCCCCCGCGCGTGGGCGGAG	6720
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Qy	6721	GCAGCTCCCCAGAGCGCCCTGACTCCCCCGCCAGCATCACCTACAAGACGGCCAACTC	6780
Db	6630	-----	6629
Qy	6781	CTACCCATCCACTTCGCGGGGCTCAGACGAGCCTCCCTGCTTCTCCCCAGGCGGGCT	6840
Db	6630	-----	6639
Qy	6841	CAGCGTGGGCTTTCCGAACACAAACGCTGCTCAGAGAGACCCCTCAGCAGCGCCCT	6900
Db	6840	CAGCGTGGGCTTTCCGAACACAAACGCTGCTCAGAGAGACCCCTCAGCAGCGCCCT	6899
Qy	6901	GGCCCTGGCTCTCGAATTTGGCTCTGACCCCTTACCTGGGGCAGCGTCTGGACAGTGAAGC	6960
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Qy	6961	CTCTGTCAAGCCCTGCTGAGGACAGCTCACTTTTCAGAGAGGCTGTGGCCACCAATC	7020
Db	6760	CTCTGTCAAGCCCTGCTGAGGACAGCTCACTTTTCAGAGAGGCTGTGGCCACCAATC	6819
Qy	7021	GGGCGGCTCTCCAGGACTTCTTACGCTGCTCCCTGACCTCCAGCTCACCCTCTCCG	7080
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Qy	7081	CCGCGTCCCAACGGTTTACCACTGCAACCTTGGGACTCAGCTCGGTGGCGGACGAGCA	7140
Db	6880	CCGCGTCCCAACGGTTTACCACTGCAACCTTGGGACTCAGCTCGGTGGCGGACGAGCA	6939
Qy	7141	CAGCTACCAACCCCTGACCAAGACCACTGGTCTAGCTGACCGTACCGCTCAGACGC	7200
Db	6940	CAGCTACCAACCCCTGACCAAGACCACTGGTCTAGCTGACCGTACCGCTCAGACGC	6999
Qy	7201	CTGCATGCAAGCAGCGTGTTCACAGTGGATGATTTTATCATCCACACGGGCGAGTCGG	7260
Db	7000	CTGCATGCAAGCAGCGTGTTCACAGTGGATGATTTTATCATCCACACGGGCGAGTCGG	7059
Qy	7261	CCCTCGGGGAGGCTTGGCCACCTTGGTGGAGGCTCTGTGGCCCTCTCCCTCCCTCTCT	7320
Db	7060	CCCTCGGGGAGGCTTGGCCACCTTGGTGGAGGCTCTGTGGCCCTCTCCCTCCCTCTCT	7119
Qy	7321	CCCTCTCTTTACTCTAGACGACGAATAAAGCCCTGTGTTGAGTGTAGTACACGC	7376
Db	7120	CCCTCTCTTTACTCTAGACGACGAATAAAGCCCTGTGTTGAGTGTAGTACACGC	7175
RESULT 7			
US-10-627-370-1			
; Sequence 1, Application US/10627370			
; Publication No. US20040081988A1			
; GENERAL INFORMATION:			
; APPLICANT: Johnson, Jason M.			
; APPLICANT: Castile, John C.			
; APPLICANT: Armour, Christopher D.			
; TITLE OF INVENTION: SPLICE VARIANT ISOFORMS OF HUMAN CALCIUM CHANNEL CACNA1B			
; FILE REFERENCE: RS0202Y			
; CURRENT APPLICATION NUMBER: US/10/627,370			
; CURRENT FILING DATE: 2003-07-25			
; NUMBER OF SEQ ID NOS: 13			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 1			
; LENGTH: 6792			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-627-370-1			
Query Match 88.6%; Score 6535; DB 17; Length 6792;			
Best Local Similarity 96.8%; Pred. No. 0;			
Matches 6792; Conservative 0; Mismatches 0; Indels 237; Gaps 2;			
Qy	146	ATGCTCCGCTTCGGGACGAGCTGGCGCGCGCTATGAGGCGCCCGGCGCGGAGAGCGG	205
Db	1	ATGCTCCGCTTCGGGACGAGCTGGCGCGCGCTATGAGGCGCCCGGCGCGGAGAGCGG	60
Qy	206	GCCCAGGCG	265
Db	61	GCCCAGGCG	120
Qy	266	CAGCGGCTCTTACAGCAATCGATCGCGACGCGCGCGCGCGCGCGCGCGCGCGCG	325
Db	121	CAGCGGCTCTTACAGCAATCGATCGCGACGCGCGCGCGCGCGCGCGCGCGCGCG	180
Qy	326	CCCATCCCGTCAAGCAGAACTGCTTCAACCGTCAACCGCTCGCTCTTCGCTTCAGCGAG	385
Db	181	CCCATCCCGTCAAGCAGAACTGCTTCAACCGTCAACCGCTCGCTCTTCGCTTCAGCGAG	240
Qy	386	GACAAGCTGCTCCGAAATAACGCAAGCGCATCACCGAGTGGCTCCATTCGAGTATATG	445
Db	241	GACAAGCTGCTCCGAAATAACGCAAGCGCATCACCGAGTGGCTCCATTCGAGTATATG	300
Qy	446	ATCTGCGCAACCATCATCGCAATCGCTGCTGGCCCTGGAGAGCAACCTCCCTGAT	505
Db	301	ATCTGCGCAACCATCATCGCAATCGCTGCTGGCCCTGGAGAGCAACCTCCCTGAT	360
Qy	506	GGGGACAAAACGCCCATGTCCGAGCGGCTGGAGCAGACGAGAGCCTATTTCATCGGATC	565
Db	361	GGGGACAAAACGCCCATGTCCGAGCGGCTGGAGCAGACGAGAGCCTATTTCATCGGATC	420

QY	566	TTTTGCTTCGAGCGAGGATCAAAATCATCGCTCGGGCTTTGTCTTCCACAAGGGCTCT	625
Db	421	TTTTGCTTCGAGCGAGGATCAAAATCATCGCTCGGGCTTTGTCTTCCACAAGGGCTCT	480
QY	626	TACCTCGCAACGGCTGGAAAGTCAATGGAATTCGTGGTCTCCTCACAGGATCCTTGCC	685
Db	481	TACCTCGCAACGGCTGGAAAGTCAATGGAATTCGTGGTCTCCTCACAGGATCCTTGCC	540
QY	686	ACGGCTGGAACATGACTTCGACCTCGCAACATCGAGGGCTGTGCTGAGGGCCCTG	745
Db	541	ACGGCTGGAACATGACTTCGACCTCGCAACATCGAGGGCTGTGCTGAGGGCCCTG	600
QY	746	AAGCTGGTCTCGGATTCGAAAGTTGAGGTGGTCTCAAGTCCATCATGAAGGCCATG	805
Db	601	AAGCTGGTCTCGGATTCGAAAGTTGAGGTGGTCTCAAGTCCATCATGAAGGCCATG	660
QY	806	GTTTCACTCCTGCAGATGGGGTCTTCTCTTTTGGCATCCTCATGTTTGGCATCAT	865
Db	661	GTTTCACTCCTGCAGATGGGGTCTTCTCTTTTGGCATCCTCATGTTTGGCATCAT	720
QY	866	GGCTTGGAGTTCTACATGGGCAAGTTCCAAAGGCTGTTTCCCAACAGCACAGATGCG	925
Db	721	GGCTTGGAGTTCTACATGGGCAAGTTCCCAAGGCTGTTTCCCAACAGCACAGATGCG	780
QY	926	GAGCCGTGGGTGACTTCCCTGTGGCAAGAGGCCCCAGCCGGCTGTGGAGGGCGAC	985
Db	781	GAGCCGTGGGTGACTTCCCTGTGGCAAGAGGCCCCAGCCGGCTGTGGAGGGCGAC	840
QY	986	ACTGAGTCGGGGAGTACTGGCCAGGACCAACTTTGGCATCACCACATTTTGACAAATATC	1045
Db	841	ACTGAGTCGGGGAGTACTGGCCAGGACCAACTTTGGCATCACCACATTTTGACAAATATC	900
QY	1046	CTGTTTGGCATCTTGACGGTGTTCAGTGCATCAACATGGAGGGCTGGACTGACATCCTC	1105
Db	901	CTGTTTGGCATCTTGACGGTGTTCAGTGCATCAACATGGAGGGCTGGACTGACATCCTC	960
QY	1106	TATATACAAACGATCGCGCGGCAACACCTGGAACTGGCTCTACTTCATCCCTCTCATC	1165
Db	961	TATATACAAACGATCGCGCGGCAACACCTGGAACTGGCTCTACTTCATCCCTCTCATC	1020
QY	1166	ATCATCGGCTCTTCTTATGCTCAACCTGGTGTGGCTGTCTCGGGGGAGTTTGGC	1225
Db	1021	ATCATCGGCTCTTCTTATGCTCAACCTGGTGTGGCTGTCTCGGGGGAGTTTGGC	1080
QY	1226	AAGAGCGAGAGAGGTGGAGAACCGCCGCGCTTCTTGAAGCTGCGCGGCGAGCAG	1285
Db	1081	AAGAGCGAGAGAGGTGGAGAACCGCCGCGCTTCTTGAAGCTGCGCGGCGAGCAG	1140
QY	1286	ATCGAGCGAGAGCTCAACGGGTACCTGGAGTGGATCTTCAAGGCGGAGGAATCATGCTG	1345
Db	1141	ATCGAGCGAGAGCTCAACGGGTACCTGGAGTGGATCTTCAAGGCGGAGGAATCATGCTG	1200
QY	1346	GCCGAGGAGGACAGGAATCCAGAGAGGAAGTCCCTTTGGACGTGCTGAAGAGAGCGGCC	1405
Db	1201	GCCGAGGAGGACAGGAATCCAGAGAGGAAGTCCCTTTGGACGTGCTGAAGAGAGCGGCC	1260
QY	1406	ACCAAGAGAGAGAGAAATGAATCATGATCCAGAGAGGAGGAGGACCGGTTTGCAGAT	1465
Db	1261	ACCAAGAGAGAGAGAAATGAATCATGATCCAGAGAGGAGGAGGACCGGTTTGCAGAT	1320
QY	1466	CTCTGTGCTGTGGATCCCTTTCGCCCGCCAGCTTCAAGAGGGGAGACAGAGAGC	1525
Db	1321	CTCTGTGCTGTGGATCCCTTTCGCCCGCCAGCTTCAAGAGGGGAGACAGAGAGC	1380
QY	1526	TCGTATATCTCCGAGGAGGAGAGATGTTCCGGTTTTTTTATCCGGCGCATGGTGAAG	1585
Db	1381	TCGTATATCTCCGAGGAGGAGAGATGTTCCGGTTTTTTTATCCGGCGCATGGTGAAG	1440
QY	1586	GCTCAGAGCTTCTACTGGGTGGTGTGCTGTGGTGGCCCTGAAACAACATGTGTGGCC	1645
Db	1441	GCTCAGAGCTTCTACTGGGTGGTGTGCTGTGGTGGCCCTGAAACAACATGTGTGGCC	1500
QY	1646	ATGGTGCAATTACACCGCCGGCGGCTTACACGACCCCTGTATTTTGCAGAGTTTGT	1705

Db	1501	ATGGTGCAATTACAAACGAGCGCGGGCTTACACGACCCCTGTATTTTGCAGAGTTTGT	1560
QY	1706	TTCTCTGGGTCTTCTTCTCACAGAGATGTCCTCTGAAGATGTATGCTGGGCGCCAGAGC	1765
Db	1561	TTCTCTGGGTCTTCTTCTCACAGAGATGTCCTCTGAAGATGTATGCTGGGCGCCAGAGC	1620
QY	1766	TACTTCCGGTCTCTCTTCAACTGCTTCGACTTTTGGGCTCATCGTGGGAGCGTCTTTGAA	1825
Db	1621	TACTTCCGGTCTCTCTTCAACTGCTTCGACTTTTGGGCTCATCGTGGGAGCGTCTTTGAA	1680
QY	1826	GTGCTGTGGGCGGCATCAAGCCGGGAAGCTCTTTTGGGATCATGTGCTGCGGGCCCTC	1885
Db	1681	GTGCTGTGGGCGGCATCAAGCCGGGAAGCTCTTTTGGGATCATGTGCTGCGGGCCCTC	1740
QY	1886	CGCTGTGTGAGGATCTTCAAAGTCAACAACTACTGGAAGTCCCTGCGGAACCTTGGTGGT	1945
Db	1741	CGCTGTGTGAGGATCTTCAAAGTCAACAACTACTGGAAGTCCCTGCGGAACCTTGGTGGT	1800
QY	1946	TCCCTGTGAACTCCATGAAAGTCCATCATCAGAGCTGCTCTTTTGTCTCTTCTTTCATT	2005
Db	1801	TCCCTGTGAACTCCATGAAAGTCCATCATCAGAGCTGCTCTTTTGTCTCTTCTTTCATT	1860
QY	2006	GTGCTCTTCCGCTGTGGGGATGAGCTGTTTGGGGGAACAGTTCAACTTCCAGGATGAG	2065
Db	1861	GTGCTCTTCCGCTGTGGGGATGAGCTGTTTGGGGGAACAGTTCAACTTCCAGGATGAG	1920
QY	2066	ACTCCCAACAACTTTCGACACCTTCCCTGCGCCCATCTCACTGTCTTCCAGATCCTG	2125
Db	1921	ACTCCCAACAACTTTCGACACCTTCCCTGCGCCCATCTCACTGTCTTCCAGATCCTG	1980
QY	2126	ACGGGAGAGACTGGAAATGCAATGATATCAGGGATCGAAATCGCAAGCGGCGTCAGC	2185
Db	1981	ACGGGAGAGACTGGAAATGCAATGATATCAGGGATCGAAATCGCAAGCGGCGTCAGC	2040
QY	2186	AAAGGCATGTTCTGCTCTTTTACTTCTTCTGACACTGTTCGGAACATACACTCTG	2245
Db	2041	AAAGGCATGTTCTGCTCTTTTACTTCTTCTGACACTGTTCGGAACATACACTCTG	2100
QY	2246	CTGAATGCTTTCTGGCCATCGCTGTGGCAACCTTGGCCAACTGGCCAACTGGCCAACT	2305
Db	2101	CTGAATGCTTTCTGGCCATCGCTGTGGCAACCTTGGCCAACTGGCCAACTGGCCAACT	2160
QY	2306	GATGAAGAGAGATGGAAGAACGAGCAATCAGAAGCTTCTCTGCAAAAAGCCAAAGAA	2365
Db	2161	GATGAAGAGAGATGGAAGAACGAGCAATCAGAAGCTTCTCTGCAAAAAGCCAAAGAA	2220
QY	2366	GTGGCTGAAGTCAAGCCCATGTCTGCGGCAACATCTCCATCGCGCCGAGGAGCAAC	2425
Db	2221	GTGGCTGAAGTCAAGCCCATGTCTGCGGCAACATCTCCATCGCGCCGAGGAGCAAC	2280
QY	2426	TCGGCCAAAGCGCGCTCGGTGTGGGAGCAGCGGGCCAGCCAGCTAGCGCTG3CAGAACTG	2485
Db	2281	TCGGCCAAAGCGCGCTCGGTGTGGGAGCAGCGGGCCAGCCAGCTAGCGCTG3CAGAACTG	2340
QY	2486	CGGGCAGCTGCGAGCGCTGTACAGCGATGGACCCCGAGAGCGGCTG3CGCTTGGCC	2545
Db	2341	CGGGCAGCTGCGAGCGCTGTACAGCGATGGACCCCGAGAGCGGCTG3CGCTTGGCC	2400
QY	2546	ACTACGGCCACTGCGGGCCGACATGAAGCCACCTGGACCGGGCGCTG3TGTGGTGGAG	2605
Db	2401	ACTACGGCCACTGCGGGCCGACATGAAGCCACCTGGACCGGGCGCTG3TGTGGTGGAG	2460
QY	2606	CTGGGCGGAGCAGCGCGGGGGCCGCTGGGAGGCAAGCCGACCTGA3GCTGCGGAG	2665
Db	2461	CTGGGCGGAGCAGCGCGGGGGCCGCTGGGAGGCAAGCCGACCTGA3GCTGCGGAG	2520
QY	2666	GCCCCGAGGGGTGCAACCTCGCGCAGGCAACACCGGCAACCGCAACAGCAAGAC	2725
Db	2521	GCCCCGAGGGGTGCAACCTCGCGCAGGCAACACCGGCAACCGCAACAGCAAGAC	2580
QY	2726	CCGCGCGGGGACAGGACCGAGCAGAGGCCCCCAAGCGGAGAGCGG3GAGCCGCT	2785

QY 4946 AAGGCCCTGCCCCTACGTGTCTGTCTCATTTGCCATGCTGTCTTCTCATCTACGCCCATCATC 5005
DB 4789 AAGGCCCTGCCCCTACGTGTCTGTCTCATTTGCCATGCTGTCTTCTCATCTACGCCCATCATC 4848
QY 5006 GGCATCGAGGTGTTTGGGAATATTGCCCTGGATGACACACAGCATCAACCGCCACAAAC 5065
DB 4849 GGCATCGAGGTGTTTGGGAATATTGCCCTGGATGACACACAGCATCAACCGCCACAAAC 4908
QY 5066 AACTTCCGGACGTTTTTGAAGCCCTGATGCTGTCTTTCAGGAGGCCACACGGGGAGGCC 5125
DB 4909 AACTTCCGGACGTTTTTGAAGCCCTGATGCTGTCTTTCAGGAGGCCACACGGGGAGGCC 4968
QY 5126 TGGCAGAGATCATGTCTGCTCCTGAGCAACCGAGCCCTGTGATGAGCAGGCCCAATGCC 5185
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QY 5186 ACCGAGTGTGGAGTACATTTGCGCTACTTCTACTTGGTCTCTTCTCATCTTCTGTGCTCC 5245
DB 5029 ACCGAGTGTGGAGTACATTTGCGCTACTTCTACTTGGTCTCTTCTCATCTTCTGTGCTCC 5088
QY 5246 TTTCTGATGTGAACCTCTTTGTGGCTGTGATCATGGACAAATTTTGAAGTACCTCACGGG 5305
DB 5089 TTTCT----- 5093
QY 5306 GACTCTTCCATCCTAGGTCTCACCACCTTGGATGAGTTCAATCCGGGTCTGGGCTGAATAC 5365
DB 5094 ----- 5093
QY 5366 GACCCGGCTGCGTGTGGGCGCATCAGTTACATGACATGCTTTGAGATGCTGAAACACATG 5425
DB 5094 ----- 5093
QY 5426 TCCCGCCTCTGGGGCTGGGGAAGAAATGCCCTGCTCGAGTTGCTTACAAGCGCCTGGTT 5485
DB 5094 -----GGCCTGGTT 5103
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DB 5704 ATGCAGAGCATAAACCCGAGAGGGGCCCTGATGGGGAGGCCACAGCCTGGCTGGAGAGCCAG 5763
QY 6146 GGTGAGGGCGCTCCATGCCCCCGCTTGGGCCGAGACTCAGCCGTCACAGATGCCAGC 6205
DB 5764 GGTGAGGGCGCTCCATGCCCCCGCTTGGGCCGAGACTCAGCCGTCACAGATGCCAGC 5823
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DB 5824 CCCATGAAGCGCTCCATCTCCAAGCTGGCCAGCGGCCCGCTGGGAATCTCATCTTTTGACG 5883
QY 6266 ACCACCCGGAGCCGCCACACCCCTAGCCAGCGGTGTGTGCAACACCAACCAACCGCTGC 6325
DB 5884 ACCACCCGGAGCCGCCACACCCCTAGCCAGCGGTGTGTGCAACACCAACCAACCGCTGC 5943
QY 6326 CACCGCCGAGGAGACAGAAAGAGGTCTCTGGAGAGGGGCCAGCCCTCTCTGCCGAT 6385
DB 5944 CACCGCCGAGGAGACAGAAAGAGGTCTCTGGAGAGGGGCCAGCCCTCTCTGCCGAT 6003
QY 6386 ATGATGCGCAACCAAGCAGTGTGTGGGCCCGGGGTGCCCCGGGAGAGAGGCTTACA 6445
DB 6004 ATGATGCGCAACCAAGCAGTGTGTGGGCCCGGGGTGCCCCGGGAGAGAGGCTTACA 6063
QY 6446 GGTCTCCGGCGGGACAGAGAGCCCGGAGAGGGGGCCGGTCCAGAGAGCCGAGGAGCAG 6505
DB 6064 GGTCTCCGGCGGGACAGAGAGCCCGGAGAGGGGGCCGGTCCAGAGAGCCGAGGAGCAG 6123
QY 6506 CCTCTCATCTCTCTCCGAGAAAGCAGCGCTTCTACTCTCTGACACGCTTTGGGGGCGGT 6565
DB 6124 CCTCTCATCTCTCTCCGAGAGAGCGCTTCTACTCTCTGCGACCGCTTTGGGGGCGGT 6183
QY 6566 GAGCCCCCGAAGCCCAAGCCTCTCAGCAGCCACCCAAAGCTCGCAACAGCTGGCCAG 6625
DB 6184 GAGCCCCCGAAGCCCAAGCCTCTCAGCAGCCACCCAAAGCTCGCAACAGCTGGCCAG 6243
QY 6626 GAGCGGGACCCCAACCCACAGGGCAGTGGTTCGTGATGGGAGCCCTTCTGTCAACA 6685
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DB 6304 TCTGCTAGTACACCCCGCGCTGGGCGGAGGAGCAGTCCCGCCAGAGCCCGCTGACT 6363
QY 6746 CCGCGCCGAGCATCACTTACAAGACGGCCAACTCCTCAACCATCCAATTGCGGGGCT 6805
DB 6364 CCGCGCCGAGCATCACTTACAAGACGGCCAACTCCTCAACCATCCAATTGCGGGGCT 6423
QY 6806 CAGACAGCCTCCTGCTTCTCCAGGCGGCTCAGCGGTGGGCTTTCCGAACCAAC 6865
DB 6424 CAGACAGCCTCCTGCTTCTCCAGGCGGCTCAGCGGTGGGCTTTCCGAACCAAC 6483
QY 6866 GCCTGTGTCAGAGAGACCCCTCAGCCAGCCCTGGCCCTGGCTCTCGAATGGCTCT 6925
DB 6484 GCCTGTGTCAGAGAGACCCCTCAGCCAGCCCTGGCCCTGGCTCTCGAATGGCTCT 6543
QY 6926 GACCCCTTACCTGGGCGAGCGTCTGGACAGTGGCCCTCTGTCAACGCCCTCTCTGAGGAC 6985
DB 6544 GACCCCTTACCTGGGCGAGCGTCTGGACAGTGGCCCTCTGTCAACGCCCTCTCTGAGGAC 6603
QY 6986 AGCCTCACTTTTCAGAGAGCGTGGGCCAACACTCGGGCGGCTCTCTCCAGACTTCTCTAC 7045
DB 6604 AGCCTCACTTTTCAGAGAGCGTGGGCCAACACTCGGGCGGCTCTCTCCAGACTTCTCTAC 6663
QY 7046 GTGCTCTGTCAGTCTCCAGTCTACCTCTCCGCGGCTGCCAAACGGTACCACTGC 7105
DB 6664 GTGCTCTGTCAGTCTCCAGTCTACCTCTCCGCGGCTGCCAAACGGTACCACTGC 6723
QY 7106 ACCCTGGGACTCAGTCTGGGTGGCGAGCAGGTCAGTACCAACCCCTGACCAAGAC 7165

Db 6724 ACCCTGGAGCTCAGCTCGGTGGCCGAGCAGCGCACAGCTACCAACCCTTGACCAAGAC 6783
Qy 7166 CACTGGTGC 7174
Db 6784 CACTGGTGC 6792

RESULT 8
US-10-033-026-9
; Sequence 9, Application US/10033026
; Publication No. US20020147309A1
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/10/033,026
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 7011
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..7008
US-10-033-026-9

Query Match 71.7%; Score 5289.8; DB 14; Length 7011;
Best Local Similarity 85.5%; Pred. No. 0;
Matches 6045; Conservative 0; Mismatches 927; Indels 99; Gaps 10;

Qy 146 ATGCTCCGCTTCGGGGACGAGCTCGGCGCGCGCTATGGAGCCCGCGCGGAGCGG 205
Db 1 ATGCTCCGCTTCGGGGACGAGCTAGGCGCGCTATGGGCGCACCGCGCGGAGCGG 60

Qy 206 GCCCGGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 265
Db 61 GCTCGGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 120

Qy 266 CAGCGGTCTCTACAAGCAATCATCGCGAGCGCGCGGACCATGGCGCTGTACAAC 325
Db 121 CAGCGGTCTCTACAAGCAATCATCGCGAGCGCGCGGACCATGGCGCTGTACAAC 180

Qy 326 CCCATCCCGGTCAAGCAGAACTGCTTCAACCGTCAACCGCTCGCTCTTCGTTTCAGCGGAG 385
Db 181 CCCATCCCGGTCAAGCAGAACTGCTTCAACCGTCAACCGCTCGCTCTTCGTTTCAGCGGAG 240

Qy 386 GACAACTGTCGCCAAATACCGAAGCGCATACCGAGTGGCTCCATTCGAGTATATG 445
Db 241 GACAACTGTCGCCAAATATGCTAAGCGCATCAACCGAATGGCGCGCTTCGATATATG 300

Qy 446 ATCTGCGCCACCATCATCGCCAACTGCATCGTGTGGCCCTGGAGCAGCACCTCCCTGAT 505
Db 301 ATCTGCGCCACCATCATCGCCAACTGCATCGTGTGGCCCTGGAGCAGCACCTCCCTGAT 360

Qy 506 GGGGACAAAACGCCCATGTCCGAGCGGTGGAGCAGACCGAGCCCTATTTTCATCGGGATC 565
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Qy 566 TTTTGTCTTCAGGCGAGGATCAAAATCATCGCTCTGGGCTTTGTTCACAAGGGCTCT 625
Db 421 TTTTGTCTTCAGGCGGCGATCAAGATCATAGCTCTGGGCTTCGTGTTCACAAGGGCTCC 480

Qy 626 TACCTCGGACCGCTGGAGCTCATGCACTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 685
Db 481 TACCTCGGAAATGGCTGGAAGCTCATGGACTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540

Qy 686 ACGGCTGGAACTGACTTTCGACCTTCGGAACA CTGAGGGCTGTGCTGTGCTGAGGGCCCTG 745
Db 541 ACAGCTGGAACTGACTTTCGATCTCGCACCTTCGAGGCTGTGCTGTGCTTAGGCCCTG 600

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Db 601 AAGTGGTGTCTGGAAATTCGAAGCTTTCGAAGTGGTGTCTCAAGTCCATCATGAAGGCCATG 660

Qy 806 GTTCCCACTCTGAGATTTGGGCTGCTCTCTTTTGGCAATCTCTCATCTGTTTGGCATCAT 865
Db 661 GTCCCGCTGTGAGATCGGCTGCTCTCTCTTCGCAATCTCTCATCTGTTTGGCATCATC 720

Qy 866 GGCTTGAGTTTACATGGGCAAGTTCCACAAGGCTCTTTCCCAACAGCAGACAGATGCG 925
Db 721 GGCTCGAGTTCTATATGGCAAAATTCATAAGGCTCTGCTTCCCAACAGCAGACAGATGCA 780

Qy 926 GAGCGCTGGGTGACTTCCCTGTGCGAGGAGGCCCGCCAGCCGGCTGTGCGAGGGCGAC 985
Db 781 GAGCGCTGGGTGACTTCCCTGTGCGAGGAGGCCCGCTGCTCTGTGTGTGACAGTGAC 840

Qy 986 ACTGAGTGGCGGAGTACTGCGCCAGGACCCAACTTTGGGCAATCAACCACTTTGACAATATC 1045
Db 841 ACCGAATGGCGGAGTACTGCGCCAGGACCCAACTTTGGGCAATCAACCACTTTGACACATC 900

Qy 1046 CTGTTTGCCATCTTGACGGTTCCTCAAGTGATCACCATGGAGGGCTGGAATGACATCCTC 1105
Db 901 CTGTTTGCCATCTTGACGGTTCCTCAAGTGATCACCATGGAGGGCTGGAATGACATCCTC 960

Qy 1106 TATAATACAAACGATCGCGCGGCAACACTGGAACCTGGCTCTACTTCACTCCCTCTCATC 1165
Db 961 TACAATACAANTGATCGCGCGGCAACACTGGAACCTGGTGTGTTGTTACTTCACTCCCTCTCATC 1020

Qy 1166 ATCATCGGCTCTCTTTCATGCTCAACCTGGTGTCTGCGGCTGTCTCTCGGGGAGTTTGCC 1225
Db 1021 ATCATTTGGCTCTCTTTCATGCTCAACCTGGTGTCTGCTGCTGCTTTCAGGAGTTTGCC 1080

Qy 1226 AAGGAGGAGAGAGGGTGGAGAACCGCGCGGCTTCTCTGAAGCTGCGCCCGGAGCAGAG 1285
Db 1081 AAGAGCGGAGCGAGTCGAGAAACCGCGGCTTCTCTGAAGCTTCCGAGCGGAGCAGAG 1140

Qy 1286 ATGAGGAGGAGCTCAACGGTACTTGGAGTGTATCTTCAAGCGGAGGAGTCACTGCTG 1345
Db 1141 ATTGAGCGAGAACTGAATGGGTACTTGGAGTGTATCTTCAAGCGGAGGAGTCACTGTTG 1200

Qy 1346 GCGGAGGAGCAGAGGAATGACAGAGGAAGTCCCTCTTTTGA ---CGTGTCAAAGAGAGCG 1402
Db 1201 GCAAGAGGAGCAGAAACGCAAGAGAGTCCCTCTTGGATGCACTGTTGAAGAGAGCT 1260

Qy 1403 GCCACCAAGAGAGCAAAATGACCTGATCCA CGCAGAGAGGAGGAGAGGACCGGTTTGCA 1462
Db 1261 GCTACCAAGAGAGCGMAATGACCTCATCCATGCAAGAGAGGAGGAGGACCGGTTTGTA 1320

Qy 1463 GATCTCTGTGCTTGTGATCCCTCTTCCCGCGCGGCGGCTCAAGAGCGGAGAGACAGAG 1522
Db 1321 GACCTCTGTGCTGTGGTCTCCCTTTGCTGCTGCGCAGCTCAAGAGTGGGAAGACAGAG 1380

Qy 1523 AGCTCTGCTACTTTCGAGAGAAAGAGATGTTTCGGTGTTCGAGTTCCTGCTGATGCTG 1582
Db 1381 AGCTCTGCTACTTTCGAGAGAAAGAGATGTTTCGGTTCCTTATCCGCTGATGCTG 1440

Qy 1583 AAGGCTCAGAGCTTCTACTGGGTGGTGTGCTGCTGGTGGCCCTGAAACACACTGTGTGTG 1642
Db 1441 AAAGCAGAGAGCTTCTACTGGGTGGTGTGCTGCTGGTGGCCCTGAAACAGTGTGTGTG 1500

Qy 1643 GCCATGGTGAATTAACAACGAGCCCGCGGCTTACCAAGCCCTGTATTTTTCAGAGTTT 1702
Db 1501 GCCATGGTGAATTAATACAGCCTCAGCGCTTACCACTGCTGCTGCTTTCAGAGTTT 1560

Qy 1703 GTTTTCTGGGTCTCTTCTCTCAGAGATGTCCTGAAAGATGTATGGCTTGGGGCCGAG 1762
Db 1561 GTTTTCTGGGTCTCTTCTCTCAGAGATGTCCTGAAAGATGTATCGGTCTAGGGCCGAG 1620

Qy 1763 AGCTACTTCGGGTCTCTCTCTTCAACTGCTTTGAGACTTTTGGGCTCATCGTGGGAGCGCTTTT 1822

Db 1621 AGCTACTTCGGTCTTCCCTCAACTGCTTTGACTTTGGGGTGATTGTGGGAGTATCTTT 1680
Qy 1823 GAAGTGGTCTGGCGGCGCATCAAGCCGGGAAGTCTCTTTGGGATCAGTGTGCTGGGGCC 1882
Db 1681 GAAGTAGTCTGGGCTGCCATCAAGCCAGGAACCTCTTCGGAATCAGTGTGCTGGGGCT 1740
Qy 1883 CTCGGCTCTGAGGATCTTCAAAGTCACGAAGTACTGGAGTCCCTCGGGAACCTGGTG 1942
Db 1741 CTCGGACTGCTGAGGATTTCAAAGTCACGAAGTATGGAATCTCCTGAGGAACCTGGTT 1800
Qy 1943 GTGTCCTCTGTAACCTCAATGAAGTCCATCATCAGCCTCTCTTTGCTCTTCCTGTTTC 2002
Db 1801 GTTTCCTCTCTCAACTCCATGAAGTCCATCATCAGCCTCTCTCTGCTTTCTCTTTC 1860
Qy 2003 ATTGTGGTCTTCGCTCTGGGATGACAGTCTGTTTGGGGGACAGTTCAACTTCCAGAT 2062
Db 1861 ATTGTGGTCTTCGCTCTGTGTGGGATGACAGTCTGTTTGGGGGACAGTTCAACTTTC 1920
Qy 2063 GAGACTCCCAACCAACTTTCGACACTTCCCTGCGCCATCTCACTGTCTTCAGATC 2122
Db 1921 GAGACTCCCAACCAACTTTTGATACCTTCCAGCTGCCATCTCACTGTGTTTCAAGAT 1980
Qy 2123 CTGACGGGAGAGACTGGAATGATGATGATATCACGGGATCGAATCGCAAGCGCGCTC 2182
Db 1981 CTGACAGGAGAGACTGGAATGATGATGATATCATGATGATGATGATGATGATGATG 2040
Qy 2183 AGCAAAAGGATGTTCTGCTGCTTCTTACTTCAATGCTGACACTCTTGGAAACTACACT 2242
Db 2041 AGCAAAAGGATGTTTCTATCTTCTTACTTCACTGCTGACACTGTTGGAAACTACACC 2100
Qy 2243 CTGCTGAATGTTCTTCTGCGCCATCGCTGTGGCAAACTTGGCCAAAGCCGAGCTGACC 2302
Db 2101 CTGTTGAACGTTTCTTGGCCATGCTGTGGCAAACTTGGCCAAAGCCGAGTTGACC 2160
Qy 2303 AAGGATGAAGAGAGAGATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2362
Db 2161 AAGGATGAAGAGAGAGATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Qy 2363 GAAGTGGCTGAAGTCAAGCCCACTGCTGCGCGAATCTCCATCGCCGAGGAGAGAGAG 2422
Db 2221 GAAGTGAAGTCAAGTCAAGCCCACTGCTGCTGCAAACTCTCCATGCTGCGAGGAGAG 2280
Qy 2423 AACTCGGCAAGCGCGCTCGTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2482
Db 2281 AACTCGGCAAGCGCGCTCAGTATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Qy 2483 CTGCGGCGCAGCTGCGAGGCGCTGTACAGAGAGATGGAACCCGAGGAGGCGCTGCGCTTC 2542
Db 2341 CTGCGTGCAGCTGTGAGGCACTGTACAGTGAATGGAACCCGAGGAGGCGCTGCGTTAT 2400
Qy 2543 GCCACTAGCGCCACTTGGCGCCGACATGAAGAGCAGCACTGGACCGGCGCTGTTGGTG 2602
Db 2401 GCCAGCAGCGCCACTTGGGCGCAGCATGAAGACACACATGGAACCCGAGGAGAGAG 2460
Qy 2603 GAGCTGGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2662
Db 2461 GAACCTGTGCGGATGCGGCTGCGGCGGAGCCGCGGCGGAGCAAAAGTCAAAAGCCTGAGG 2520
Qy 2663 GAGGCGCGGAGGCGCTGCAACCTCCGCGAGGAGCAGCCGAGGAGGAGGAGGAGGAGGAG 2722
Db 2521 GAGGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2580
Qy 2723 -----ACCCCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2770
Db 2581 ACCTCAGCTCAACCCCTGCTGGAGGCGAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
Qy 2771 AGCGGGAGAGCGGCTGCGCGGAGAGAGGCGGCGGCGGCGGAGGAGGAGGAGGAGGAGG 2830
Db 2641 AGCAGGAGAGCGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2700
Qy 2831 GCGCGGCGGCGCGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2890

Db 2701 GCTCCAGGGCT-----GACACACAAGTGCCTTGTGTGAGGCGAGT 2739
Qy 2891 CGGCGGAGACACCGCGGGGCTCCCGGAGAGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAG 2950
Db 2740 AGAGCTCACCACCGCGCGGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2799
Qy 2951 CGCGCGACCGGCGC-----CAGGATCCGAGCAAGGAGTGCCTGCGCGG----- 2993
Db 2800 CGTCCACACCGGACCGCAGGAGTCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2859
Qy 2994 -----CAGGAGGAGCGGCGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3046
Db 2860 CTTGTATCCCAAGGCGAGCGTTCGCGCAAGACATC---GAGGCGCGGCTACGGGCGCGCT 2916
Qy 3047 GAGCGGAGAGCGGAGGAGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3106
Db 2917 GAGACAGAGAACAGTGAAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2976
Qy 3107 GCTCACGAGGCTGTGGAGAGGAGACACCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3166
Db 2977 ACATTTGAGCCCCAGAGAGGAGGTTTGCAGAGAGAGGAGAGGAGGAGGAGGAGGAGG 3031
Qy 3167 ATAGTGAAGCGGAGAAAGGAGCTCCGGAACACCGAGCGGCGGCGGCGGCGGCGGCGG 3226
Db 3032 -----GGGATTAAGMAACTCGAAATCACCGCCCAAGGAACTCGCTGT 3075
Qy 3227 GACCTGAGAGACAGTGGGACTGTGACTGTGGGTCCCATGCAACACATGCGCCAGGACCTGT 3286
Db 3076 GACCTGAGGCGCATTTGCGGTTACAGGCGTGGGCTCTTGCACATGCTGCGCTAGCACCTGT 3135
Qy 3287 CTCAGAAAGGTGGAGGAACAGCCAGAGATGCGAGACAAATCAGCGGAACGTCATCTCGCATG 3346
Db 3136 CTCAGAAAGTGGAGGAACAGCCAGAGATGCGAGAGATGCGAGACAAACAGCGTAAATGTCA 3195
Qy 3347 GCGAGTCAAGCCCCAGACCCGAAACATATTGTATATATCCAGTGTATGCTTACCGGCGCT 3406
Db 3196 GCGAGTCAAGCCCCAGACCCGAAACATATTGTATATATCCAGTGTATGCTTACCGGCGCT 3255
Qy 3407 CTTGGGGAAGCGGCTGTTCCAGTGTAACTGAGCTGGAAGAGGAGGAGGAGGAGGAGGAG 3466
Db 3256 CCGGAGGAGGCGGCTGTTAGTTCAGTGTAAACAGGAGGAGGAGGAGGAGGAGGAGGAG 3315
Qy 3467 AAGAGGAGTGAAGCGGATGAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3526
Db 3316 AAGAGGAGGAGGAGGCTGACGATGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3375
Qy 3527 AGCTCCATGTTCTTTAAGCCCCCAACAGCTGCTGCGCGCTTCTGCGCATACATCGTG 3586
Db 3376 AGTTCCATGTTCTGCGCTCAGCCCCCAGCAACTACTCCTGCTGCTTCTGCCATACATTTGTG 3435
Qy 3587 ACCATGAGGTACTTTCAGAGTGGTCACTTCTGCTGCTCATCGCTTTCAGAGAGATCGGCGCTG 3646
Db 3436 ACCATGCGGTACTTTGAGATGGTATCTTGTGCTCATCGCTTTCAGAGAGATTCGCGCTG 3495
Qy 3647 GCTGCTGAGAACCCAGTGGGACAGACTGCGCCAGGAAACAGCTCTGAAATACCTGGAT 3706
Db 3496 GCTGCTGAGGATCCCGTGGGAGCGGACTCATTCGGAACAAATGCTCTGAAATACATGGAC 3555
Qy 3707 TACATTTTCACTGCTCTTTTACCTTTGAGATGGTGAATGAATGATCGACTTTGGGAGCTG 3766
Db 3556 TACATCTTTACAGAGTCTTTCACCTTTGAGATGGTGAATGAATGATGAGATTTGGGCGCTG 3615
Qy 3767 CTGCTTCACTCGGAGCCTATTTTCGGGAGCTTTGTGGAACATTTCTGAGCTTCAATTTGGGCT 3826
Db 3616 CTGCTGACCTTGGGCGCTTACTTCCGGAGCTGTGGAACATTTCTGAGCTTCAATTTGCTG 3675
Qy 3827 AGTGGCGGCTGCTGCTGCTTCTGAGCTTCTGAGCTTCTGAGGAGGATCCAAAGGAGGAG 3886
Db 3676 AGTGGAGCGCTGCTGCTGCTTCTGAGCTTCTGAGCTTCTGAGGAGGATCCAAAGGAGGAG 3735
Qy 3887 ATCAATACCATCAAGTCTCTGAGAGTCTTCTGCTGCTGCGGCGGCTTCAAGACCATCAA 3946
Db 3736 ATCATACCATCAAGTCTCTGAGAGTCTCTGCGGAGTCTCTGCGGCGGCTTCAAGACCATCAAG 3795

Qy	3947	CGGCTGCCAAGCTCAAGGCTGTGTTGTAAGTGTGTGTGTAACCTCCCTGGAAGAAATGTCTTC	4006
Db	3796	CGGCTGCTAAACTCAAGGCTGTGTTGACTGTGTGTGTAACCTCTCTGGAAGAAATGTCTTG	3855
Qy	4007	AACATCTTGATGTCTACATGCTCTTCAATGTTTCAATATTTCCGTCATTTGGGTGCAGCTC	4066
Db	3856	AACATCTTGATGTCTACATGCTCTTCAATGTTTATAATTTGGCGTCATCGCGGTCAAACCT	3915
Qy	4067	TTCAAAGGGAAGTTTCTTACTGCACAGATGAATCCAAAGGAGCTGGAGAGGAGCTGCAGG	4126
Db	3916	TTCAAAGGGAAGTTCTTACTGCACATGATGAGTCCAAAGGAGCTGGAGCGGAGCTGCAGG	3975
Qy	4127	GGTCAGTATTTGGATATGAGAAAGGAGAAAGTGAAGCTCAGCCCAAGGAGTGAAGAAA	4186
Db	3976	GGTCAGTATTTGGATATGAGAAAGGAGAAAGTGAAGCTCAGCCCAAGGAGTGAAGAAA	4035
Qy	4187	TACGACTTTTCACTACGCAATGCTCTGGGCTCTGCTGAGCGCTGTTCACAGTGTCCACG	4246
Db	4036	TATGACTTTTCACTATGACAAATGCTCTGGGCTTGTCTGACTCTGTTTACGGTGTCCACA	4095
Qy	4247	GGAAAGGCTGGCCATGGTGTCTGAACACATCCGCTGGATGCCATATGAGGAGCAGGGT	4306
Db	4096	GGAAAGGCTGGCCATGGTGTCTGAACACATCTGTGTGAAGCCACTATGAGGAGCAGGGG	4155
Qy	4307	CCAAAGCCCTGGGTACCGCATGGAGCTGTCCAATCTTCACTGCTGCTACTTTTGGTCTTTT	4366
Db	4156	CCAAAGCCCGGTTTCGATGGAGCTTTCCATCTTCTATGTGGTCTACTTTTGGTCTTCTC	4215
Qy	4367	CCCTTCTTCTGCTCAACATCTTTTGGCTTTGATCATCATCCTTCCAGGAGCAGGGG	4426
Db	4216	CCTTTTTCTTGTCAACATCTTTTGGCCCTTGTATCATCATCACCTTCCAGGAGCAGGGG	4275
Qy	4427	GACAAGTGTATGCTGTAATGAGCTCGAGAAAGACGAGAGGGCTTGCAATTGACTTCGCC	4486
Db	4276	GACAAGTGTATGCTGAGTGCAGTCTGGAAAGAAATGAGAGGGCTTGCATTTGACTTTGCC	4335
Qy	4487	ATCAGCGCCAAACCCCTGACACGGTATACGCTCCCAAAACCGGCAAGTCTGTTCCAGTATAAG	4546
Db	4336	ATCAGCGCCAAACCCCTGACACGGTATACGCTCCAGAAACGAGTCTGTTCCAGTATAAG	4395
Qy	4547	ACGTGGACATTTGGTGTCTCCCGCCCTTTGAAATACTTATCATATGGCCATGATAGCCCTC	4606
Db	4396	ACATGGACATTTGGTGTCTCTCCACCCCTTTGAGTACTTCAATATGGCCATGATAGCCCTC	4455
Qy	4607	AACACTGTGGTGTGATGATGAAGTCTATGATGACCCCTATGATGACGAGCTCATGCTG	4666
Db	4456	AACACAGTGTGCTGATGATGAAGTCTACGATGCCCTTATGATGAGTACGAGCTGATGCTG	4515
Qy	4667	AAATGCTGAACATCGTGTTCACATCCATGTTTCTCCATGGAATCGCTGCTGAAGATCATC	4726
Db	4516	AAGTGTGTAACATCGTCTTCAATCCATGTTTCTCTGGAGTGCATCCTCGAAGATCATC	4575
Qy	4727	GCCTTTGGGTGTGAACTATTTACAGATGCGCTGGAAATGCTTTGACTTTGTCACTGTG	4786
Db	4576	GCCTTTGGGTGTGAACTACTTACAGATGCGCTGGAAACGCTTTTGTGACTTTGTCACTGTT	4635
Qy	4787	TTGGGAAGTATTTACTGATATTTTATGTAACAGAGATTCGGGAAACGAAATTTTCATCAAC	4846
Db	4636	TTGGGAAGTATTTACTGATATTTTATGTAACGGAGATTCG-----CGAACAATTTTCATCAAC	4689
Qy	4847	CTCAGCTTCTCCGCTCTTTTCGAGCTGCGGGCTGATCAAGCTGTCTCCGCGCAGGGCTAC	4906
Db	4690	TTGAGCTTCTTCCGCTCTTCCGGCGACACGGCTGATCAAGCTCTGTGCGCCAGGGCTAC	4749
Qy	4907	ACCATTCGCATCTCTGCTGGAACCTTTGTCCAGTCTCTTCAAGGCCCTGCCCCCTAGCTGTG	4966
Db	4750	ACCATTCGCATCTTGTGTTATGACCTTTGTCCAGTCTTTTAAAGGCGCTGCCCTAGCTGTGC	4809
Qy	4967	CTGCTCATGCGCATGCTGTTCTTCTACGCCATCATCGGCATGCAAGTGTGTTGGGAAT	5026
Db	4810	CTCCTCATTGCATGCTGTTCTTCTCATCTACGCCATCATCGGCATGCAAGTGTGTTGGGAAC	4869

Qy	5027	ATTGCCCTGATGATGACACCCAGCATCAACCGCCACAAACAACTTCCGGACGTTTTTGGCAA	5086
Db	4870	ATTGCCCTTATGATGATGACACCCAGCATCAACCGCCACAAACAACTTCCGGACATTTTGGCAA	4929
Qy	5087	GCCTGATGCTGCTGTTTCAGAGCGCCACCGGGGAGGCTTGGCACAGAGATCATGCTGTCC	5146
Db	4930	GCCTTATGCTGTTGTTTCAGAGTGCACATGCGGAGGCTTGGCACAGAAATCATGCTGTCT	4989
Qy	5147	TGCTGAGCAACAGAGCTGTGTATGAGCAGGCGCAATGCCCCAGAGTGTGGAAGTGAAGTCTT	5206
Db	4990	TGCTGGGCAACCGGCTCGACCCACATGCCAAACGCGAGCGAATGCGGGAGCGACTTT	5049
Qy	5207	GCCTACTTCTACTTCTCTCTTCT	5266
Db	5050	GCCTATTTTATTTTGTCT	5109
Qy	5267	GTGGCTGTGATCATGAGCAATTTTGTAGTACTCACCGGGGACTCTTCCATCTCTAGGTCCT	5326
Db	5110	GTTTGTGTGATCATGAGCAATTTTGTATACCTCACCGGGGATTTCTTCCATCTCTAGGCGG	5169
Qy	5327	CACCACCTTGGATGAGTTCATCCGGGTCTGGGTGGAATACGACCCGGCTGCTGTGGGCGC	5386
Db	5170	CACCACCTCGATGAATTCATTTCCGCTCTGGGTGGAATACGACCCAGCTGCTGTGGGCGC	5229
Qy	5387	ATCAGTTTAAATGACATGTTTGTAGATGCTGAAACACATGTCCCCGCTCTGCGGCTGGGG	5446
Db	5230	ATCAGTTTAAATGACATGTTTGTAGATGCTGAAACACATGTCCCCACCTCTTGGGTTTGGGG	5289
Qy	5447	AAGAAATGCCCTCGAGTTGCTTACAGCGCTGTTTCGATGACATGACATGCCATCTCC	5506
Db	5290	AAGAAATGCCCGCTCGAGTTGCTTACAGCGCTGTTTCGAAATGAACATGCCCCATATCC	5349
Qy	5507	AAGCAGGACATGACTGTTTCACTTTCAGCTCCACCTGATGGCCCTCATCCGGAGGGCACTG	5566
Db	5350	AATGAGGACATGAGGTACACTTTTACATCCACTGATGSCCTCATCCGAGCGGCACTG	5409
Qy	5567	GAGATCAAGCTGGCCCGCTGGGACAAAGCAGATCAGTGTGACGCGGAGTTGAGGAAG	5626
Db	5410	GAGATCAAGCTTGGCCCGCTGGGACAAACAGCACCATGTGTGCTGAGCTGAGGAAG	5469
Qy	5627	GAGATTTCCGTTGTGGGCGCAATCTGCCCCAGAGACTTTTGGACTTGTGTTGTTACACCC	5686
Db	5470	GAGATCTTCTGTGTGGGTAAATCTGCCCCAGAGACTCTGGACTTACTTGGTGGCCACCC	5529
Qy	5687	CATAAGCCTGATGAGATGACAGTGGGGAAGTTTATGACGCTCTGATGATATTTGACTTC	5746
Db	5530	CACAACTTGACGAGATGACAGTGGGGAAGTCTATGCGGCTCTCATGATATTTGACTTC	5589
Qy	5747	TACAGCAGAAACAAACACACAGAGACAGATGAGAGGCTCTGTGAGGCTCTTCCAG	5806
Db	5590	TACAAACAGAAACAAACACACAGAGATCAGACTCACCAAGCTCTGTGGAGGCTGTGCCAG	5649
Qy	5807	ATGGGTCTGTGCTCTGTTCACCTCTCGAAGCCACCTTGAGGACAGACACAGCCGCT	5866
Db	5650	ATGGGTCTGTTCCTTATTCATCTCTGAAAGCCACCTTGAGGACAGACACAGCCGCT	5709
Qy	5867	GTGCTCGAGGAGCCCGGGTTTTCTTTCGACAGAAAGTTCACCTCCCTCAGCAATGGC	5926
Db	5710	GTGCTCGAGGAGCTCGGGTTTTCTTTCGACAAAGAGTGCNACTTCCCTCAGCAATGGG	5769
Qy	5927	GGGGCCATACAAACCAAGAGATGGGATCAAAAGATGCTGTCTCTGGGGCATCAAAAGG	5986
Db	5770	GGGGCCATACAAACCCAGGAAAGTGGCATCAAGAGATGCCCTGTCTGGGGCAGCGCAGG	5829
Qy	5987	ACCCAGGATGCAACCCATGAGGCGAGCCACCTTGAGGCTGGCCACTCCACAGAGATC	6046
Db	5830	ACCCAGGATGCAACCCATGAGGCGAGGACCTCTTGAAGCTGGCCATCTCTGAGAGATC	5889
Qy	6047	CTGTGGGGGGGTGAGGACATGCTGTGTGAGCTTTCAGATGAGAGATCAACCCCGAGG	6106
Db	5890	CTGTGGGGGGGCGCAGGAGACCTGGCTGTAGATGTCCAGATGAGAGACATGACATGAGA	5949
Qy	6107	GGCCCTGATGGGAGCCCCAGCTGGGCTGGAGAGCCAGGGTGCAGCGGCTCTCATGCCCC	6166

Db 721 GGCCTGAGATTCTACATGGGCAAGTTCCACAAAGGCCTGTTTCCCAACAGCAGACAGATGGG 780
Qy 926 GAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGCCCCAGCCCGGCTGTGTGAGGGCGAC 985
Db 781 GAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGCCCCAGCCCGGCTGTGTGAGGGCGAC 840
Qy 986 ACTGAGTGC CGGGAGTACTGGCCAGGACCCAACTTTGGCATFACCAACTTTTGACAAATATC 1045
Db 841 ACTGAGTGC CGGGAGTACTGGCCAGGACCCAACTTTGGCATFACCAACTTTTGACAAATATC 900
Qy 1046 CTGTTTCCCATCTTGA CGGTGTTCCAGTGCATACCATGAGGAGGCTGAGCTGACATCCTC 1105
Db 901 CTGTTTCCCATCTTGA CGGTGTTCCAGTGCATACCATGAGGAGGCTGAGCTGACATCCTC 960
Qy 1106 TATAATAACAAACGATGCGGCGGCAACACCTGGAACTGGCTCTACTTTCATCCCTCTCATC 1165
Db 961 TATAATAACAAACGATGCGGCGGCAACACCTGGAACTGGCTCTACTTTCATCCCTCTCATC 1020
Qy 1166 ATCATCGGCTCTTCTTCATGCTCAACTGGTGTGGGGTGCTCTCGGGGAGTTTGGC 1225
Db 1021 ATCATCGGCTCTTCTTCATGCTCAACTGGTGTGGGGTGCTCTCGGGGAGTTTGGC 1080
Qy 1226 AAGGAGCGAGAGGGTGGAAACCGCGCGCTTCTGAAAGCTGCGCGCAGCAGCAG 1285
Db 1081 AAGGAGCGAGAGGGTGGAAACCGCGCGCTTCTGAAAGCTGCGCGCAGCAGCAG 1140
Qy 1286 ATCGAGCGAGAGCTCAACGGGTACTCGAGTGGATCTTCAAGCGGAGGAGTCACTCG 1345
Db 1141 ATCGAGCGAGAGCTCAACGGGTACTCGAGTGGATCTTCAAGCGGAGGAGTCACTCG 1200
Qy 1346 GCGGAGGAGACAGGAATGCAGAGGAGAAGTCCCTTTTGGACGTGTGAAGAGCGGCC 1405
Db 1201 GCGGAGGAGACAGGAATGCAGAGGAGAAGTCCCTTTTGGACGTGTGAAGAGAGCGGCC 1260
Qy 1406 ACCAAGAAGACGAGAAATGCATGCTACCGCAGAGGAGGAGGACCGGTTTGCAGAT 1465
Db 1261 ACCAAGAAGACGAGAAATGCATGCTACCGCAGAGGAGGAGGACCGGTTTGCAGAT 1320
Qy 1466 CTCTGTGCTGTGGATCCCTCTTCGCGCGGCCAGCTCAAGAGCGGGAAGACAGAGAGC 1525
Db 1321 CTCTGTGCTGTGGATCCCTCTTCGCGCGGCCAGCTCAAGAGCGGGAAGACAGAGAGC 1380
Qy 1526 TCGTCACTATTCGGGAGGAAGGAGAAGATGTTCCGGTTTTTATCCGGCGCATGGTGAAG 1585
Db 1381 TCGTCACTATTCGGGAGGAAGGAGAAGATGTTCCGGTTTTTATCCGGCGCATGGTGAAG 1440
Qy 1586 GCTCAGAGCTTCTACTGGGTGGTCTGTGGTGGTGGCCCTGAACACACTGTGTGTGGCC 1645
Db 1441 GCTCAGAGCTTCTACTGGGTGGTGGTGTGGTGGCCCTGAACACACTGTGTGTGGCC 1500
Qy 1646 ATGGTGCATTACAAACAGCCGCGGCTTACACAGACCTGTATTTTGCAGAGTTTGT 1705
Db 1501 ATGGTGCATTACAAACAGCCGCGGCTTACACAGACCTGTATTTTGCAGAGTTTGT 1560
Qy 1706 TTCTCTGGGTCTTCTCTCAGAGAGATGTCCTGAAGATGTATGGCTTGGGGCCAGAAAGC 1765
Db 1561 TTCTCTGGGTCTTCTCTCAGAGAGATGTCCTGAAGATGTATGGCTTGGGGCCAGAAAGC 1620
Qy 1766 TACTTCCGGTCTCTCTTCAACTGCTTCGACTTTGGGGTCACTGTGGGAGCGTCTTTGAA 1825
Db 1621 TACTTCCGGTCTCTCTTCAACTGCTTCGACTTTGGGGTCACTGTGGGAGCGTCTTTGAA 1680
Qy 1826 GTGCTCTGGGCGGCATCAAGCCGGGAAGCTCTTTTGGGATCAGTGTGCTGCGGGGCCCTC 1885
Db 1681 GTGCTCTGGGCGGCATCAAGCCGGGAAGCTCTTTTGGGATCAGTGTGCTGCGGGGCCCTC 1740
Qy 1886 GCGCTGTGAGGATCTTCAAGTCAAGATGTA CTGGAGTCCCTGCGGAACCTGGTGGTG 1945
Db 1741 GCGCTGTGAGGATCTTCAAGTCAAGATGTA CTGGAGTCCCTGCGGAACCTGGTGGTG 1800
Qy 1946 TCCTGTGTAATCCATGAAGTCCATCATCAGCTGTCTCTTGTCTTCTCTCTCTCTTCAAT 2005
Db 1801 TCCTGTGTAATCCATGAAGTCCATCATCAGCTGTCTCTTGTCTTCTCTCTCTCTTCAAT 1960

Qy 2006 GTGGTCTTCCCTGCTGCTGGGATCGAGCTGTGTTGGGGA CAGTTCAACTTCCAGGATGAG 2065
Db 1861 GTGGTCTTCCCTGCTGCTGGGATCGAGCTGTGTTGGGGA CAGTTCAACTTCCAGGATGAG 1920
Qy 2066 ACTCCCAACAACCACTTCGACACTTTCCTGCGCCATCTCTCACTGTCTTCCAGATCCTG 2125
Db 1921 ACTCCCAACAACCACTTCGACACTTTCCTGCGCCATCTCTCACTGTCTTCCAGATCCTG 1980
Qy 2126 ACCGGAGAGACTGGAAATGAGTATCA CGGGATCGAATCGAAGCGGCGTCAAGC 2185
Db 1981 ACCGGAGAGACTGGAAATGAGTATCA CGGGATCGAATCGAAGCGGCGTCAAGC 2040
Qy 2186 AAAGGCATGTTCTGCTCTTTTACTTCA TTGTCTGACACTGTTCGGAATACTACACTCTG 2245
Db 2041 AAAGGCATGTTCTGCTCTTTTACTTCA TTGTCTGACACTGTTCGGAATACTACACTCTG 2100
Qy 2246 CTGAATGTCTTTCTGGCCATCGCTGTGGACAACTTGGCCAAAGCCCAAGAGCTGACCAAG 2305
Db 2101 CTGAATGTCTTTCTGGCCATCGCTGTGGACAACTTGGCCAAAGCCCAAGAGCTGACCAAG 2160
Qy 2306 GATGAAGAGAGATGGAAGAGCAGCAATCAGAAGCTTGTCTGTGCAAAAAGGCCAAAGAA 2365
Db 2161 GATGAAGAGAGATGGAAGAGCAGCAATCAGAAGCTTGTCTGTGCAAAAAGGCCAAAGAA 2220
Qy 2366 GTGGCTGAAGTCAAGCCCCCATGTCTGCGGAA CATCTCCATCGCCGCCAGGACAGCAAC 2425
Db 2221 GTGGCTGAAGTCAAGCCCCCATGTCTGCGGAA CATCTCCATCGCCGCCAGGACAGCAAC 2280
Qy 2426 TCGGCCAAAGCGCGCTCGGTGTGGAGCAGCGGCCAGCCAGCTACGGCTGCAAGACCTG 2485
Db 2281 TCGGCCAAAGCGCGCTCGGTGTGGAGCAGCGGCCAGCCAGCTACGGCTGCAAGACCTG 2340
Qy 2486 CCGGCGCAGCTGCGAGCGCTGTACGAGATGGAACCGGAGGAGCGGCTGCGCTTCGCC 2545
Db 2341 CCGGCGCAGCTGCGAGCGCTGTACGAGATGGAACCGGAGGAGCGGCTGCGCTTCGCC 2400
Qy 2546 ACTACGCGCACCTGCGGCCCGA CATGAAGACACCTTGGACCGCGCTGTGTGGTGGAG 2605
Db 2401 ACTACGCGCACCTGCGGCCCGA CATGAAGACACCTTGGACCGCGCTGTGTGGTGGAG 2460
Qy 2606 CTGGGCGGAGCGCGCGCGGGGCCCTGTGGAGGCAAGCCCGACTGAGGCTGCGGAG 2665
Db 2461 CTGGGCGGAGCGCGCGCGGGGCCCTGTGGAGGCAAGCCCGACTGAGGCTGCGGAG 2520
Qy 2666 GCCCGCAGGGCTCGACCTCCGCGCAGSCACACCGGCAACCGGAGGAGCAAGACC 2725
Db 2521 GCCCGCAGGGCTCGACCTCCGCGCAGSCACACCGGCAACCGGAGGAGCAAGACC 2580
Qy 2726 CCGCGCGGGGACCAAGGACCGGAGCGGCCCGGAAAGCGGAGAGCGGGAGCCCGGT 2785
Db 2581 CCGCGCGGGGACCAAGGACCGGAGCGGCCCGGAAAGCGGAGAGCGGGAGCCCGGT 2640
Qy 2786 GCCCGGAGAGCGCGCGCGGCCCGGAGCGGAGCGGAGGAGCGCGGGGCCCGG 2845
Db 2641 GCCCGGAGAGCGCGCGGGCGGAGCGGAGCGGAGCGGAGGAGCGCGGGGCCCGG 2700
Qy 2846 GAGGCGCGAGCGAGCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 2905
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Qy 2906 GCGGGTCTCCCGGAGAGCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 2965
Db 2761 GCGGGTCTCCCGGAGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 2820
Qy 2966 CAGGATCCAGCAGAGAGTGTCCCGCGGCAAGAGGCGAGCGGCGCGGAGCGGAGCGG 3025
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Qy 3026 GCGCCCCGAGCGGGGCCCGGAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 3085
Db 2881 GCGCCCCGAGCGGGGCCCGGAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 2940

Db 5089 TTTCTGATGTTGAACCTCTTTGTGGCTGTGATCATGGACAAATTTTGTAGTACCTCAACCGG 5148
Qy 5306 GACTCTTCCATCTTAGTCTCACCACCTTGGATGAGTTCATCCGGGTCTCGGCTGAATAC 5365
Db 5149 GACTCTTCCATCTTAGTCTCACCACCTTGGATGAGTTCATCCGGGTCTCGGCTGAATAC 5208
Qy 5366 GACCGGCTGGGTGTG 5381
Db 5209 GACCGGCTGGGTGCG 5224

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; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1586
; LENGTH: 6639
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012918
US-09-917-800A-1586

Query Match 35.0%; Score 2582.6; DB 9; Length 6639;
Best Local Similarity 68.3%; Pred. No. 0;
Matches 3955; Conservative 0; Mismatches 1639; Indels 199; Gaps 19;
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RESULT 11

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US-10-375-253-33
; Sequence 33, Application US/10375253
; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10/375,253
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751
; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
; PRIOR FILING DATE: 1993-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PAI
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 7808
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (237)...(7769)
; OTHER INFORMATION: standard name = Alpha-1A-1
US-10-375-253-33

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	Query Match	34.0%;	Score 2507.2;	DB 16;	Length 7808;
	Best Local Similarity	63.8%;	Pred. No. 0;		
	Matches 4457;	Conservative 0;	Mismatches 2093;	Indels 434;	Gaps 26;
QY	146	ATGGTCGGCTTCGGGGACGAGCTGGGGCGCGCGCTATGGAGGCCCGCGCGCGGACGAGCGG	205		
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QY	206	GCCCGGGCGCGCGGGCCGGCGGGGGCGGGGGCCCGGGTCCCGGGGGGGCTGCAGAGCCCGCC	265		
Db	297	GCCGGGTGTGTGTGGGCAGCGAGCGCGCGCGAGAGCCGGGGGACCGCGGCGCGG	356		
QY	266	CAGCGGGTCC-----TCTACAGCAATCATCGCGAGCGCGCGGAGCCATCGG	316		
Db	357	CAGCCCGGGCGCAAGGATGTACAGCACTCAATGCCGAGAGAGCGGGHACCATGCA	416		
QY	317	CTGTACAAACCCATCCCGGTCAAGCAGAACTGTTCAACCGTCAACCGTCTTCTTC	376		
Db	417	CTCTACAAACCCATCCCGGTCCGACAGAACTGCTCAACGGTTAAACGGTCTCTTCTTC	476		

QY	377	TTTACGGAGGACAAACGTCGTCCGGCAAAATATACGGGAAGCGCATCACGAGTGCCTCCCATTC	433
DB	477	TTTACGGAGGACAAACGTCGTGAGAAAAATATCGCCAAAAAGATCATCCGAATGGCCTCCCTTT	536
QY	437	GAGTATATGATCCTGGCCACCATCATCGCCAACTGCATCGTGTGGGCCCTTGAGGACAGAC	496
DB	537	GAATATATGATTTTAGCCACCATCATAGCGAATTTGCATTCGTCTCGCACTGGAGCAGCAT	596
QY	497	CTCCCTGATGGGGACAAAACGCCCATATGTCGAGGGCTGGACGACACGGAGCCCTATTTC	556
DB	597	CTGCCCTGATGATGACAAGACCCCGATGCTGAACGGCTGGATGACACAGAACCATACATTC	656
QY	557	ATCGGGATCTTTTGCCTTCGAGCGAGGATCAAAATCATCGCTCTGGGCTTTGTCTTCAC	616
DB	657	ATTGGAATTTTTTGTTCGAGGCTGGAAATAAAATCATTTGCCCTTGGGTTTGGCCTTCAC	716
QY	617	AAGGGCTCTTACCTGCGGAAACGGCTGGAACCGTCATGGACTTCGTGGTCTCCTCACAGG	676
DB	717	AAAGGCTCCTACTTTAGGAATGGCTGGAAATGTCATGACTTTGTGTGGTCTCTAAACGGGC	776
QY	677	ATCCTTGGCACGGCTGGAACTGACTTCGAACTCTGGAAACACTGAGGGCTGTTCGTGTGCTG	736
DB	777	ATCTTGGCGACAGTTGGGACCGAGATTTGAACTACCGACCGCTGAGGGCAGTTCGAGTCTG	836
QY	737	AGGCCCTTGAAAGCTGGTGTCTGGGATTTCCAAATTTGCAAGTGGTGGTCTCAAATCCCATCATG	796
DB	837	CGCGCGCTCAGGCTGGTCTCTGGAAATCCCAAGTTTACAAGTCGTCTGAAATCGATCATG	896
QY	797	AAGGCATATGTTTCCACTCTCTGCAGATTTGGGTGCTTCTCTTTTGGCATCTCATATGTTT	856
DB	897	AAGCGGATGATCCCTTTGTCTGCAGATCGGCTCTCCCTATTTTTTGGCAATCTTATTTTT	956
QY	857	GCCATCATTTGGCCTGGAGTTCTCATCGGCAAGTTCCACAGGCGCTGTTTCCCCAACAGC	916
DB	957	GCAATCATAGGTTAGAAATTTTATGGGAAATTTCTATCCACTCTCTTTGAAGAGGGG	1016
QY	917	ACAGATG---CGGAGCCGTTGGGTGACTTCCCTGTGGCAAGGAGGCCACGCCCGGCTG	973
DB	1017	ACAGATGACATTCAGGGTGAATCTCCGGCTCCATGTGGGACAGAAGAGCCGCGCCGACC	1076
QY	974	TGCGAGGGGACACTGAGTCGGGAGTACTGGCCAGGACCCAACTTTGGATCATCACCAAC	1033
DB	1077	TGCCCAATGGGACCAAATGTACGCCCTACTCTGGGAAGGGCCCAACACGGGATCATCTCAG	1136
QY	1034	TTTGACAAATATCCTGTTTGGCATCTTGACGGTGTTCAGTGCATCAACATGAGGGGCTGG	1093
DB	1137	TTGACAAACATCCTGTTTGGAGTCTGACTGTTTCCAGTGCATTAACCATGGAAGGTGG	1196
QY	1094	ACTGACATCTCTATATAACAAGATGGGGCGGGCAACACTTGGAACTGGTCTACTTTC	1153
DB	1197	ACTGATCTCTCTACAAATAGCAACGATGCGCTCAGGGAAACACTTGGAACTGTTGTACTTC	1256
QY	1154	ATCCCTCTCATCATCATCGGCTCCTTCTTCATGCTCAACTGTGTCTGGGCGTCTCTCG	1213
DB	1257	ATCCCCCTCATCATCATCGGCTCCTTTTTTATGCTGAACTGTGTCTGGGCTGCTGCTCA	1316
QY	1214	GGGAGTTTCCCAAGGACGAGAGAGGGTGGAAACCGCGCGCTTTCCTCAAGCTGCGC	1273
DB	1317	GGGAGTTTCCCAAGAAAGAGGAAACGGGTGGAAACCGGCGGGCTTTTCTCAAGCTGAGG	1376
QY	1274	CGGCAGCAGCAGATTCGAGCGAGGCTCAACGGGTACTTGGAGTGGATCTTCAAGGCGGAG	1333
DB	1377	CGGCACACACAGATTGAACGTGAGCTCAATGGGTAATGGAATTGGATCTCAAAAGCAGAA	1436
QY	1334	GAAGTCATGTGTGCCGAGGAGGACAGGAATGACAGAGGAAAGTCCCTCTTTCGA---CGTG	1390
DB	1437	GAGTGAATCTCTCCCGAGGATGAAACTGACGGGGACGAGGCAATCCCTTTGATGGAGCT	1496
QY	1391	CTGAAGAGGCGGCCCAAGAGACAGCAAAATGACTCTGATCCACCGCAGACGAGGAGAG	1450
DB	1497	CTCGGAGAACCAACCAATAAGAAAGAACAGACAGATTTTGTCTCAACCCGAAAGGCTGAG	1556
QY	1451	GACCGGTTTGCAGATCTCTGTGCTGTGGATCCCCCTCTCGCCGCGCCAGCTCTCAAGAGC	1510

QY 3400 GGSCCCTCTTGGGAAAGCCACGGTCTGTCCTCCAGTGTAAACGTGGAC-----CTGGA 3450
Db |||||
3773 ACCCCCTCTCAACCAACACCGTGTGTAAGTGAACAAAGCCCAACCCAGACCCACTGCC 3832
QY 3451 AAGCCAAAGCAGAGGGAAGAGAGGTGGAAGCGGATGACGTGATGAGAGCGGCCCGG 3510
Db |||||
3833 AAAAAAGAGGAGAGAGAAGAGAGGAGGAGAAAGACGACCGTGGGGAAGAGCGCCCTAA 3892
QY 3511 GCCTATCGTCCCATACAGCTCCATGTTCTGTTTAAAGCCCCACCAACCTGCTCCGCGGCTT 3570
Db |||||
3893 GCCAATGCCCTCCCTATAGTCTCATGTTTCACTCTGTCACGACCAACCCCTTCGCGCGCT 3952
QY 3571 CTGCCACTACATCGTACCATGAGTACTTTCAGAGTGTGTCATTTCTCGTGGTCATCGCCCTT 3630
Db |||||
3953 GTGCCATTACCTCTGAACCTCGCTACTTTGAGATGTGCATCTCTCATGGTCATTTGCCAT 4012
QY 3631 GAGCAGATCGCCCTGGCTGCTGAGGACCCAGTGGGCAAGAGCTGCCCGAGAAACAAAGC 3690
Db |||||
4013 GAGCAGATCGCCCTGGCCGCGGAGGACCTGTGAGCCCAACGACCTCGGNAACAAGT 4072
QY 3691 TCTGAAATACCTTGGATTACATTTTCACTGGTCTCTTTACCTTTGAGATGGTGATAAAGT 3750
Db |||||
4073 GCTGCGATACTTCTACTAGCTTTTACAGCGCTCTTCACTTTGAGATGGTGATCAAGAT 4132
QY 3751 GATCGACTTGGGACTGCTGCTTCACTCGGAGCTATTTTCGGGACTTTGTGGAAATTTCT 3810
Db |||||
4133 GATTGACCTGGGGCTGCTCTGCATCAGGGTSCCTACTTCCGTGACCTCTGGAATTTCT 4192
QY 3811 GGACTTTCATGTTGTCAGTGGCGCCCTGGTGGGCTTTGTTTCTCGAGCTTCGTGGGAGG 3870
Db |||||
4193 CGACTTTCATGTTGTTGAGTGGGGCCCTGGTGAACCTTTGCG-----CTTCACTGGCAA 4243
QY 3871 ATCCAAAGGGAAGACATCAATACCATCAAGTCTCTGAGAGTCTTTGCTGCTGGCGCC 3930
Db |||||
4244 TAGCAAAAGGAAGACATCAACAGTTAAATCCCTCCGAGTCTCCGGGTGCTACGACC 4303
QY 3931 CTTCAAGACCATCAAAACCGCTCCCAAGCTCAAGGCTGTGTTTGAAGTGTGTTGAACTC 3990
Db |||||
4304 TCTTAAACCATCAAGCGCTGCCAAGCTCAAGGCTGTGTTTGAAGTGTGTTGAACTC 4363
QY 3991 CTTGAGAGATGCTTCAACATCTTGAATGTTCTACAGTCTCTTCATGTTTATTTGCGGT 4050
Db |||||
4364 ACTTAAACAGTCTTCAACATCCTCATGCTTACATGTTTCAATGTTTCAATGTTTCACTTGGCGGT 4423
QY 4051 CATTCGGTGTGAGCTCTTCAAGGGAAGTCTTCTACTGCAAGATGAATCCAAGGAGCT 4110
Db |||||
4424 GGTGGCTGTGACAGCTCTTCAAGGGAATTTCTTCACTGCACTGACGAGTCCAAGAGTT 4483
QY 4111 GGAGAGGACTGCAAGGCTCAGTATTTGGATATGAGAAAGGAGGAGTGGAAAGTCAAGC 4170
Db |||||
4484 TGAGAAAGATTGTGAGGCAAAATACCTCTCTACGAGAAAGTGAAGTGAAGCGCGAGA 4543
QY 4171 CAGGCAGTGGAAAGAAATACGATTTTCACTACGAAATGTGCTTGGGCTCTGCTGACGCT 4230
Db |||||
4544 CCGGAGTGGAAAGATGAAATCCATTAAGCAATGTGCTGAGGCTCTGCTGACCCCT 4603
QY 4231 GTTCAAGTGTCCACGGGAGAGGCTGGCCCATGCTGCTGAAACAACCTCCGTTGAGTGCAC 4290
Db |||||
4604 CTTTACCCGTGTCCACGGGAGAGGCTGGCCACAGGTCTCAAGCATTTGGTGGAGCCAC 4663
QY 4291 CTAAGAGAGAGGCTCAAGCCCTGGGTAACGATGAGGCTGTCCATCTTCTACGTGGT 4350
Db |||||
4664 CTTTGAAGAACCGGGGCCACGCGCGGGTACCGATGGAGATGTCCATTTTCTACGTCTGT 4723
QY 4351 CTACTTGTGTCTTCTCTCTCTCTCTCAATCTTTTGTGCTTTGATCATCATCAC 4410
Db |||||
4724 CTACTTGTGTGTCTCTCTCTCTCTCTCAATCTTTTGTGCTTTGATCATCATCAC 4783
QY 4411 CTTCCAGAGAGGAGGGAACAAGTGTGATGTTCTGAATGACGCTGGAGAAAGACGAGGGC 4470
Db |||||
4784 CTTCCAGAGAGCAAGGGGACAAAGATGATGAGAGGAATACAGCTCTGGAGAAATGAGAGGGC 4843

QY 4471 TTGATTGACTTTCGCATCAGCGCAAAACCCCTGACACGGTACATGCCCAAAACCGSCA 4530
Db |||||
4844 CTGCATTGATTTTCGCATCAGCGCAAGCGCTGACCGGACACATGCCGAGAAACAAGCA 4903
QY 4531 GTCCTTCCAGTATGAAGCAGTGGACATTTGTGGTCTCCCGCCCTTTGAATATTTCAAT 4590
Db |||||
4904 GAGCTTCCAGTACCGCATGTGGCAGTTTCTGGTGTCTCGCCCTTTCGAGTACACGATCAT 4963
QY 4591 GGCCATGATAGCCCTCAACACTGTGGTGTGATGATGAAGTCTATGATCCACCTATGA 4650
Db |||||
4964 GGCCATGATAGCCCTCAACACCATCGTGTCTTATGATGAAGTCTATGGGCTTCTGTGTC 5023
QY 4651 GTACGAGCTGATGTGAAATGCTTGAACATCGTGTTCACATCCATGTTCTCCATGGAATG 4710
Db |||||
5024 TTATGAAATGCTTGGGGTGTTCACATGCTTCACTCTCTCTCTCTCTCTGGAATG 5083
QY 4711 CGTCTGAAAGATCATCGCCCTTTGGGGTGTGAACTATTTTCAAGATGCTTGGAAATGCTT 4770
Db |||||
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QY 4771 TGACTTTGTCACTGTGTGGGAGTATTAAGTATTTTGAATACAGAGATTTGGGAAAC 4830
Db |||||
5144 CGACTTTGTGACTGTCTGGGAGCATCAACGATATCTCTGACTGAGTTGGGAATCC 5203
QY 4831 GAACAATTTTCATCAACCTCAGCTTTCCTCCGCCCTTTTCGAGCTGCGCGCTGATCAAGCT 4890
Db |||||
5204 GAATAACTTTTCATCAACCTGAGCTTTCCTCCGCCCTTTCGAGCTGCGCGCTCATCAACT 5263
QY 4891 GCTCCGCGAGGCTACACCATCCGCAATCCGCAATCTTCTCGAGCTTGTGCAAGTCTTCAAGGC 4950
Db |||||
5264 TCTCCGTCAGGTTTACACCATCCGCAATCTTCTCGAGCTTGTGCAAGTCTTCAAGGC 5323
QY 4951 CTTGCCCTCAGTGTCTGCTCATTCGCAATGCTTCTTCTCATGAGCTTGTGCAAGTCTTCAAGGC 5010
Db |||||
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QY 5011 GCAGTGTTTGGGAATTTGCCCCT-----GGATGATGACAC 5046
Db |||||
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QY 5047 CAGATCAACCGGCAACAACTTCCGAGCTTTTGGAGCCCTGATGCTGTGTTTCAAG 5106
Db |||||
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QY 5107 GAGCGCCACCGGGGAGGCTTGGCAAGATCAATGCTGCTGCTGAGCAACAGGCGCTG 5166
Db |||||
5504 GAGTGCCAACCGGGAGGCTTGGCAACATCAATGCTTCTGCTGCTGAGGAGGAAACCGTG 5563
QY 5167 TGATGAGCAGGC-----CAATGCCACCGAGTGTGGAAGTGAATTTGCTTCTTACTT 5220
Db |||||
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QY 5221 CGTCTCTTCACTTCTGCTGCTCTTCTGATGTTGAACTTCTTGTGGCTGTGATCAT 5280
Db |||||
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QY 5281 GGACAAATTTGAGTACTCAACCGGAGCTTCTTCCATCTTAGGTCCTCACCACCTTGGATGA 5340
Db |||||
5684 GGACAACTTTGAGTACTCAACCGGAGCTTCTTCCATCTTGGGCCCCCAACCACTGGATGA 5743
QY 5341 GTTTCATCCGGGTCTGGGCTGAAATACGACCCGGTGGTGTGGGCGCATCAATGATGA 5400
Db |||||
5744 GTACGTGCGTGTCTGGGCGAGTATGACCCGAGCTTGGGCGCGCATGCTTACCTGGA 5803
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Db |||||
5804 CATGTATCAGTCTGAGACATGTTCTCGGCCCTTGGGCTCTGGGGAAGATGTCCTGGC 5863
QY 5461 TCGAGTGTCTTCAAGCGCTTGTGCTGCAATGAACATGCCCCATCTCCAAACGAGGACATGAC 5520
Db |||||
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QY 5521 TGTTCACCTTCAAGTCCACGCTGATGGCCCTCATTCGGAACGCGACTGGAGATCAAGCTGGC 5580

Db 357 CAGCCCGGGCGCAAAAGGATGTACAAAGCAGTCAATGGCGCAGAGAGCGCGACCATTGGCA 416
QY 317 CTGTACAAACCCATCCCGGTCAAGCAGAACTGCTTCCACCGTCAACCGCTCGCTCTTCGTC 376
Db 417 CTCTACAAACCCATCCCGGTCCGACAGAACTGCTTCCACCGTCAACCGCTCTTCGTC 476
QY 377 TTCCAGCGAGGACAAACGTCGTCGCGAAATACGGGAAGCGCATCACCGAGTGGGCTCCATTTC 436
Db 477 TTCCAGCGAGGACAAACGTCGTCGCGAAATACGGGAAGCGCATCACCGAGTGGGCTCCATTTC 536
QY 437 GAGTATATATCTTGGCCACATCATCGCCAACTGCAATCGTGTGGGCTGGGCTCGGCTTTC 496
Db 537 GAATATATATATTTAGCCACCATCATAGCGAAATGTCATCGTCTCGCATGCGAGCAGCAT 596
QY 497 CTCCTGTATGGGACAAAACGCCCATGTCGAGCGGCTGGAGCAGACCGAGCCCTATTTC 556
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QY 677 ATCTTGGCACCGCTGGAATGACTTTCGACCTGCGAACAACCTGAGGCTGTGCTGCTG 736
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QY 1871 GTGCTCGGCGCTCTCGGCTCTGAGATCTTCAAAGTACAGAACTGAGTCTGAGTCTCCGTG 1930
Db 1977 GTGTTACGAGCCCTCAGGTTATTTGCGTATTTTCAAAGTCTCAAAGTACTGCGCATCTCTC 2036
QY 1931 CGGAACCTGTTGTCTCCCTGCTGAACTCCATCAAGTCCATCATCAGCCTGCTCTTCTTCTG 1990
Db 2037 AGAAACCTGTTGTCT 2096
QY 1991 CT 2050
Db 2097 CT 2156
QY 2051 AACTTCAGAGATGAGACTCCCAACCAACTTCGACACCTTCCCTGCGGCTATCTCTCACT 2110
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QY 2111 GTCTTCCAGATCCTGACGGGAGAGGACTGGAATGCAAGTGTATGATGATGATGATGATGATG 2170
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Qy 2962 -----GCAACAGGATCCGAGCAGGAGTGCGC 2988
Db 3173 GAGGCGCGGCACCGCGAGGCGACGCGCGCGCGCGCGCGGCGGCGGCGGCGGAGGG 3232
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Db 3293 GGACCGCGGAGGAGGACAAGGAGCGGAGGCATCGGAGGAGGAAGAGAACCCAGGGGCTC 3352
Qy 3081 -----ACCGGGC 3087
Db 3353 CGGGGTCTGTGTGGGCCCCAACCTGTCAACACCGCGGCCAATCGAGCAGGACCTGGG 3412
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Qy 3268 CACACTGCCAGCACCTGTCTCCAGAGGCTGGAGGAACAG----- 3307
Db 3593 CCCCAGAACCGCGGACGCGCGGACGCCCAACAAACCGGGGAAACCCATCCANTCCCGG 3652
Qy 3308 ----CCAGAGGATGACACAATACGCGGAACGTCACTCGCATGGGC----- 3349

Db 3653 CCCCCCAAGACCCCGAGAATAGCTTATCGTCACCAACCCGAGCGGACCCAGACCAA 3712
Qy 3350 -----AGTCAGCCCCCAGACCGGA--ACACTATTGTACATATCCAGTGTGCTGAC 3399
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Qy 3400 GGGCCCTCTTGGGGAGCCACGGTGGTCCAGTGGTAACGTGGAC-----CTGGA 3450
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Qy 3571 CTGCCACTACATCGTGACCATGAGGTACTTCGAGGTGGTCAATTCGTGTGTCATCGCTT 3630
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Qy 3691 TCTGAATACTCGATTACATTTTCACTGTGTCTTTACCTTTGAGATGTTGATAAAGAT 3750
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Db 4133 GATTGACTGGGCTCGTCTGTCATCAGGCTGCTACTTCCGTGACCTCTGGAATATCT 4192
Qy 3811 GGAATTCAATTGCTGAGTGGCGCCCTGTTGGTGTGCTTCTCGAGCTTCTGTTGGAGG 3870
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Qy 3931 CCTCAAGACATCAAAACGGCTGCCAAGCTCAAGGCTGTGTTGACTGTGTGTTGAACTC 3990
Db 4304 TCTTAAACCATCAAGCGGCTGCCAAAGCTCAAGGCTGTGTTGACTGTGTGTTGAACTC 4363
Qy 3991 CCTGAAGAAATGCTCTCAACATCTTGAATGTTCTACATGCTCTTCAATGTTATTTGCCG 4050
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Qy 4051 CATTGGGCTGAGCTCTTCAAAGGGAAGTTTTCTACTGCACAGATGAATCCAAAGAGCT 4110
Db 4424 GGTGGCTGTGAGCTCTTCAAAGGGAATTTCTTCCACTGCACCTGACGATCCAAAGATT 4483
Qy 4111 GGAAGAGGACTGAGGGGTCAAGTATTGGATTATGAGAAGGAAAGTGAAGCTCAGCC 4170
Db 4484 TGAGAAAGATTGCGAGGCAAAATACCTCTCTACGAGAAGAAATGAGGTGAAGCGCGAGA 4543
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Db 4604 CTTTCACGTGTCCACGGGGAAGGCTGGCCACAGGCTCTCAAGCATTCGTGGAGCCAC 4663
Qy 4291 CTATGAGGAGCAGGCTCCAGGCCCTGGGTACCGCATGGAGCTGTCCATCTTCTACGTGGT 4350
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Qy 4411 CTTCCAGGACAGGGGACAAAGTGATGTCGTAATCAGCTGGAGAAAGACGAGGGC 4470
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Db 4964 GGCCATGATCGCCCTCAACACCATCTGTCTTATGATGAAGTTCTATGGGGCTTCTGTTC 5023
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Db 7143 CTA 7145
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Matches 4441; Conservative 0; Mismatches 2103; Indels 431; Gaps 26;
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Db 6226 CCAGAACGCCCTCCCTCCACCCAGCTGGACCCAGGAGGAGCCCTGATGGCTCACGAAG 6285
QY 5950 TGGCATCAAGAGTCTGTCTCTGGGCACTCAAGGACCCAGGATGACCCCTAGAGGC 6009
Db 6286 CGGCTTCAAGGAGAGCCCGTCTGGGTGACCCAGCGTCCCAAGGAGATGTTCCAGAAAG 6345
QY 6010 CAGGCCA----CCCCTGGAGCGTGGCACTCCACAGAGATCCCTGTGGGCGGTCAGGAGC 6066
Db 6346 GGGCACAATGGAGTCGGACAGAGCCCGCTTACCGACATGCCAACAGCCGCTTAATCT 6405
QY 6067 ACTGGCTGGAGCTTCAGATCAGAGCATACCCGAGGGGCCCTGATGGGGGCCCA 6126
Db 6406 TCAGTCCGTTGAGATGCGAGAGATGGCAGA---GATGGCTACTCCGACAGCGAGCACTA 6462
QY 6127 GCTGGGCTGGAGAGCAGGCTCGAGCGGCTCCATGCCCGCTTGGCGGCGGAGACTCA 6186
Db 6463 CTCCCCATGGAGGCGAGGCGCGGCTGCTTCCATGCCCGCTTCCCTGCGAGAAACA 6522
QY 6187 GC-----CCGTCACAGATGCCAGCCCAT 6210
Db 6523 GAGGAGAGGGCCGSCACAGTGGGATAACTCAGTACCATCTCAGACACAGGCCCAT 6582
QY 6211 GAAGGCTCCATCTCAAGCTGCGCCAGCGGCGCCGCTGGAGTCACTTTGAGACACAC 6270
Db 6583 GAAGGCTTCAGCTTCGCTGGGCGCCCAAGCGCCGAGCTGAGCAATTAATCGCTGGA 6642
QY 6271 CCGGAGCGCCACCCCTAGCAGGCTCGTCGACCAACACACACCGCTGCCACCG 6330
Db 6643 GGGGTTCGCGCCGAGGAGAACACGGGACCAACAGCGGCGCCGAGCCGAGCCACCG 6702
QY 6331 CCGCAGGACAGGAAGCAGAGTCCCTGGAGAGGGGCCAGCTGTCTGCGGATATGGA 6390
Db 6703 CGCTCTGAGCGCTCCCTGGGCGCTACACCGATGTGGACACAGGCTTTGGGACAGACCT 6762
QY 6391 TGGCGCACCAAGCAGTGTGTGGGCGCGGGCTGCCCGGGAGGGGCGCTACAGGCTG 6450
Db 6763 GAGCATGACCCCAATCCGGGGACCTCGCTCGAAGAGCGGGACCAAGGAGCGGGCGG 6822
QY 6451 CCGGCGGGAACAGAGCGCGGAGGCGGGCGGCTCCAGAGCGGAGCGGAGCGCCCTC 6510
Db 6823 GCCAAGGATCGGAAGCATCGACAGCACCAACACCAACACACACACACATCCCCC 6882
QY 6511 ATCTCTCTCTCGGAGAGCAGCGTTCTATCTCTGACACCGCTTTGGGGCCGCTGAGCC 6570
Db 6883 GCGCCCGACAAAGACCGCTATGCCAGGAAGCGGCGGACACACCGCGGGCAACGGGCTCG 6942
QY 6571 CCCGAAGCCCAAGCCCTCCCTCAGCAGCCACCAACGTCGCGCAACAGCTGGCCAGGAGCC 6630
Db 6943 GGAACAGCGCTGTGTCGCG-----TCGCCAGCGAGGGCCGAGAGCA 6984
QY 6631 GGGACCCCAACCAAGGCGAGTGGTTCCGTAAGTGGGAGCCCTTGTGTCAACATCTGG 6690
Db 6985 CATGGCGCACCGGACGAGGAGTAGTTCCGTAAGTGGAGCCAGCCCGCTCAACATCTGG 7044
QY 6691 TGCTAGCAACCCCGGCGGCTGGGCGGAGGAGCTCCCCCAGACGCGCCCTGACTCCCGG 6750
Db 7045 TACCAGCACTCCGCGGCGGGCGCGCG---CAGCTCCCCCAGACCCCTCCACCCCGG 7101
QY 6751 CCCAGCATCACTCA 6765
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Db 7102 GCCACAGGTGTCCTA 7116
RESULT 14
US-10-322-696-83
; Sequence 83, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322.696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 7291
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-696-83
Query Match 32.7%; Score 2408.4; DB 17; Length 7291;
Best Local Similarity 65.1%; Pred. No. 0;
Matches 3790; Conservative 0; Mismatches 1946; Indels 34; Gaps 13;
QY 4 GCGCGGCTCGCGGCTGGGGCGGGGAGGTCCGCTCCGCTCCCGCGGCTCCCGCGGCTCCGCTGGCT 63
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QY 64 GCTCCGCTCTGAGCGCTCGCGCGCCCGCGGCTCCCTCCCGGGCGGCTGGGGCCGGG 123
Db 326 CGGGCGCGGGGCTCATCGAGCAGCGGCAATCATCAAGGCCACAGGCGCACAG 385
QY 124 ATGACGCGGGGCGGGAGCCATGTCTGCTTCGGGAGCAGAGTGGGCGGCTCGCTATGG 183
Db 386 ATGCA-GAGCACCCCGCGGCGGCGGCAAGGAATGGGAGATGGCTCGCTTCGGGGAGG 444
QY 184 AGCCCCCGGGCGGAGAGCGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 243
Db 445 GTGTGTGCGCAGCGCAGGCTCCGCGATGAGACTCGACAGAGAGGAAACCGGAGG 504
QY 244 TCCCGGGGGCTGACGCGCGGCGGCGGCTCTCTACAAGCAATCGATCGCAGCGCGC 303
Db 505 AACCCCGTCCGCGCTCGGGCAGCGCGCGCTTACAGCAGACGAAAGACAGAGGGC 564
QY 304 GCGGACATGGCGCTGTACACCCCATCCCGGTCAAGCAGAACTGCTTCAACCG 363
Db 565 GCGGACTATGGCTTTGTACAAACCCCATTCGCTCCGCGAGAACTGTTTCAACG 624
QY 364 CTGCTCTTCTGCTTTCAGCGAGGACAACTGCTCGCAAAATAGCGAAGGCTACACCG 423
Db 625 ATCCCTGTTCACTTCGGAGAGATTAACATTGTGAGAAATATGCCAGAGTCAATCGA 684
QY 424 GTGCGCTCCATTCGAGTATATGATCTGGCCACCATCATCGCAACTGCACTGCTGGC 483
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Db 865 GTTCATCTTCCATAAGGGCTTTTACCTCGGCAATGGCTGGAATGTGATGATCTTCACT 924
QY 664 CGTCTCTCACAGGATCTTTGCGCAGCGCTGACTGCTC-----GACCTGG 711
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Db 925 GGTCTCAGTGGGCATCTCGGCCACTGCAGGAACCCACTTCAATACTCACGTGACCTGAG 984
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Qy 772 GCAGTGGTGTCAAGTCCATCATGAAGGCCATGGTTCCACTCTCTGCAGATTTGGGCTGCT 831
Db 1045 GCAGATTTGTGAAGTCCATCATGAAGGCCATGGTTACCTCTTCTGCAGATTTGGCCTTCT 1104
Qy 832 TCTCTTCTTTGGCACTCTCATGTTTGGCATCATTTGGCTGGCTGGATTTCTACATGGSCAAGTT 891
Db 1105 GCTCTTCTTTGGCACTCTCATGTTTGGCATCATTTGGCTGGATTTCTACAGTGGCAAGTT 1164
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Qy 952 CAAGGAGGCCAGCCCGCTGTGCGAGGGGACACTGAGTGCAGGAGTACTGGCCAGG 1011
Db 1219 ---TCACCCCATGTGTGCGAGGCTGCCAGCTGGTTATGAATGCAAGGACTGGATCGG 1275
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Qy 1252 CCGGCTCTTCTGAAGCTGGCCGCGAGCAGCAGATCGAGCGAGCTCAACGGGTACCT 1311
Db 1516 AAGGCTTTTATGAAGTGTGGGCCAGCAGCAGATTTGAGCGTGAATGGCTACCG 1575
Qy 1312 GGAGTGAATCTTAAAGGGGAGGAAGTCACTGTGCGCGAGGAGACAGGAATGCAGAGGA 1371
Db 1576 TGCCTGTGATAGACAAAGCAGAGGAAGTCACTGCTCGCTCAAGAAATTAATAATGC- 1632
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Db 1633 AACATCCGCTTAGAAGTGTCTTCAAGGGCAACCATCAAGAGGAGCCGGACAGAGGCCAT 1692
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Db 1813 GCTTCTGGCATCTCCATTTGCCACATGGTTTAAATCCCAAGTGTTTTACTGGATTTGCT 1872
Qy 1612 GTGGTGGTGGCCCTGAACACACTGTGTGTGGCCATGGTGCATTAACAACAGCCCGCGCG 1671
Db 1873 GAGCTTTGTGGCACTCAACACTGCTGTGTGGCCATTTGTCCATCACAAACAGCCCAAGT 1932
Qy 1672 GCTTACCAACGACCTGTATTTTGCAGAGTTTGTGTTTCTGCGGTCTCTTCTCAAGAGAT 1731
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Qy 1732 GTCCCTGAAGTGTATGGCTGGGGCCAGAGTACTTCCGCTCTCTTCACTGCTT 1791
Db 1993 GTCCCTGAAGATGTATGGCATGGGGCCCTCGCCCTTTATTTTCACTCTTCAATTCACCTGCTT 2052

Qy 1792 CGACTTTTGGGGTCATCGTGGGGAGCGCTCTTTGAAGTGGTCTGGGGCGGCCATCAAGCCGGG 1851
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Qy 1852 AAGCTCTTTTGGGATCAGTGTGCTGGGGCCCTCCGCTGCTGAGGATCTTCAAAGTCA 1911
Db 2113 TAGCTCTTTTGGAAATCAGTGTCTTGGAGCCCTCCGGCTTCTAAGAAATATTTAAATAAC 2172
Qy 1912 GAAGTACTGAGCTCCCTGCGAAACCTGGTGGTGTCCCTGCTGAACTCCATGAAGTCCAT 1971
Db 2173 CAGATATTTGGCTTCCCTACGGAAATTTGGTGGTCTCTTGTATGAGCTCAATGAATCTAT 2232
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Db 2233 CATCAGTTTGTCTTCT 2292
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Qy 2092 CCCTGCGCCCATCTCTCACTGTCTTCCAGATCTCTGACGGGAGGAGACTTGAATTCAGTGTAT 2151
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Qy 2212 CATGTCTGTGACTGTTTGGAAACTTACACTCTGCTGTAATGTCTTTCGGCCATCCGTGT 2271
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3118 CCAACGGCGC--AGCGGCGATCGCGGTGACGACAGAGGCAAGGAGTCTTTCAGC 3174
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4422 AATTTCACTACGACAACATTTATCTGGGCCCTGTGACCTCTTTCACGCTCTCCACAGGG 4481
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Db 5382 GCCTTGGGAGAGGGCTGTGAGCTGACACCGGCACCATCAGGGGAGAACGAGAACG 5441
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RESULT 15
US-10-375-253-37
; Sequence 37, Application US/10375253
; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10/375,253
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751

; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
; PRIOR FILING DATE: 1993-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 7032
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)...(6921)
; OTHER INFORMATION: standard name = Alpha-1B-1
US-10-375-253-37

Query Match 32.6%; Score 2402.4; DB 16; Length 7032;
Best Local Similarity 65.9%; Pred. No. 0;
Matches 3710; Conservative 0; Mismatches 1841; Indels 83; Gaps 12;
Qy 190 CGCGCGGAGAGCGGGCCCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 249
Db 192 CGCGCGGAGAGCGGGCCCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 251
Qy 250 GGGGCTGCGAGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 309
Db 252 CGTGGCGGGCTCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 311
Qy 310 CATGGGCGCTCAACACCCCATCCCGGTCAAGCAGAGAACTGCTTCAACGCTCAACGCTCG 369
Db 312 TATGGCTTTGTACACCCCATTCCTGCGCGAGAACTGTTTCAACGCTCAACGATCCCT 371
Qy 370 CTTTCGTCTTCAGCGAGGACAAAGCTGCTCGCAAAATACGCAAGCGCATCACCGAGTG 429
Db 372 GTTCATCTTCGAGAGAGATAACATTGTGAGGAAATATGCCAAGAGCTCATGATTGGCC 431
Qy 430 TCATTTCGAGTATATGATCTCTGGCGACCATCATCGCAACTGATCGTGTGCGCCCTGGA 489
Db 432 GCCATTGTAGTATGATCTCTGGCGACCATCATTTGCCAACTGATCGTCTGCGCCCTGGA 491
Qy 490 GCAGCAGCTCCCTGATGGGGGACAAAGCGCCCATGTCGAGCGGCTGCACGACGAGGCC 549
Db 492 GCAGCATCTTCCTGAGAGATGACAGACCCCATGTCCGAGAGACTGGAGAGACAGAAC 551
Qy 550 CTATTTTCATCGGATCTTTTGTCTTCGAGGCGAGGATCAAAATCATCGCTCTGGGCTTTGT 609
Db 552 TTATTTTCATTTGGATCTTTTGTCTTTGAAGCTGGGATCAAAATTTGTGCGCTGGGTT 611
Qy 610 CTTTCCAGAGGCTCTTATCTCTGGGAAAGCGCTGGAAAGCTCATGGAATCTGCTGTGCT 669
Db 612 CTTTCCATAGGCTCTTATCTCTGGCAATGGCTGGAATGTCTGGAATCTCATGCTGTGCT 671
Qy 670 CACAGGAGCTCTTGGCCACCGGCTGGAATGACTTTC-----GACCTGCGAACT 717
Db 672 CAGTGGCATCTCTGGCCACTGACAGAACCCACTTCAATATCTACGTGAGCTGAGGACCT 731
Qy 718 GAGGCTGTGCTGTGCTGAGGCGCCCTGAAAGCTGGTGTCTGGGATTCCAAAGTTTGAGGT 777
Db 732 CCGGCTGTGCTGTCTCTGGGCTTTTGAAGCTCGTGTGAGGATACCTAGCTGCGAGAT 791
Qy 778 GGTGCTCAAGTCCATCATGAAAGCCCATGGTTCCACTCTCTGAGATTTGGGCTGCTTCT 837
Db 792 TGTGTTGAAGTCCATCATGAAAGCCCATGGTACCTCTTCTGCAATTTGGCTTCTGCTCT 851
Qy 838 CTTTGGCATCTCTGCTGCTGAGGCGCCCTGAGGTTTCTACATGGGCAAGTTTCCACAA 897
Db 852 CTTTGGCATCTCTGCTGCTGAGGTTTCTACATGGGCAAGTTTACATCG 911

QY	998	GGCCTGTTTCCCAACACGACAGATGCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGA	957
Db	912	AGCGTGTCTTATGAACCAATTCAGGTATTCTAGAAGGATTTGACCCCC-----TCA	962
QY	958	GGCCCCAGCCCGGTGTGCGAGGGCGACACTAGTGC GGGAGTACTTGGCCAGGACCCAA	1017
Db	963	CCCATGTGGTGTGAGGGCTCCCGACGTGGTTATGAATGCAGAGACTGGATCGGCCCCAA	1022
QY	1018	CTTTGGCATCAACCACTTTGACAATATCTCTTTTGCCATCTTGTACGGTGTTCAGTGCAT	1077
Db	1023	TGATGGGATCACCCAGTTTGATAACATCTTTTGGCTGTGCTGACTGTCTTCAGTGCAT	1082
QY	1078	CACCATGGAGGGCTGGACTGACATCTCTCTATATAATACAAACGATCGGCGCGCAACACTG	1137
Db	1083	CACCATGGAGGGTGGACCACTGTGCTGTGTACAAATACCAATGATGCCTTAGGAGCCACTG	1142
QY	1138	GAACTGCTCTACTTTCATCTCCCTCTCATCATCATCGGCTCTCTTCTCATGCTCAACCTGGT	1197
Db	1143	GAATTGCTGTACTTTCATCTCCCTCTCATCATCTTGGATCTCTTCTTCTTCTCAACCTTAGT	1202
QY	1198	GCTGGGGTGTCTCTCGGGGGAGTTTGGCAAGGACGAGAGAGGGGTGAGAAACCGCCGCGC	1257
Db	1203	CTTGGGAGTGTCTTTCGGGGAAATTGGCAAGAGAGAGAGAGTGGAGAACCGAAGGGC	1262
QY	1258	CTTCTGAAGTGTGCGCGGACGACGAGATCGAGCGAGAGTCAACGGGTACTCTGGAGTG	1317
Db	1263	TTTTCATGAAGTGTGCGCGCCAGCAGCAGATTGAGCGTGAGCTGAATGGCTACCGTGCGTG	1322
QY	1318	GATCTTCAAGCGGAGGAAGTCACTGTGCGCGGAGGAGGACAGGAATCGCAGGAGAGATC	1377
Db	1323	GATAGACAAAGCAGAGGAAGTCACTGCTGCTGAAGAAAAATAAAATGC---TCGAAACATC	1379
QY	1378	CCCTTTGGACGTGTCTGAAGAGAGCGGCCCAACAAAGAGACAGAAAAATGACCTGATCCACGC	1437
Db	1380	CGCCTTAGAAGTGTCTCGAAGGGCAACCATCAAGAGAGCGGACAGAGGCCATGACTCG	1439
QY	1438	AGAGGAGGAGAGACCGGTTTGAGATCTCTGTGCTGTGGATCCCTTCGCCCGCGCGC	1497
Db	1440	AGACTCCAGTGTATGACACTGTGTGTGATATCTCTCTGTGGGCACACTCTGTGCCCGAGC	1499
QY	1498	CAGCTCAAGCGGGAAGACAGAGACTCGTCACTATCTTCGGAGGACAGAGAAGATGTT	1557
Db	1500	CAGTATCAAAAGTGCAAAGGTAGA CCGGGTCTCTTATTTCCGGGCACAAAGAAAGGCTTCT	1559
QY	1558	CCGGTTTTTATCCGGCGCATGTGTGAAGGCTCAGAGCTTCTACTGGGTGGTGTCTGTGCGT	1617
Db	1560	GCGCATCTCCATTGCGCACATGTTAAATCCAGAGTGTTTTACTGGATTTGTCTGAGCCT	1619
QY	1618	GGTGGCCCTGAAACACTGTGTGTGGCCATGGTGTGCAATTAACACGACCGCGCGGCTTAC	1677
Db	1620	TGTGGCACTCAACACTGCTGTGTGGCCATTGTCCATCAACACGACCCCGAGTGGCTCAC	1679
QY	1678	CACGACCTTGATTTTTCAGAGTTTGTTCCTGGGTCTCTTCTCTCACAGAGATGTCCT	1737
Db	1680	CCACCTCTCTACTATGACAGAAATTTCTGTCTTCTGGGACTCTTCTCTCTGGAGATGTCCCT	1739
QY	1738	GAAGATGTATGGCTCGGGGCCAGAAAGTACTTCCGGTCTCTCTCAACTGCTTCGACTT	1797
Db	1740	GAAGATGTATGGCATATGGGGCTCGCCTTTATTTTCACTCTTCAATCAACTGCTTTGATTT	1799
QY	1798	TGGGGTCATCTGTGGGAGCGGTCTTTGAAGTGGTCTGGGGGGCCATCAAGCCGGGAAGCTC	1857
Db	1800	TGGGGTCACAGTGGGCAGTATCTTTGAAGTGGTCTGGGCAATCTTCAGACCTGGTACGTC	1859
QY	1858	CTTTGGGATCAGTGTCTGTGGGGCCCTCGCGCTGTGTGAGGATCTTCAAAAGTCAACGAATG	1917
Db	1860	TTTGTGAATCAGTGTCTTGGAGCCCTCGCGCTTCTTAAGAAATATTTAAATAATACCAAGTA	1919
QY	1918	CTGGAGCTCCCTCGGAACTGTGTGTGTCCTGTCTGAACTCCATGAAGTCCATCATCAG	1977
Db	1920	TTGGGCTTCCCTACGGAAATTTGGTGGTCTCTCTGTGATGAGCTCAATGAGTCTATCATCAG	1979

QY	1978	CCTGCTCTTTCGTCTCTTCTCTGTTTCATTTGTGGTCTTCGCGCTCTCTGGGGATGCAGCTGTT	203
Db	1980	TTTGTCTTTTCCCTCTCTCTCTCTCACTCGTGTGCTTGTCTCTCTAGGAATGCAGTATT	2039
QY	2038	TGGGGGACAGTTCAACTTCCAGGATGAGATCCCAAAACCAACTTTCAGACCTTCCCTGC	2097
Db	2040	TGGAGGCAAGGTTTAACTTTTAAATGATGGGACTCTCTTCGGCAAAATTTTGATACCTTCCCTGC	2099
QY	2098	CGCCATCCTCACTCTTTCAGATCTCTGACGGGAGGAGCTTGAATTCGAGTGTATATCA	2157
Db	2100	AGCCATCATGACTGTGTTCCAGATCTCTGACGGGTGAGCACTGGANATGAGTGATGACAA	2159
QY	2158	CGGGATCGAATTCGCAAGCGCGGTTCAGCAAGGATGTTTCTGTCCTTTTACTTCAATTGT	2217
Db	2160	TGGGATCCGCTCCACGGGTGGGTTCAGTCAGGCATGTGTGCTGTGCCATCTACTTCAATTGT	2219
QY	2218	CCTGACACTGTTTCGGAACTTACACTCTGCTGTAATGTTCTTTCTGGCCATCGCTGTGACAA	2277
Db	2220	GCTCACCTTGTTTGGCAACTACACGCTACTGAAATGTTCTTTGGCTATCGCTGTGGATAA	2279
QY	2278	CCTGGCCAAAGCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGAGCAGCCAAATCA	2337
Db	2280	TCTCGCCCAAAGCCCAAGGAACTGACCAAGGATGAACAGGAGGAAGAAGAGGCTTTCAAACA	2339
QY	2338	GAAGCTTGTCTCTGCAAAAGGCCAAAGAGTGGCTGAAAGTCAGCCCATGTCTGCGCGGAA	2397
Db	2340	GAACAATGCACTGCAGAAGGCCAA-----GGAGGTTCAGCCGATGTCTTGCAACCAA	2399
QY	2398	CATCTCCATCGCGCCAGGACGAGCAACTCGGCCAAGGCGCGCTCGGTGTGGAGCAGCG	2457
Db	2391	CATGCCCTTCGATCGAGAGGAGCGGAGGCGCGGCCACCAATGTCGTGTGGAGCAGCG	2459
QY	2458	GGCCAGCAGCTACGGCTGCAGAACTTCGGGGCAGCTCGCAGGGCGCTGTACAGCGAGAT	2517
Db	2451	TACCAGCCAGCTGAGGAGCAATGCAGATGTCCAGCCAGGAGGCCCTCAAACAGAGAGA	2519
QY	2518	GGACCCCGAGGAGCGGTGCGCTTCGCCACTACGCGCCACCTTCGCGGCCCGACATGAAGAC	2577
Db	2511	GGCGCCGACCATGAACCCGCTCAACCCC-----CTCAACCCGCTCAGCTCTCTCAACCC	2564
QY	2578	GCACCTGGACCGGCGCGTGTGTGTGAGCTTGGGCGCGGACGGCGCGCGGGGCGCGTGG	2637
Db	2565	GCTCAATGCCCACCCACCGCTTTATCGCGGACCCACAGGCCATTGAGGGCTTCGCGCTGG	2624
QY	2638	AGGCAAAAGCCGACCTGAGGCTGCGGAGGCCCGCGAGGGCGTTCGACCTTCGCGCAGCA	2697
Db	2625	CCTGGCCCTGGAGAAATTTCAGAGAGAGGCGCATCAGCCGTGGGGGTCTCTCAAGGGGA	2684
QY	2698	CCAACCGGCACCGGCAAGGACAAAGACCCCGCGCGGGGACCAGGACCTCAGCAGAGGC	2757
Db	2685	TGGAGGGACCGGATCAGTGCCTCTGACAAACAGAGGACCCCTTTGTCTCTTCGCGCCAGCG	2744
QY	2758	CCCGAAGGCGGACGCGGGAGCCCGGTGCCCGGAGGAGCGGCGCGCGGCTGCACCGGAG	2817
Db	2745	GGAGCCACCATGCTGCGCGAGGCCCTGTCTATGGAACTGTGACCCGCACTCAGCAGGAGGC	2804
QY	2818	CCACAGCAAGGAGCGCGCGGCGCCCGAGAGCGGAGCGAGCGCGGCGCGAGGCCGAGG	2877
Db	2805	AGGGGAGGAGAGGCTGTGTGACCTTTTGAAGACCGGCGCAGGCAAGGCAAGGCGAAG	2864
QY	2878	CCCGAGGGCGGCGCGGCAACACCGGCGCGGCTCCCGGAGGAGGGGGTCGAGCGGGA	2937
Db	2865	GCGC--AGCGGCACTCGCGGTTCAGGACAGAAAGCAAGGATCTCTTTAGCTCTCCG	2921
QY	2938	GCCCCAGCGCACCGCGCGCAACCGGACACAGGATCCGAGCAAGGAGTGCCTCGCGCGCAA	2997
Db	2922	GAGCAGGTCTTCGACGACAGAAACCGAGTCTGGATGAAGCCATGCCCCACTGTAAGGGGAGAA	2981
QY	2998	GGCGAGCGCGCGCGCGCACCGCGGGGCGCCCCGAGCGGGGCCCCGGGAGGCG-GAGA	3056
Db	2982	GGACCATGAGCTCAGGGGCAACCATGTTGCCAAGGAGCCACGATCCCAAGAGAGAGAGC	3041
QY	3057	CGCGGGAGGAGCGCGCGCGGCAACCGGCGCCCGGCAACAAGCGCGAGCTCTCTACGAGG	3116

Db	3042	CCAGGATTTAAGGAGGACCAACAGTCTGATGGTGTCCAGAGGCTCCGGGTGCGCAGGAGG	3101
Qy	3117	CTGTGGAGAAAGGAGACCAACGAGAGGAGGAGCCACGGAGAAAGGAGGCTTGAGATAGTGTGAAG	3176
Db	3102	CCTTGTATGAGGCTGACACCCCTTAGTCTTGCCC-----CATCCTTGAGCTGGAGTGG	3154
Qy	3177	CCGACAAAGGAAAGGAGCTCCGGAACCAACAGAGCCCGGGAGCCACACTGTGACCTGTGAGA	3236
Db	3155	GGAAGCAGCTGGTGTCTGACGAGCAGGAGCCAGAAAGCAGCAGTGTAGCAGGCCCCCTGCTGG	3214
Qy	3237	CCAGTGGGAGCTGTGACTGTGGTCCCATGCACACACTGCCAGCACCTGTCTCCAGAAAG	3296
Db	3215	GGAATGTGCAGCTTAGACATGGCCCGGGTCAATCAGCCAGAGCGAGCTCTCTCTGTGCA	3274
Qy	3297	TGGAGGAACAGCCAGAGGATGCAGACAATCAGCGGAAACGTCACTCGCATGGGAGTCAAGC	3356
Db	3275	TCACGGCCAAACAGGACACAGGCCACACAGAGAGCACAGGCTCACCGTCGCCA-----	3328
Qy	3357	CCCAGACCCGGAACAATAATTGTACATATCCAGTGTACTGTAGCGGGCCCTCTTTGGGGAAG	3416
Db	3329	TCCCCGACGTGGACCCCTTGTGTGACTCAACCGTGTGTGCAATTAGCAACAAGACGGATG	3388
Qy	3417	CCACGGTCTGTTCCAGTGGTAAAGCTGTGAACCTGTGNAACCAAGCAGAGGGGAGAAAGAGG	3476
Db	3389	GGGAAGCCAGTCCCTTGAAGGAGGACAGATCAAGAGAGATGAGAGGAGGTGGAGAAGA	3448
Qy	3477	TGGAAGCGGATGAGCTGATGAGGAGCGGCCCGCGCTATCTGCTCCCATACAGCTCCCATGT	3536
Db	3449	AGAAGCAGAAAGGAGAGAGCTGTAGACAGGCAAGCCATGTGTGCCCCACAGCTCAATGT	3508
Qy	3537	TCTGTTTAAAGCCCAACAACTGTCCGCGCTTTCTGCCATCACTCGTGACCATGAGGT	3596
Db	3509	TCATCTTTCAGCACACCAACCGATCCGAGGGGCTGCCACTACATGTTGAACCTGCGCT	3568
Qy	3597	ACTTCGAGGTGGTCAATCTCGTGTGTATCGCTTGACAGAGATCGCCCTGGCTGCTGAGG	3656
Db	3569	ACTTTGAGATGTGCATCTCTCGTGTATGTCAGCAGCAGCATGCCCCTGGCGCAGAGG	3628
Qy	3657	ACCAGTGGCCACAGACTCGCCACGGAACAACGCTCTGAAATACCTGGATTAACATTTTCA	3716
Db	3629	ACCCGCTCTGACCAACTCGAGCGCAACAAAGTCTTGAGGTATTTTGACTATGTGTTCA	3688
Qy	3717	CTGGTGTCTTTACCTTTTGAGATGGTGATAAGATGTACGACTTTGGGACTGCTGCTTCACC	3776
Db	3689	CGGCGGTGTTCACTTTTGAGATGGTATATAAGATGTATAGACCAAGGCTTGATCCTGCAGG	3748
Qy	3777	CTGAGAGCCTATTTCCGGGACTTTGTGGAACATTTCTGGACTTCAATTGTGTTGTCAGTGGCGCCC	3836
Db	3749	ATGGGTCTCTACTTCCGAGACTTTGTGGAACATCTCTGGACTTTGTGTGTGCTGTTGGCGCAT	3808
Qy	3837	TGTTGGGCTTTGCTTCTTCGAGCTTCTGTGGAGGATCCAAAGGGAAGACATCAATACCA	3896
Db	3809	TGTTGGGCTTTGCTCTCGGCAACCTTTGGGAACCAACAAAGGACGGGACATCAAGACCA	3868
Qy	3897	TCAAGTCTCTGAGAGTCTTCTGTCCTCGGGGCCCTCAAGACCATCAAAACGGCTGCCCCA	3956
Db	3869	TCAAGTCTCTGCGGTGCTCCGAGTTCTAAGGCCACTGAAACCAATCAAGGCTTGCCCCA	3928
Qy	3957	AGCTCAAGGCTGTGTTGTGACTGTGTGTGGAATCTCCCTGGAAGAAATGCTCTCAACATCTTGA	4016
Db	3929	AGCTCAAGGCGCTTTCGACTGCGTAGTGACCTCTTGGAAGAAATGCTTCAACATACTCA	3988
Qy	4017	TTGCTCTACATGCTCTTCATGTTCTATATTTGCCGTCAATTGCGGTGCAGCTCTTCAAGGGA	4076
Db	3989	TTGTGTCAAGCTCTTCATGTTCTATCTTTGCTGTCTATCGCAGTTCAGCTCTTCAAGGGA	4048
Qy	4077	AGTTTTTCTACTGCACAGATGAATCCAAAGAGCTGGAGAGGAGCTGCAGGGGTCAAGTATT	4136
Db	4049	AGTTCTTTTATTTGACCGGACAGTTCCAAAGACACAGAGAAAGGAGTGCATAGGCACATATG	4108
Qy	4137	TGGAATTATGAAAGGAGGAAGTGGAACTCAGCCCGAGGAGTGGAAAGAAATACGACTTTC	4196

4109	DB	TAGATCA	CAGAAAAA	ACAAGATG	AGGCGCGG	GAATGGA	AGCGCCATGA	ATTTC	4166	
4197	QY	ACTACGA	CAATATG	CTCTGGG	CTCTG	CTGACG	CTGTGTTAC	AGTGTCCA	CGGAGAAAGCCT	4256
4169	DB	ACTACGA	CAACAAT	TATCTGG	GCCTG	CTGAC	CCCTTTC	ACCGTCTC	CACAGGGAAGGAT	4228
4257	QY	GGCCCAT	TGGTGTGA	AAACAT	CTCCGT	TGGATGCC	ACCTTATG	AGGACAGGGT	CTCAAGCCCTG	4316
4229	DB	GGCCTCA	AGTTCTG	CAACACT	CTGTG	ATAGTGA	CAGAGGA	AGACCCG	AGGCGCCAAAGCCGCA	4288
4317	QY	GGTACCG	CATGGAG	CTGTCC	ATCTTAC	GTGGTGT	TACTTTT	TGGTCTTT	TCCCTCTTCTTCT	4376
4289	DB	GCAACCG	CATGGAG	ATGTCT	ATCTTTAT	TGTAGT	TACTATTTT	TGGTCTTT	TCCCTCTTCTTCT	4348
4377	QY	TCGTCAA	CATCTTT	TGTGGCTT	TGATCAT	ATCATCA	CTTTC	CAGGACAGG	GGGCAAGGTGA	4436
4349	DB	TTGTCAAT	ATCTTTG	TGGCTCT	CATCAT	CATCACTT	C	CAGGACAGG	GGGTAAGATGA	4408
4437	QY	TGCTGA	ATCGAGC	CTTGGA	AGAAACG	AGAGGCTT	GCATTG	ATTCGCC	ATCAGCGCCA	4496
4409	DB	TGGAGG	AGTGCAG	CTTGAG	GAAGAA	TGAGAGG	CGTGCAT	CGACTT	TCGCCATCAGCGCCA	4468
4497	QY	AACCC	CTGACAC	CGGTAC	ATCCCA	AAACGG	CAGTCTG	TTC	CAAGTATAAGACGTGGACAT	4556
4469	DB	AACCT	CTCA	CCCGCTAC	ATCCG	CAGAAC	CACACCTT	TTC	CAAGTACCGCGTGTGGCACT	4528
4557	QY	TTTGGT	CTCTCC	CGCCCTTT	TGAATACT	TTCA	TCAATG	GCATGAG	CCCTCAACACATGTGTG	4616
4529	DB	TTTGGT	GTCTCG	TCTCTTT	TGATAC	CACCA	TATATG	GCATGAT	CGCTTGAATCTGTTG	4588
4617	QY	TGCTGAT	GTGAAG	TCTAT	TGATG	TCAC	CCCTAT	TGATG	CTGAATGCTCTGA	4676
4589	DB	TGCTGAT	GTGAAG	TATTA	TTCTG	CTCC	TGTAC	CTATG	AGCTTGGCCCTGAAATGTA	4648
4677	QY	ACATCG	TGTTCA	CATCC	ATGTTT	CCATG	GAATGCG	TGTG	AGATCATCGCCTTTGGGG	4736
4649	DB	ATATCG	CCCTTCA	CAATGG	TGTTT	TCC	CTGGAATGT	CTC	TGAAGGTCA	4708
4737	QY	TGCTGAA	CTATTT	CAGAGAT	GCCTT	GGAATG	CTCTT	TGACTTT	TGTCACTGTGTGGGAAGTA	4796
4709	DB	TTTTTGA	CTATTT	CCGAGAC	CACCTG	GNATAT	CTTTG	ACTT	CATCA	4768
4797	QY	TTACTG	ATATTT	TAGTA	CAGAGAT	TGCG	GAACGAA	CAATTT	CACTCA	4853
4769	DB	TCACAG	AAATTA	TCTCT	GACAGAC	GACG	CTGCTG	TAACAC	CAGTGGCTTCAATATGAGCT	4828
4854	QY	TCCTCCG	CCCTTT	TCGAG	CTGCG	GGCTGAT	CAAGTGT	CTCCG	CAGGGCTACACCATCC	4913
4829	DB	TTCTGAA	GTCTTT	CCGAGCT	TGCCG	GCCTCA	TAAAGCT	CTCTG	CGTCAAGGGCTATACCATAC	4888
4914	QY	GCATCTG	CTGTG	GAACCTTT	TGTC	ACGTC	TTCAAG	GCCTT	CAGCTGTGTCTGCTCA	4973
4889	DB	GCAATTT	TGCTGTG	AGACCTTT	TGTG	AGTCTC	TTTAA	GGCCCTCC	CTTATGTCTGCTCTTTAA	4948
4974	QY	TTGCCAT	GTCTGTT	CTTCA	TCTAC	CGCCAT	CATCG	GCATG	CTGAGTGTGTGGAAATATTGCC	5033
4949	DB	TTGCCAT	GTCTTT	CTTCA	TCTTAT	TGCC	CATCAT	TGGGAT	TGCAAGTATTTGGAAACATAAAAT	5008
5034	QY	TGGAATG	ATGAC	CACG	AGATCA	ACCG	CAACAA	CACTT	TCGGAGCTTTTTTTCGAGGCCCTGA	5093
5009	DB	TAGACG	AGGAGAGT	CTCAT	CAAC	CGGCAC	AAACACTT	TC	CGGAGTCTTTTGGGGTCCCTAA	5068
5094	QY	TGCTGCT	GTTC	CAGAGCG	CAACG	GGGAGCC	TGGCA	CGAGAT	CATGCTGTCTCTGCTGTA	5153
5069	DB	TGCTACT	CTTTC	CAGAGTG	CCAC	AGGTG	AGGCC	TGG	CAGGAGATTTGCTGTCA	5128
5154	QY	GCAAC	CAGGCGCTGT	GATG	AGCAG	CGCAAT	TGCC	ACCGAG	-----T	5192
5129	DB	GGGAG	AGGGCTGT	GAGC	CTTGAC	CA	CCACCG	CACCAT	CAGGCGACGAGATG	5188
5193	QY	GTGGA	AGTGA	CTTTG	CTACTT	CTG	CTCTT	CA	CTTCTCTGCTGCTCTTCTGTA	5252
5189	DB	GCAGCA	CCGATCT	TGGCC	CTAG	CTGATCTT	TGCTCT	CTTCA	CTTCTCTGCTCTCTTCTGTA	5248

QY	5253	TGTTGAACCTCTTTTGTGGCTGTGATCATGGACAATTTTGAGTACCTCACGCGGACTCTT	5312
Db	5249	TGCTCAACCTGTTTGTGGCGTTCATCATGGACAACCTTGAGTACCTGACTCGGGACTCT	5308
QY	5313	CNATCCTAGGTCTCAACCACTTGGATGAGTTTCATCCGGGTCTGGGTGAATACGACCCGG	5372
Db	5309	CCATCCTGGGGCTCAACCACTTGGACGAGTTTGTCCGCGTCTGGGCAGAATATGACCGAG	5368
QY	5373	CTGCGTGTGGGCGCATCAGTTACAATGACATGTTTGAGATGCTGAAACACATGTCCCGC	5432
Db	5369	CAGCATGTGGCGCATCCATTCATCTGAGATGATGAATGCTGACTCTCATGTACCTC	5428
QY	5433	CTCTGGGGCTGGGGAAGAAATGCCCTGCTCGAGTTGCTTACAAGGCGCCTGGTTGCAATGA	5492
Db	5429	CGCTAGGCCCTGGCAAGAGATGTCCCTCCAAAGTGGCATATAAGAGTTGGTCTGATGA	5488
QY	5493	ACATGCCCATCTCCACAGGAGATGACTGTTTCACTTCAAGTCCAGGTGATGGCCCTCA	5552
Db	5489	ACATGCCAGTAGC---TGAGGACATGACGCTCCACTTCACTCCACACTTATGGCTCTGA	5545
QY	5553	TCCGACGGCACTGGGAGATCAAGCTGGGCCCCAGCTGGGACAAAGCAGCATCAGTGTGACG	5612
Db	5546	TCCGACAGCTCTGGACATTAAATTGCCAAAGGTGGTGACACAGGCAGCAGCTAGACT	5605
QY	5613	CGGAGTTGAGGAAGGAGATTTCCGTTGTGTGGGCCAAATCTGCCCCAGAAGACTTTGGACT	5672
Db	5606	CAGAGCTACAAAGGAGACCTTAGCCATCTGSCCTCACCTATCCCAGAAGATGCTGGATC	5665
QY	5673	TGCTGGTACCCACCCCATAGCCTGATGATGACAGTGGGGAAGGTTTATGCAGCTCTGA	5732
Db	5666	TGCTTGTGCCCATGCCCAAGGCTCTGACCTGACTGTGGGCAAAATCTATGCAGCAATGA	5725
QY	5733	TGATATTTGACTTCTACAGCAGAACAAACCAACAGAGACCAGATGCAGCAGG	5786
Db	5726	TGATCATGACTACTATATAAGCAGATAGGTGAAGAGCAGGAGCAGCAGCTGG	5779

Search completed: September 27, 2004, 07:05:53
Job time : 2214 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2004, 15:36:42 ; Search time 11188 Seconds
(without alignments)
19687.473 Million cell updates/sec

Title: US-10-033-026-3
Perfect score: 7376
Sequence: 1 gggcgccgcgtcgcgggt.....tgcttgagtacgtaccgc 7376

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gsl:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1987.6	26.9	6813	29	AY406056 Homo sapi
2	1940.8	26.3	6822	29	AY406058 Mus muscu
3	1787	24.2	6675	29	AY406057 Pan trogl
4	1128	15.3	2617	11	AK081230 Mus muscu

5	692	9.4	735	12	BG472603
6	666.4	9.0	802	14	CK000994
7	663	9.0	6035	11	BC051413
8	633.4	8.6	4058	11	AK039991 Mus muscu
9	628.4	8.5	848	14	CF182756 UI-M-EYO-
10	625	8.5	807	14	CF743150 UI-M-GVO-
11	624.8	8.5	815	14	CD804209 UI-M-GVO-
12	623	8.4	636	11	BC043482 Mus muscu
13	605	8.2	795	14	CB521867 UI-M-GHO-
14	597.6	8.1	754	14	CF537761 UI-M-GHO-
15	570.6	7.7	756	14	CB518919 UI-M-GHO-
16	569.8	7.7	696	10	BE266069 601190737
17	557.2	7.6	683	12	BM941798 UI-M-CGOp
18	538	7.3	654	14	CA324977 UI-M-FYO-
19	528.6	7.2	942	12	B1905728 603169205
20	525.4	7.1	872	13	BU364873 603586745
21	514.2	7.0	690	14	CF538264 UI-M-GHO-
22	509.8	6.9	610	14	CF533828 UI-M-GHO-
23	506.2	6.9	957	13	BQ886304 AGENCOURT
24	504.6	6.8	747	14	CF743227 UI-M-GVO-
25	504.2	6.8	600	14	CF534054 UI-M-GHO-
26	500	6.8	645	14	CF518720 UI-M-GHO-
27	500	6.8	657	10	BB621795 BB621795
28	494.6	6.7	958	13	BQ882047 AGENCOURT
29	492.2	6.7	608	14	CB580917 AMGNNUC.N
30	491	6.7	705	13	BU056303 UI-M-FOO-
31	489	6.6	711	13	BY728171 BY728171
32	473.8	6.4	811	14	CA318259 UI-M-FWO-
33	466.4	6.3	1150	11	AK052625 Mus muscu
34	464.8	6.3	684	14	CB520731 UI-M-GIO-
35	462.2	6.3	646	13	BQ444257 UI-M-EXO-
36	461	6.2	613	14	CF537036 UI-M-FYO-
37	452.6	6.1	2560	11	AK044695 Mus muscu
38	444	6.0	645	14	CB576173 AMGNNUC.C
39	443.4	6.0	658	14	CF739159 UI-M-HDO-
40	443	6.0	524	10	BE234696 141896 MA
41	427.8	5.8	438	9	AA776162 ae80b04.8
42	424.8	5.8	649	14	CD762997 GGE2SM103
43	417.2	5.7	1012	12	BG820937 602780845
44	416.4	5.6	853	9	AU169553 AU169553
45	415.8	5.6	877	13	BU367254 603584475

ALIGNMENTS

RESULT 1	AY406056	6813 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	Homo sapiens CACNA1E gene, VIRTUAL TRANSCRIPT, partial sequence,				
DEFINITION	genomic survey sequence.				
ACCESSION	AY406056				
VERSION	AY406056.1	GI:39762030			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 6813)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 6813)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				

QY 2098 GGCATCCTCACTGCTTCCAGATCCTGACGGGAGAGACTGGAATCGAGTGATGATCA 2157
Db 1935 AGCCATCATGACTGTGTTCAGATCCTGACCGGTGAGGACTGGAAATGAGGTGATCAAA 1994
QY 2158 CGGGATCGAATCGCAAGCGCGGTGACAAAGGATGTTCTCGTCTTTTACTTTCATTGT 2217
Db 1995 TGGATTCGGCTCCAGGGTGGGTCACTCAGGATGTGTCTGCCATCTACTTTCATTGT 2054
QY 2218 CTTGACACTGTTCCGAAACTACACTGCTGCTGAATGTTCTTTGSCCATCGCTGTGGCAA 2277
Db 2055 GCTCACCTTGTGGAACATACACGCTACTGAAATGTTCTTGGCTATCGCTGTGGATAA 2114
QY 2278 CTTGGCCAAAGCCCAAGAGCTGACCAAGGATGAAGAGAGATGGAAGAACAGCCCAATCA 2337
Db 2115 TCTGCCAAAGCCCAAGAGCTGACCAAGGATGAAGAGAGAGAGAGCCCTTCAACCA 2174
QY 2338 GAAGCTTGTCTGCAAAAGGCCAAAGAGTGGCTGAAAGTCAAGCCCATGCTGTGCGCGAA 2397
Db 2175 GAAACATGCACTGCAGAAAGGCCAAGGAG-----GTACGCCGATGTTCTGCACCCAA 2225
QY 2398 CATCTCCATCGCCCGCAGGACGACAGAACTCGGCCAAGCGCGCTTCGGTGTGGAGCAGCG 2457
Db 2226 CATGCTTCGATCGAAAGAGACAGAAAGAGACACCAATGTCGATGTGGAGCCACG 2285
QY 2458 GCGCAGCCAGCTACGGCTGAGAAACCTGCGGGCCAGC-----TGCAGGCGCTGTA 2508
Db 2286 CAGCAGCCACTGAGGGAGCGGAGCGCCGACCAATGTCGCTGTGGGAGCAGCGTAC 2345
QY 2509 CAGCGAGTGGACCCCGAGGAGCGGCTGCGTTGCGCCACTACGCGCACCTCGGCCCCGA 2568
Db 2346 CAGCCAGCTGAGGAGACATGCAATGTCAGTGTCCAGCAGGAGGCCCTCAACAGAGAGGAGC 2405
QY 2569 CATGAAGACGCACTGACCGCGCGCTGTGTGTGGAGCTGGGCGCGACCGCGCGCGGG 2628
Db 2406 GCGACCATGAACCCGCTCAACCCCTCAACCGCTCAGCTCCCTCAACCGCTCAATGC 2465
QY 2629 GCGCGTGGGAGGCAAGCCGACCTGAGGCTGTGGAGGCC---CCGAGGGCGTGCACCC 2685
Db 2466 CCAACCCAGCGCTTATCGGGGACCCAGGGGCCATTGAGGGCTGTGCCCTGTGGCCCT 2525
QY 2686 TCGCGCAGGACCCACCGGACCGCAGCAAGGACCAAGACCCCGCGGCGGGGACACAGGA 2745
Db 2526 GGAAGTTTCAGAGAGAGCGCATCAGCCGTGTGGGGTTCCTCAGGGGATGAGGGGA 2585
QY 2746 CCGAGCAGAGCCCCCGAAGCGGAGAGCGGGAGCCCGGTGCCGGGAGGAGCGCGCGC 2805
Db 2586 CCGATCAGTGCCTTGACAAACACAGAGGCCCTTTGTCCCTGGGCCAGCGGAGCCACC 2645
QY 2806 GCGCACCGCAGCCACAG-----CAAGAGGCGCGCGGGCC 2841
Db 2646 ATGCTGGCCAGGCGCTGTATGGAACCTGTGACCCGACTCAGCAGGAGCAGGGGAGG 2705
QY 2842 CCGGAGCGCGGAGCAGCGCGCCGAGGCCAGGCCCGGAGGGCGCGCGGACCA 2901
Db 2706 AGAGGCTGTGTGACCTTTGAGGACCGGGGCCAGGCAAGGAGAGCCAAAGCGGAGCCG 2765
QY 2902 CCGGCGCGGCTCCCGGAGAGGCGCGGAGCGGAGCCCGAGCCCAAGCGCGCACCG 2961
Db 2766 GCATCGCGGTGAGGACAGAGCAAGGAGTCTCTTTCAGCTCCCGGAGCAGTCTGC 2825
QY 2962 GCACAGGATCCGAGCAAGAGTGTCGCGCGCGCAAGGGGAGCGCGCGCGGACCG 3021
Db 2826 CAGCCAGGAAGCGAGTCTGGATGAAGCCATGCCCACTGAAAGGGGAGAGGACCATGAGCT 2885
QY 3022 CGGCGGCCCCGAGCGGGCCCCCGGAGGCGGAGAGCGGGGAGAGCGGCGCGCGGCA 3081
Db 2886 CAGGGGCAACCATGCTGCCAAGGAGCCAAAGATCCAAAGAGAGAGAGCCCGAGATTTAAG 2945
QY 3082 CCGGGCCCGGCAAGCGCGAGCTGTCTCAGAGGCTGTGGAGAAGGAGACCAAGGAGAA 3141
Db 2946 GAGACCAACAGTCTGATGTGTCCAGAGGCTCGGGCTGGCAGGAGGCTTGTGAGGC 3005
QY 3142 GGAGGCCACGGAGAGGAGGCTGAGATAGTGAAGCCGACAAAGAGGAGCTCGGAA 3201

Db 3006 TGACACCCCTTAGTCTCTGCCCATCTCTGAGCTGGAAGTGGGAAGCACGTGTGTCTGAC 3065
QY 3202 CCACCAAGCCCGGGAGCCACACTGTGACTCTGGAGACCAAGTGGGACTGTGACTGTGGTCC 3261
Db 3066 GGAGCAGGAGCCAGAGGAGCAGTGTGAGAGGCCCTGTGGGGAATGTGCGACTAGACAT 3125
QY 3262 CATGCAACACTGCCCAGCACTGTCTCCAGAAAGTGGAGAAACAGCCAGAGATGAGA 3321
Db 3126 GGGCCGGTCTATCAGCCAGAGCAGCTGACCTCTCTGTCATCAGCGCCAAACGAGCAA 3185
QY 3322 CAATCAGCGGAACGTCACTCGCATGGCAGTCAAGCCAGCGTCTTCCCAGTGGTAACGT 3381
Db 3186 GGCACACAGAGAGCAGACGCTCACCGTCGCCATCCCCGAGCTGACCCCTTGAAGAGGC 3245
QY 3382 TATCCCACTGATCTCTGACGGGCCCTCTTGGGGAAGCCACGCTCTTCCCAGTGGTAACGT 3441
Db 3246 CTCAAACGTTGGTGCATATTAGCAACAAGACGATGGGAAGCCAGTCCCCTTGAAGAGGC 3305
QY 3442 GGACCTGGAAAGCAAGCAGAGAGGGGAAGAGGAGTGGAAAGCGGATGACGTGATGAGGAG 3501
Db 3306 AGAGATCAGAGAGATCAGGAGGAGGTGGAGAAAGAAAGACAGAAAGAGAGCGTGA 3365
QY 3502 CGGCCCCCGCTTATCGTCCCATACAGCTCCATGTTCTGTTTAAAGCCCAACCACTGCT 3561
Db 3366 GACAGGCAAGCCATGGTGCCTCCACAGCTCAATGTTCACTCTTCAGCACCAACCAACCGAT 3425
QY 3562 CCGCGCTTCTGCACTTACATCGTGAACCATGAGGTACTTCGAGGTGTCATTCTCTGTTGT 3621
Db 3426 CCGAGGGCTGCCACTACATCGTGAACCTGCGTACTTGTGATGTGCATCTCTCTGTT 3485
QY 3622 CATCGCTTGTAGCAGATCGCTCGCTGTGTGAGGACCCAGTCGCGCAGCAGACTCGCCAG 3681
Db 3486 GATTGAGCAGCAGCATCGCTCGCGGAGAGGACCCGCTCTGTACCAACTCGGAGCG 3545
QY 3682 GAACAAGCTCTGAATACCTGATTTACATTTTCACTGGTGTCTTTACCTTTTGTGAGTGT 3741
Db 3546 CAACAAGTCTGAGTATTTGACTATGTGTTTCAAGGGCGTGTTCACCTTTTGTGAGTGT 3605
QY 3742 GATAAAGATGATCGACTTGGGACTGTGCTTCACTCCCTGGAGCCTATTTCGCGGACTTGTG 3801
Db 3606 TATAAAGATGATAGACCAAGGCTTGTATCTGCAAGGATGGTCTTACTTCCGAGACTTGTG 3665
QY 3802 GAACAATTCGACTTCATTGTGTGAGTGTGCGCCCTGTGTGGCGTGTGCTTTTCGAGCTT 3861
Db 3666 GAACATCTCGACTTTGTGTGTGTGTCGCGCATTTGGTGGCTTGTCTGCGGCTTGTCTG 3725
QY 3862 CGTGGAGGATCCAAAGGGAAGACATCAATCAATCAAGTCTCTGAGAGTCTTCTGTTGT 3921
Db 3726 NNNNNNAACCAACAAAGGAGCGGACATCAAGACCATCAAGTCTCTGCGGTGTCTCGAGT 3785
QY 3922 CTTGCGGCGCTCAAGACCATCAACCGGTGCGCAAGCTCAAGGCTGTGTTGACTGATC 3981
Db 3786 TCTAAGGCCACTGAAACCATCAAGCGCTTGGCCAAAGCTCAAGNNNNNNNNNNNNNNNN 3845
QY 3982 GGTGAATCTCCCTGAAGAATGTCTCAACATCTTTGATTGTCTACATGCTCTTCAATGTT 4041
Db 3846 NNN 3905
QY 4042 ATTTGCGGTCAATTGCGGTGAGCTCTTCAAGGGAAGTTTCTACTGACACATGAATC 4101
Db 3906 NNN 3965
QY 4102 CAAGGAGCTGGAGAGGAGCTGCAAGGGGTCAAGTATTGGATTATGAGAGAGGAGAGTGA 4161
Db 3966 NNN 4025
QY 4162 AGCTCAGCCCGAGCAGTGGAGAAATACGACTTTTCACTACGACAAATGTGCTCTGGGCT 4221
Db 4026 NNN 4085
QY 4222 GCTGACGCTTTCACAGTGTCCAGGGAGAGGCTCGGCCCATGCTGAAACACTCCGT 4281

ORIGIN

Query Match 26.3%; Score 1940.8; DB 29; Length 6822;
Best Local Similarity 57.1%; Pred. No. 4.7e-291;
Matches 3272; Conservative 0; Mismatches 2316; Indels 145; Gaps 18;

QY 146 ATGCTCCGCTTCGGGAGGAGCTGGGCGCGCTATGGAGCCCGCGGCGGAGACGG 205
DB 1 ATGGCTCGCTTCGGGAGGCGGTGGTGGTGGCAGCGCCAGGCTCAGGCGATGGAGACTCG 60

QY 206 GCCCGGCG 265
DB 61 GACCAGAGCAG-----GAA CCGACAAGAAACCCCGTCCCGGCTCGGG 105

QY 266 CAGCGGTCCTTCAAGACAAATCGATCGCGCAGCGCGCGCGGACCAATGGCGCTGTACAAC 325
DB 106 CCGCGCGCGCTTCAAGCAGTCAAAAGCGCAGAGGCGCGGACATATGGCTTTGTACAAC 165

QY 326 CCCATCCGGTCAAGCAGACTGCTTACCCTGCAACCGCTCGCTCTTCTTTCAGCGAG 385
DB 166 CCCATACAGTCCGGCAGACTGTTTACGGTCAACAGATCCCTGTTTCATCTTCCGAGAA 225

QY 386 GACAACTGCTCCGCAATACGGAAGCGCATCACGAGTGGCTCCATTCGAGTATATG 445
DB 226 GATAACATGTGAGAAATACGCCAGAGACTCATCGATTGGCCGCCATTTGAGTACATG 285

QY 446 ATCTGCGCCACCATCATCGCAACTGCACTGCTGTCGCCCTTGGAGCAGCACTCCCTGAT 505
DB 286 ATCTGCGCCACCATCATTTGCCAACTGCACTGCTTGGCCCTTGGAGCAGCATCTTCTGAG 345

QY 506 GGGGACAAAGCCCATGTCCGAGGCGTGCAGACGACGAGCGGCTATTTTCATCGGGATC 565
DB 346 GATGACAAGACCCCAATGTCTCGAAGACTTGGAGAAGACAGAACCATATTTCAATTGGGATC 405

QY 566 TTTTGTCTCAGGAGGAGTCAAAATCATCGCTCTGGGCTTGTCTTCCAAAGGGCTCT 625
DB 406 TTTGCTTTGAAGCTGGATCAAAATTTGTGGCTCTAGAGTTTCACTTCCATAAGGGTTCA 465

QY 626 TACCTGCGGAAACGGCTGGAACGTGATGAGACTTGTGTCGTCCTTCAAGGATCCTTGCC 685
DB 466 TACCTCGTAATGCTGGAATGTGATGAGACTTATCGTGTGCTTGTAGTGGCATCCTGGCC 525

QY 686 ACGGTGGAATGACTTC-----GACCTGGGAACACTGAGGGCTGTGCGTGTG 733
DB 526 ACTGCGGGAACCCACTTCAACACCCACGCTGAGACCTTGGGACCCCTCGGGCTGTGCGTGTG 585

QY 734 CTGAGGCCCCGAGAGTGTCTGCGGATTCAGATTTGCAAGTGTGCTCAAGTCCATC 793
DB 586 CTGAGGCCCCTTAAAGCTGGATATCAGGAATACCTAGCTGCAAGATCGTGTGAGTCTATC 645

QY 794 ATGAAGGSCATGGTTCCACTCTCGAGATTGGGCTGTCTTCTTTTGGCATCCTCATG 853
DB 646 ATGAAGGCCATGGTGGCTCTTTCGAGATTGGCTTCTGTCTTCTTTGGCATCCTCATG 705

QY 854 TTTGCGCATATGGCTGGAGTTCTACATGGGGAAGTTCCAAAGGCTGTGTTTCCCAAC 913
DB 706 TTTGCTATCATTTGGCTTGGAGTTCTACAGTGGCAAGTTGCAATCGAGCATGCTTCAAGAAC 765

QY 914 AGCAGATGCGGAGCCGCTGGGTGACTTCCCTGTGCGAAGAGGCGCCAGCCGCGCTG 973
DB 766 AATTGAGGTATTTAGAGGGTTTGAATCCTCTCACCCGCTGTGTGCAAGGCTGCCCCG 825

QY 974 TCGAGGCGGACACTGAGTGGCGGAGTACTGGCCAGGACCAACTTTGGCATCACCAAC 1033
DB 826 -----GCTGGTTATGAATGTAAAGACTGGATCGGCCCAATGAGGGATCACCCAG 876

QY 1034 TTTGCAATATCTGTTTGGCATTTGACCGGTGTTCCAGTGTGATCAACATGGAGGGCTGG 1093
DB 877 TTTGACAAACATCTTTTGGCGGTGTGACTGTCTTTCCAAATGCATCACTATGGAAGGGTGG 936

QY 1094 ACTGACATCTTATAATAAAGATGGCGCGGCAACACTGGACTGCTTACTTTC 1153
DB 937 ACCATGTGCTGTACAATACCAATGATGCTTTAGAGGACCACTTGGAACTGGCTGTACTTC 996

QY 1154 ATCCCTCTCATCATCATCGGCTCTTTCATGCTCAACCTGGTGTGGCGGTGCTCTCG 1213
DB 997 ATCCCTCTCATCATCATCGGATCCTTCTTGTGTCTCAACCTGCTCTGGAGTGTCTTC 1056

QY 1214 GGGGAGTTTGGCAAGGAGCGAGAGGCTGGAGAACCGCGCGCTTCTCTGAAAGCTGCGC 1273
DB 1057 GGGGAATTTGCCAAGAGAGAGAGTGGAGAACCGAAGAGCGTTTCATGAAGCTCCGG 1116

QY 1274 CGGACAGCAGATCGAGCGAGAGCTCAACGGGTA CTTGGAGTGGATCTTCAAGGCGGAG 1333
DB 1117 CGGCAGCAACAGATTGAGCGAGAAATTGAACGGCTACCTGCTCGTGTAGATAGACAAGCAGAG 1176

QY 1334 GAGTCTATGCTGCCAGGAGGACAGGAATGACAGAGAGTCCCTCTTGGACGTGCTG 1393
DB 1177 GAAGTCTATGCTTGAAGAAATAAATCAATC---GGGAA CATTACAGCTTGGAGTGTCTT 1233

QY 1394 AAGAGCGGCGCCACCAAGAGAGCAGAAATGACTGATCCACGACAGAGGAGGAGGAC 1453
DB 1234 CGAAGGCGCAACCATCAAAAGGAGCGGACGCGGCATGACCCGAGACTCCAGGATGAG 1293

QY 1454 CGGTTTTCAGATCTCTGTGCTGTGATCCCTTTCGCCGCGCGCAGCTCAAGAGGGGG 1513
DB 1294 CACTGCGTTGATATCTCTTCAGTGGGCACACCTCTTGGCAGAGCCAGTATCAAGAGCACA 1353

QY 1514 AAGACAGAGAGCTCGTCTATCTTCCGAGGAAGAGAGTGTTCGGTCTTTTATCCGG 1573
DB 1354 AAGATGATGGGCGCTCTTATTTCCGGCAACAGGAA CCGGCTCTTGGCGATCTCTATCCCG 1413

QY 1574 CGCATGCTGAAGGCTCAGAGCTTCTACTGGGTGGTGTGCTGTGGTGGCCCTGAAACACA 1633
DB 1414 CACATGCTCAAGTCCCAAGTCTTTTACTGATCGTCTGAGTGTGTGGCTCTTATACT 1473

QY 1634 CTGTGTGGCCATGGTGCAATTAACAACGCGCGCGGCTTACCAGACCCCTGTATTTT 1693
DB 1474 GCCTGTGGGCCATTGTTCAATCAACAACGAGCCACAGTGGCTCACTACCTCTCTACTAT 1533

QY 1694 GCAAGTTTGTCTTCTGGTCTCTTCTCAGAGATGTCTCTGAGATGTATGGCTG 1753
DB 1534 GCAGAGTTTGTCTTCTGGGACTCTTCTGTTGGAGATGTCTCTGAGAGATGTATGGCATG 1593

QY 1754 GGGCCAGAGAGTACTTTCGGTCTCTCTCAACTGCTTTCAGTCTTGGGGTCACTCGTGGG 1813
DB 1594 GGGCCAGCGCTTATTTTCACTCATCTTCACTGCTTTGATTTTGGGNNNNNNNNNNNN 1853

QY 1814 AGCGTCTTTGAAAGTGTCTGGGCGGCGCATCAAGCCGCGAGACTCTTTGGGATCAGTGTG 1873
DB 1654 NNN 1713

QY 1874 CTGGGGCCCTCGCGCTGTGAGATCTTCAAAGTCAAGAGTACTGGAGCTCCCTGCGG 1933
DB 1714 NNN 1773

QY 1934 AACCTGTGTGTGCTCCCTGCTGAACTCCATGAAGTCCATCATCAGCTGTCTCTTCTGCTC 1993
DB 1774 NNN 1833

QY 1994 TTCGTGTTCACTGTGTCTTTCGCCCTGCTGGGATGCACTGTTTGGGGGACAGTTCAC 2053
DB 1834 NNN 1893

QY 2054 TTCAGGATGAGACTCCCAACAACCTTCGACACCTTCCCTGCGGCATCTCTCAGTGTG 2113
DB 1894 TTTAAATGATGGGACTCTTTCAGCTAAATTTTGAACACCTTCCCTGAGCTATCATGACAGTG 1953

QY 2114 TTCAGATCTGACGGGAGGAGTGAATGCAATGATGTATCATCGGATCGAATCGCAA 2173
DB 1954 TTCAGATCTGACGGGGAAGACTGGAATGAGGTGATGTACATGGCATTCGCTCCAG 2013

QY 2174 GGGGCGCTCAGCAAGGAGTGTCTCGTCTTTTACTTTTCACTGTCTGACACTGTTCGGA 2233
DB 2014 GGTGGGTCAGCTCAGGCGATGTGTCTGCCACTTACTTCACTTGTGTCTCACTTGTGTTGA 2073

Db 4211 TCCTTTATGGGTCTACTTTGTGTGTCCTCCCTTTCTTCTTTGTCAATATCTTCGTGGCTC 4270
Qy 4398 TGATCATCATCACCTTCACGAGCAGGGGACAAAGTGATGCTCTGAATGCAGCCTCGAGA 4457
Db 4271 TCATTATCATCACCTTCACGAGCAAGGGACAAAGATGATGGAGGAGTGATAGCCTGGAGA 4330
Qy 4458 AGAACGAGAGGGCTTGATGACTTTCGCCATCAGCGCCAAACCCCTGACAGGTCATGTC 4517
Db 4331 AGAATGAGCGGCATGATGACTTCGCCATTAGTGCCAAACCTCTCACCGCTACATGC 4390
Qy 4518 CCAAAAACCGCAGTCGTTCCAGTATAAGACGTGGACATTTGTGCTCTCCCGCCCTTTG 4577
Db 4391 CACGAAACAGGCACACCTTCAGTACCGTGTGGGCACTTTGTAGTCTCCCATCCTTTG 4450
Qy 4578 AATACTTCATCATGCCCATGATGCCCTCAACACTGTGGTCTGATGATGAAGTTCATG 4637
Db 4451 AGTATACCATCATGCGCATGATTGCCCTTGAACACTGTGCTGATGATGAAGTACTACT 4510
Qy 4638 ATGCACCTATGATGACGCTGATGCTGAATGCCTGAACATCGTGTTCACATCCATGT 4597
Db 4511 CTGCTCCTTGCACTATGAGCTGCGCTTAAAGTACCTGAAACATCGCCTTCACCTATG 4570
Qy 4698 TCTCCATGGAATGCTGCTGAAGATCATCGCTTGTGGGTGCTGAACATTTTCAGAGATG 4757
Db 4571 TTTCCCTGGAGTGCTGCTAAAGTCAATGCTTTCCGCTTCCCTGNNNNNNNNNNNNNN 4630
Qy 4758 CTGGAAATGCTTTGACTTTGTCACTGTGTGGGAAGTATTACTGATATTATTAAGTAA 4817
Db 4631 NNN 4690
Qy 4818 AGATTGC---GGAAACGAAACAATTTCACTCAAGCTTCCTCGGCTCTTCGAGCTG 4874
Db 4691 NNNNNNNCTGGTGAACACCAAGTGGCTTCAATATGAGCTTCTGAAAGCTCTTCGAGCTG 4750
Qy 4875 CGGGCTGATCAAGCTGCTCGCAGGCTACACCATCCGCTCTGCTGTGAGCCTTTG 4934
Db 4751 CACGGCTATAAAGCTTCTGAGCAGGGCTACACATCCGCACTTACTGTGACCTTCG 4810
Qy 4935 TCCAGTCTTCAAGGCCCTGCGCTACGTGTGTGCTCATTTGCCATGCTGTCTTCACTC 4994
Db 4811 TGCAGTCTTTAAGGCTCTTCCCTACGCTGCTGCTTCTCATTTGCCATGCTTTTCTCATCT 4870
Qy 4995 ACGCCATCATCGGCATGAGGTGTTGGGAATATATGCCCCTGATGATGACACAGCATCA 5054
Db 4871 ACGCCATCATTTGGATGAGGTGTTGGAAACATAAAGTTAGATGAGGAGATCAACATCA 4930
Qy 5055 ACCGCCACAACTTCGGAGCTTTTTCGAAGCCCTGATGCTGCTTCAGGAGCGCCA 5114
Db 4931 ACCGGCACAACTTCGGAGTTTCTTTGGGTCCCTCATGCTGCTTTTCAGGAGTGCCA 4990
Qy 5115 CGGGGAGGCTGCGCAGATCATGCTGCTCCCTGAGCAACACGAGCCTGTGATGAGC 5174
Db 4991 CGGGGAGGCTTGGCAGAGATTATGCTGCTCTCGGTGAGAAAGGTTGTGAGCCTG 5050
Qy 5175 AGGCCAATGCCACCGAG-----TGTGGAAGTGACTTTGCCCTACT 5213
Db 5051 ACACCACTGCACCCCTCAGGGCAGAATGAGGTGAGCGCTGGGCACCTGACCTGGCCTACG 5110
Qy 5214 TCTACTTCTGCTCTCTCATCTCTGCTGCTCTTTCTGATGTTGAACCTCTTTGTGGCTG 5273
Db 5111 TTTATTTTGTCTCTCTCATCTCTTCTGCTCTCTTCTGATGCTCAACCTGTTCGTGGCTG 5170
Qy 5274 TGATCATGGACAAATTTTGAATACCTCAGCGGGACTCTTCATCTTAGTCTCCTACCACT 5333
Db 5171 TCATCATGGACAACTTTGAGTACTGACTCGAGATTCTCCTCATCTCGGGGCTCACCACT 5230
Qy 5334 TGGATGATTCATCCGGGTCTGGGCTGAAATACGACCCGGCTGCTGTGGGCGCATCATGTT 5393
Db 5231 TAGATGAGTTTGTCCGTGCTGGGCGAATATGACAGACGAGCATGTGGCGGCATTCATT 5290
Qy 5394 ACAATGACATGTTTGAATGCTGAAACACATGTCCTCCGCTCTGGGCTGGGAGNAAT 5453
Db 5291 ACATGAGATGTATGAAATGCTGACTCTCATGTCAACACCGCTAGGCTCGGGAAGAT 5350

Qy 5454 GCCTCTCGAGTTGTTTAAAGCGCCTGTTTCGCATGAACATGCCCATCTCCAACGAGG 5513
Db 5351 GTCCCTCCAAGTGGCTATTAAGAGGCTGCTCTGATGAACATGCCAGTGGC---TGAGG 5407
Qy 5514 ACATGACTGTTTCACTTCCAGTCCACGCTGATGAGCCCTCATCCGAGGCACTGGAGATCA 5573
Db 5408 ACATGACAGTCCACTTTCACCTCCACACTTATGCTCTGATCCGAGACGCTCTGGACATTA 5467
Qy 5574 AGCTGCCCCAGCTGGGCAAAAGCAGCATCAGTGTGACGCGAGTTTGAGGAAGAGATTT 5633
Db 5468 AATTCGCCAAAGTGTGCGACAGACAGCAGCTAGACTCGGAGCTGCAAAAAGAGACCC 5527
Qy 5634 CCCTTGTGTGGGCAATCTGCCCCAGAAAGACTTTTGACTTGTGATACCAACCAATAGC 5693
Db 5528 TGGCCATTTGGCTCACCTGTCTCCAAAAGATGTTGGATCTGCTTGTGCCCATGCCAAAG 5587
Qy 5694 CTGATGAGATGACAGTGGGGAAGGTTTATGCAGCTCTGATGATATTGATCTTCTACAAGC 5753
Db 5588 CCTCTGACCTGACTGTGGGCAAGATCTATGCACAAATGATGATCATGGACTACTATAAAC 5647
Qy 5754 AGAACAAAACCCAGACAGACAGATGCAGCAGG 5786
Db 5648 AGATTAAGTTAAAGAAACAGACAGACAGCTGG 5680
RESULT 3
AY406057 6675 bp DNA linear GSS 15-DEC-2003
LOCUS Pan troglodytes CACNA1E gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406057
VERSION AY406057.1 GI:39762031
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 6675)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 6675)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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AK081230
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CALCIUM CHANNEL PORE-FORMING SUBUNIT ALPHA 1B (FRAGMENT) [Rattus
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ACCESSION
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VERSION
AK081230.1 GI:26099772
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HTC; CAP trapper.
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Mus musculus
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REFERENCE
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED
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2
REFERENCE
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED
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3
REFERENCE
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED
11076861
4
REFERENCE
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
REFERENCE
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6
REFERENCE
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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Okazaki,Y., Saico,R., Saichon,H., Sakai,C., Sakai,K., Sakazume,N.,
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Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan [E-mail: genome-res@ac.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216]

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

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evidence: FASTY, 77.5%ID, 97.1%length, match=531)"

Query Match 15.3%; Score 1128; DB 11; Length 2617;
Best Local Similarity 81.9%; Pred. No. 7,5e-165;
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cloned. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. Average insert size
4.5kb. Adaptors 5' (AATTCGACAGGAGG) 3' and 5' d
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Sequencing primers 3' end: T3 promoter primer 5'd
(ATTAACCTCCTAAAGGA) 3'. 5' End: T7 promoter primer 5'd
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laboratory of M. Bento Soares. Note: this is a NIH_MGC
Library"

ORIGIN

Query Match          9.0%; Score 666.4; DB 14; Length 802;
Best Local Similarity 99.1%; Pred. No. 2.7e-93;
Matches 670; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 6114 ATGGGAGAGCCACGCTGGGCTGGAGAGCAGAGGTTCGAGGGCTCCATGCGCCGCTTG 6173
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Db 541 CGGCCGAGACTACGCCGCTCACAGATGCCAGCCCCCATGAAGCGCTCCATCTCCACGCTGG 600
QY 6234 CCGAGCGCCCCGTTGGGACTCATTTTGCAGCACACCCCGGAGCCGCCACCCCTAGCC 6293
Db 601 CCGAGCGCCCCGTTGGGACTCATTTTGCAGCACACCCCGGAGCCGCCACCCCTAGCC 660
QY 6294 AGGCGTCTGTCACACACACACCGCTGTCACACCCCGGAGGAGGAGGAGGAGG 6353
Db 661 AGGCGTCTGTCACACACACACCGCTGTCACACCCCGGAGGAGGAGGAGGAGG 720
QY 6354 CCCTGGAGAGGGGCC 6369
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Db 721 CCTTGAAGAGGGGCC 736

RESULT 7
BC051413
LOCUS
DEFINITION
BC051413
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT

BC051413 6035 bp mRNA linear HTC 19-NOV-2003
Mus musculus calcium channel, voltage-dependent, alpha 1F subunit,
mRNA (CDNA clone IMAGE:6493332), containing frame-shift errors.

BC051413.1 GI:30802106
HTC.
Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 6035)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schneetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raja,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 6035)
Strausberg,R.
Direct Submission
Submitted (25-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 108 Row: 0 Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9624972
This clone has the following problem: frame shifted.
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FEATURES

Location/Qualifiers
1. .6035
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6493332"
/issue_type="Eye, retina, mouse strain C57Bl/6"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Watch 9.0%; Score 663; DB 11; Length 6035;
Best Local Similarity 58.2%; Pred. No. 2.1e-92;
Matches 1334; Conservative 0; Mismatches 895; Indels 64; Gaps 7;
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QY 3572 TGCACATACATCGTGACCATGAGTACTTTCGAGGTGGTCAATTCGTGTCATGCGCTTG 3631
DB 2616 TGCACACACTATACATCACCATATCTTCCAGGTCTCATCTAGTGTTCATCATCTC 2675
QY 3632 AGAGCATCGCCTGCTGCTGAGGACCCAGTGCACAGACTCCGCCAGGAAACAGCT 3691
DB 2676 AGTAGTGTGCTGCTGCTGCTGAGGACCCATCCGAGCTCACTCTCCGAAACCATATT 2735
QY 3692 CTGAATACCTCGATTACATTTTCACTGGTGTCTTACCTTTGAGATGGTGAATGATG 3751
DB 2736 CTGGGATATTTGATTATGCTTCACTCCATATTCATCTGTGGAGATTCTACTCAAGATG 2795
QY 3752 ATCGACTTGGGACTGTGCTTCAACCTCGAGGCTATTTCCGGGACTGTGGAACATTCTG 3811
DB 2796 ACAGTGTTTGGGCTTCTGCAACGAGCTCTTTCGCGTGTAGTGTGTTCAATCTGTTG 2855
QY 3812 GACTTATTTGGTCACTGGGCGCTGCTGGGCTGTTGCTTTCGAGCTTCGAGGAGGA 3871
DB 2856 GATCTCTTGTGGTCACTGTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2894
QY 3872 TCCAAAGGGAAGACATCAATACCATCAAGTCTCTGAGAGCTCTGCTCGCGGCC 3931
DB 2895 ATCCACTCGAGTCCCATCTAGTGTGAAGATTCTCCGAGTCTCCGAGTCTCGCGGCT 2954
QY 3932 CTCAGACCATCAAA CGGCTGCCAAGCTCAAGGCTGTGTTGACTGTGTGGTGAATCC 3991
DB 2955 CTCGAGCCATCAACAGAGCCAAAGGACTCAAGCATGTGTCAGTGTGTGTCGTGCCC 3014
QY 3992 CTGAAGATATGCTCTCAACATCTTGTATGTCTACATGCTCTTCATGTTCAATTTGCGGTC 4051
DB 3015 ATCCGGACCATCGGAAACATCATGATTGTCAACACCTCTTTCAGCTTCATGTTGCGCTGC 3074
QY 4052 ATTGGGTGACGCTCTTCAAGGGAAGTTTCTACTGCACAGATGAATCCAAAGAGCTG 4111
DB 3075 ATTGTGTTCAGCTGTTCAAGGGAATTTCTAGCTGTCACTGATGAGGCCAAACACACC 3134
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DB 3255 ATGGCCCTGTTTCACTGTTCTTACCTTTGAGGCTGGGCTGGCTACTATACAAAGCCATA 3314
QY 4283 GATGCCACTATGAGAGCAGGCTCAAGCCCTGGGTACCGCATCGAGCTGTTCATCTTC 4342
DB 3315 GATGCAACGCAAGATGAGGGCCCTATCTACAATTAACCATGTTGGAGATATCAGTATTC 3374
QY 4343 TACGTGGTCTACTTGTGGTCTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4402

DB 3375 TTCAATGTCTACATCATCATCGCTTCTTTCATGTAACATCTTTGTGGCTTTGTT 3434
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DB 3435 ATCATCACTTCCGTCGCCAGGAGAGCAGAGTACCAAACTGTGAACCTGGACAAAGAAC 3494
QY 4463 GAGAGGCTGTGCAATTTGATCTTCGCCATCAGCGCCAAACCCCTGACACAGCTATCATGCCCAA 4522
DB 3495 CAGCGCAGTGTGGGAATATGCCCTCAAAGCTCAGCACTCCGCCGATCATCCCTTAAG 3554
QY 4523 AACCGGAGTGTTCAGTATAAGACGTTGGACATTTTGTGTCTCCCGCCCTTTGAATAC 4582
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QY 4583 TTCAATCATGGCCATGATAGCCCTCAACACTGTGGTGTCTGATGATGAAGTGTCTATGATGCA 4642
DB 3609 CTCATGTTTCTGCTCATCTCTCTCAACACAGTGGCCCTAGCCATGCAAGCACTATGAACAG 3668
QY 4643 CCTATGAGTACAGACTGATGCTGAATGCTGAACATCGTGTTCACATCCATGTTCTCC 4702
DB 3669 ACTGCTCCTTTAACTATGCAATGGACATCTCTCAACATGCTCTTCACTGGCTCTTCACC 3728
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DB 3729 ATTGAGATGCTGCTCAAAATCATCGCTTTAAACCCCAAGCATTTACTTTGAGATGCCCTGG 3788
QY 4763 AATGCTTTTACATTTGTCACTGTGTTGGGAAGTATTTACTGATATTTTAGTAAACAGATTT 4822
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DB 3848 CAATAGACAGCTCCCGCATATCTATCACGTTCTTTGCGCTCTTCCGAGTATGAGGCTG 3907
QY 4883 ATCAAGTGTCTCGCAGAGGCTACAACATCCGCACTCTGCTGTGTGAGACCTTTGTCAGTCC 4942
DB 3908 GTCAAGCTTCTGAGTAAGGTTGAGGGGATCCGCACACTGTCTTGGAATTCATCAAGTCT 3967
QY 4943 TTCAAGGCCCTGCTTACGTTGTCTGCTCATTTGCGCATGTGTTCTTCACTATGAGCATC 5002
DB 3968 TTCAGGCCCTTGGCTTATGTTGGCACTTCTCATAGCAATGATATTTCTTCACTATGAGCT 4027
QY 5003 ATCGCATGCAAGTGTGTTGGGAATATTTGCGCTGAGCAACCGCCCTGTA----- 5169
DB 4028 ATTGGCATGCAGATGTTTGGCAAGTGGCTTTCAGGACGCGCAGAGATTAATCGAAAC 4087
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QY 5170 --TGAGCAGGCCAATGCCAGGAGTGTGGAAGTGAATTTTGGCTTACTTCTAATTCGCTCC 5227
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QY 5348 CGGCTCTGGCTGAATACGACCGGCTGCTGTGGGCGCATCAGTTTACAAAGCATGTTT 5407
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Qy 5768 AGACACAGATGC 5780

Db 4796 AAAGAAAAGGGGC 4808

RESULT 8

AK039991

LOCUS AK039991 4058 bp mRNA linear HTC 19-SEP-2003

DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430040I15 product:unclassifiable, full insert sequence.

ACCESSION AK039991

VERSION AK039991.1 GI:26087546

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20493374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4058)

AUTHORS Adachi, G., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/

FEATURES

source Location/Qualifiers

1..4058

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM DB:A430040I15"

/db_xref="MGI:2404562"

/db_xref="taxon:10090"

/clone="A430040I15"

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/dev_stage="0 day neonate"

misc_feature 1..4058

/note="unclassifiable"

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Matches 938; Conservative 0; Mismatches 376; Indels 39; Gaps 4;

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QY 1387 CTTGCTGAAGAGAGCGGCCCCACCAAGACGAGAAATGACCTGTATCCACGAGAGGAGG 1446
Db 1752 AGTGTCTGAAGGGCAACCATCAAAAGGAGCGGACGAGGCCATGACCCGAGACTCCAG 1811
QY 1447 AGAGACCGGTTTGCAGATCTCTGTGCTGTGG 1479
Db 1812 CGATGAGCACTCGGTTGATATCTCTTCAGTGG 1844
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RESULT 9
CFI82756 848 bp mRNA linear EST 29-JUL-2003
LOCUS UI-M-EY0-bwz-j-10-0-UI.r1 NIH BMAP_EY0 Mus musculus cDNA clone
DEFINITION IMAGE: 5705193 5', mRNA sequence.
ACCESSION CFI82756
VERSION CFI82756.1 GI:33314545
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 848)
NTH-MGC http://ngc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Straubeberg, Ph.D.
COMMENT Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this cDNA
sequence: 468-529, >CHARLEI#DNA/MERI_type (matched compliment)
Seq primer: pYX-5.
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/db_xref="taxon:10090"
/clone="IMAGE: 5705193"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_EY0"
/notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is GTGCGTGAA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."
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ORIGIN

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Query Match 8.5%; Score 628.4; DB 14; Length 848;
Best Local Similarity 88.8%; Pred. No. 2.3e-87;
Matches 691; Conservative 0; Mismatches 86; Indels 1; Gaps 1;
QY 4061 CAGCTCTTCAAGGGGAAGTTTCTTACTGCACAGATGAATCCAAGGAGCTGGAGAGGGAC 4120
Db 1 CAGCTCTTCAAGGGGAAGTTCTTTTACTGTATGATGAATCCAAGGAGCTGGAGAGGGAC 60
QY 4121 TGCAGGGGTGAGTATTTGGATTATGAGAGGAGGAAGTGGAAAGCTCAGCCAGGCTAGTGG 4180
Db 61 TGCAGGGGTGAGTATTTGGATTATGAGAGGAGGAAGTGGAAAGCTCAGCCAGGCTAGTGG 120
QY 4181 AGAAATAGCATTTTCACTACGCAATGTCTCTGGGCTCTGCTGACGCTGTTTCAGATG 4240
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Db 121 AAGAAATATGACTTCCACTATGACAAATGTTCTCTGGGCTTGTGACGCTGTTCCACAGTG 180
Qy 4241 TCACGGGAGAGGCTGGCCCATGGTCTGAAACACTCCGTTGGATGCCACTATGAGGAG 4300
Db 181 TCACGGGAGAGGCTGGCCCATGGTCTGAAACACTCTGTGGATGCCACTATGAGGAA 240
Qy 4301 CAGGGTCACAGCCTGGGTACCGCATGGAGCTGTCATCTCTACGTGGTCTACTTTGTG 4360
Db 241 CAGGGGCCCATGCTCCGGGTTCCGGATGGAGCTCTCCATCTTCTACGTGGTCTACTTTGTG 300
Qy 4361 GTCTTTCCCTTCTTCTCGTCAACATCTTGTGTGCTTTGTATCATCATCACTTCCAGGAG 4420
Db 301 GTCTTCCCTTCTTCTTGTGCAACATCTTGTGTGCTTTGTATCATCATCACTTCCAGGAA 360
Qy 4421 CAGGGGACAGGTGATGTCTGAATCAGCCTCGAGAAAGACGAGAGGCTTGCATTGAC 4480
Db 361 CAGGGAGATAAGGTGATGTCTGAATCAGCTTAGAAAAGAAATGAGAGGCTTGCATTGAT 420
Qy 4481 TTGCCCATCAGCGCAACCCCTACACGGTACATGCTGCCCAAAACCCGGCAGTCTTCCAG 4540
Db 421 TTTGCCCATCAGTGCACAGCCCTGACACGGTACATGCTCAAAACAAACAGTCTGTTCCAG 480
Qy 4541 TATAAGACGTGACATTTGTGTCTCCCGCCCTTTGAATACTTTCATCATGCGCCATGATA 4600
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Qy 4601 GCCCTCAACACTGTGTGCTGATGATGAAGTTCTATGATGACCCCTATGATGACGCTG 4660
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Qy 4721 ATCATGCTTGGGGTCTGAACTATTTCAGAGATGCTGGATGCTTTGACTTTGTC 4780
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Qy 4781 ACTGTGTTGGGAATATTACTGATATTATTAGTAAACAGAGATGCGGAAACGAACT 4838
Db 721 ACGGTTTGGGAAGTA-TACTGATATTAGTAAACAGAGATGCGGAAACACTTCACT 777

RESULT 10
CF743150
LOCUS
DEFINITION
UI-M-GVO-cln-m-16-0-UI_r1 NIH_BMAP_GV0 Mus musculus cDNA clone
IMAGE:30616527 5', mRNA sequence.
CF743150
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 807)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefi.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this cDNA
sequence: 133-194, >CHARLIE14DNA/MER1_type (matched complement)
Seq primer: pYX-5.
Location/Qualifiers
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source 1. .807
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30616527"
/tissue_type="whole brain"
/dev_stage="1,5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP GV0"
/notes="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTCAAT. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
```

ORIGIN

Query Match	8.5%;	Score 625;	DB 14;	Length 807;
Best Local Similarity	89.4%;	Pred. No. 7.5e-87;		
Matches 686;	Conservative 0;	Mismatches 75;	Indels 6;	Gaps 1;
Qy 4397	TTGATCATCATCACTTCCAGGAGCGGGGACAAAGTGTCTGAATCGACGCTGGAG	4456		
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Db 62	AGAATGAGAGGCTTGCATTGATTTGCCATCAGTGCCAAAGCCCTGACACGCTACATG	121		
Qy 4517	CCCCAAACCGGACGTCGTTCCAGTATAAGACCGTGACATTTGTGTCTCCCCGCCCTTT	4576		
Db 122	CCTCAAAACAAACAGTCGTTCCAGTATAGACATGGACATTCGTGGTCTCTCCACCCCTT	181		
Qy 4577	GAATACTTCATCATGCCCATGATAGCCCTCAACACTGTGTGTGTGATGATGAAGTTCTAT	4636		
Db 182	GAGTACTTTCATCATGCTGATAGCCCTCAACACAGTGTGTGTGATGATGAAGTTCTAT	241		
Qy 4637	GATGACCCCTATCAGTACGAGCTGATGCTGAATGCTGAACTCGTGTTCACATCCATG	4696		
Db 242	GATGACCCCTTATGATACGAGCTGATGCTGAATGCTGAAATGCTGAACTTGTCTTCA	301		
Qy 4697	TTCTCCATGGAATGCTGCTGAAGATCATCGCTTTGGGGTGTCTGAACTATTTTCAGAGAT	4756		
Db 302	TTCTCCATGGAATGCTGCTGAAGATCATCGCTTTGGGGTGTCTGAACTATTTTCAGAGAT	361		
Qy 4757	GCCTGGAATGCTTTGACTTTGTCTGCTGTTGGGAAGTATTACTGATATTTTAGTAACA	4816		
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.D., Scheetz, T.E., Brownstein, M.J., Udén, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Young, A.C., Shevchenko, Y., Bouckard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smal, D.E., Schnerch, A., Schein, J.B., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477332

2 (bases 1 to 6636)

Strausberg, R.

Direct Submission

Submitted (09-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-romail.nih.gov

Tissue Procurement: The Celko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Varon Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saesdi, Jacqueline Schein, Duane Smal, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC plate: 86 Row: 0 Column: 1

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9624972

This clone has the following problem: frame shifted.

Location/Qualifiers

1. 6636

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/clone="IMAGE:5369391"

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/lab_host="DH10B"

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FEATURES

source

ORIGIN

Query Match 8.4%; Score 623; DB 11; Length 6636;

Best Local Similarity 57.5%; Pred. No. 3.6e-86;

Matches 1308; Conservative 0; Mismatches 875; Indels 90; Gaps 7;

Qy 3559 GCTCCGGGCTTCGCCACTACATCGTGACCATGAGGTACTTCGAGGTGTCATTCTCGT 3618

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Qy 3619 GGTTCATCGCTTGGAGCAGCATCGCCCTGGCTGAGGAGCCAGTGGCGACAGCTCGCC 3678

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Qy 3679 CAGGAACAACGCTCTGAAATACCTGGGATTAATTTTCACTGGTGTCTTTTACCTTTGAGAT 3738

Db 3298 CCGAAACCAATATTTCTGGGATTAATTTTCACTGGTGTCTTTTACCTTTGAGAT 3357

Qy 3739 GGTGATAAAGATGATCGACTTTGGGAGCTGCTGCTTCACTGGGAGCTTATTTCCGGGACTT 3798

Db 3358 TCTACTCAAGATGACAGTGTGTTGGGGCTTCTTGCACCGAGGCTTCTTTTTCGCGGTAGCTG 3417

Qy 3799 GTGGAAATTTCTGGACTTTCAATTTGGTGTGCTGAGTGGCGCTTGTGCTGCTTTCTTCGAG 3858

Db 3418 GTTCAATCTGTTGGATCTCTTGTGGTGTGCTGCTGCTCATCTCTTCTCGGATCCACTC 3477

Qy 3859 CTTCTGTGGGAGGATCCAAAGGGGAAGACATCAATACCATCAAGTCTCTGAGAGTCTCTTCG 3918

Db 3478 C-----AGTGCCATCTCAGTTGTGAAGATTCTCGGAGTCTCTCCG 3516

Qy 3919 TGTCTTGGGGCCCTCAAGACCATCAAAAGGCTGCCCCAGCTCAAGGCTGTGTTGACTG 3978

Db 3517 AGTCTTGGGGCCCTCTCGAGCCATCAACAGAGCAAGGAGTCAAGCATGTGTTGCACTG 3576

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Db 3637 CATGTTGCGCTGCAATGTTGTTGAGTGTTCAGTGTTCAGGGGAAATTTTACAGTTTGCATGATGA 3696

Qy 4099 ATCCAGGAGCTGGAGGAGGAGTCTGAGGCTGAGTATTTGGATTTATGAGAAGGAGGAGT 4158

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Qy 4159 GGAA-----GCTCAGCCAGGAGTGGAAAGAAATAGACATTTTCACTACGACATGT 4209

Db 3757 GTACAGACCTTTGCTCGGAGCGGCTCTGGGTCAACAGTGAATTTTAACTTTGACAACGT 3816

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Qy 4270 GAAACACTCGTGGATGCCACCTATGAGGAGGAGGTCCAAAGCCCTGGGTACCGCATGGA 4329

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Qy 4450 CTTGGAGAGAGAGAGAGGCTTGCATTTGCTGCGCATCAGGCCCAAAACCTTGCACAG 4509

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Qy 4510 GTACATGCCCAAAACCGCGCAGTGTGTTCAGTATAAGACGTGAGACATTTGTGTCTTCCCC 4569

Db 4117 ATACATCCCTTGAAGTCTCA-----TCAGTACCGGCTGTGGGCCACTGTGAATCTGC 4170

Qy 4570 GCCCTTTGAATACTTTCATCATGCGCCATGATAGCCCTCAACACTGTGTGTGTGATGATGA 4629

Db 4171 TGCCTTTGAGTACTCATGTTTCTGCTCATCTCTGCTCAACAGGCTGGCCCTGAGCATGCA 4230

Qy 4630 GTTCTATGATGACACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4689

Db 4231 GCACATGAACAGACGTCT 4290

Qy 4690 ATCCATGTTCTCCATGGAATGCGTGTGGAAGATCATCGCCTTTGGGGTGTGTAATCTTT 4749

Db 4291 TGGCCTCTTCAACATTTGAGATGTTGTTCTCAAAATCATCGCCTTTTAAACCCCAAGCATCTT 4350

